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(54) Title: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE
AND NUCLEIC ACID COMPOSITIONS

(57) Abstract: This invention uses our knowledge of the mechanisms by which antigen is recognized by T cells to identify and pre-
pare human immunodeficiency virus (HIV) epitopes, and to develop epitope-based vaccines directed towards HIV. More specifically,
this application communicates our discovery of pharmaceutical compositions and methods of use in the prevention and treatment of
HIV infection.

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**INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN
IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID
COMPOSITIONS**

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CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority to U.S. Application No. 09/412,863 filed October 5, 1999, which is herein incorporated by reference.

FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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I. BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

5 The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant
10 virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV
15 infection.

Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, Nature 321:239, 1989; Jamieson *et al.*, J. Virol. 61:3930, 1987; Yap *et al.*, Nature 273:238, 1978; Lukacher *et al.*, J. Exp. Med. 160:814,
20 1994; McMichael *et al.*, N. Engl. J. Med. 309:13, 1983; Sethi *et al.*, J. Gen. Virol. 64:443, 1983; Watari *et al.*, J. Exp. Med. 165:459, 1987; Yasukawa *et al.*, J. Immunol. 143:2051, 1989; Tigges *et al.*, J. Virol. 66:1622, 1993; Reddenhase *et al.*, J. Virol. 55:263, 1985; Quinnan *et al.*, N. Engl. J. Med. 307:6, 1982). HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens,
25 epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

30 While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, Nature 370:463, 1994; Walker *et al.*, Proc. Natl.

Acad. Sci. 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g., Tsubota et al., J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*,
5 *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g., Borrow et al., Nature Med.* 3:205-211, 1997; Price *et al., Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al., Nature Med.* 1:330-336, 1995;
10 and Haas *et al., J. Immunol.* 157:4212-4221, 1996)

Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus
15 replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al., New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g., Rosenberg et al., Science* 278:1447, 1997).

20 A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like other retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow *et al., Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g.,*
25 Lukashov *et al., AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of
30 sufficient breadth and vigor to prevent and/or clear HIV infection.

The epitope approach, as we have described, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine compositions. Such a composition may

simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of specific epitope pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

Upon development of appropriate technology, the use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The epitopes for inclusion in an epitope-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which thereby reduces the likelihood of escape mutants. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion

of epitopes from multiple antigens from the pathogen in a vaccine composition. In the case of HIV, epitopes derived from multiple strains may also be included. A "pathogen" may be an infectious agent or a tumor associated molecule.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA antigens do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of 500 nM or less for HLA class I molecules or an IC_{50} of 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response. Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analogued to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to HIV in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising an HIV epitope that has an amino acid sequence described in
5 Tables VII to Table XX which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the
10 invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution)
15 and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

20 III. BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Figure 1 provides a graph of total frequency of genotypes as a function of the number of PF candidate epitopes bound by HLA-A and B molecules, in an average population.

Figure 2: Figure 2 illustrates the position of peptide epitopes in an experimental
25 model minigene construct.

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to HIV by stimulating the
30 production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native HIV protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to HIV. The complete sequence of the HIV proteins to be analyzed can be obtained from Genbank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently

be discovered for heretofore unknown variants of HIV, as will be clear from the disclosure provided below.

The peptide epitopes of the invention have been identified in a number of ways, as will be discussed below. Also discussed in greater detail is that analog peptides have been derived and the binding activity for HLA molecules modulated by modifying specific amino acid residues to create peptide analogs exhibiting altered immunogenicity. Further, the present invention provides compositions and combinations of compositions that enable epitope-based vaccines that are capable of interacting with HLA molecules encoded by various genetic alleles to provide broader population coverage than prior vaccines.

IV.A. Definitions

The invention can be better understood with reference to the following definitions, which are listed alphabetically:

A "computer" or "computer system" generally includes: a processor; at least one information storage/retrieval apparatus such as, for example, a hard drive, a disk drive or a tape drive; at least one input apparatus such as, for example, a keyboard, a mouse, a touch screen, or a microphone; and display structure. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

A "construct" as used herein generally denotes a composition that does not occur in nature. A construct can be produced by synthetic technologies, *e.g.*, recombinant DNA preparation and expression or chemical synthetic techniques for nucleic or amino acids. A construct can also be produced by the addition or affiliation of one material with another such that the result is not found in nature in that form.

"Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein which comprises the epitope is used as an antigen.

A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (*see, e.g., Sercarz, et al., Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

It is to be appreciated that protein or peptide molecules that comprise an epitope of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, there is a limitation on the length of a peptide of the invention which is not otherwise a construct. An embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, *e.g.*, on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence (and is not otherwise a construct), the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment of (49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5) down to 5 amino acids.

Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence, if they are not otherwise a construct. For any peptide that has five contiguous residues or

less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a CTL epitope be less than 600 residues long in any increment down to eight amino acid residues.

- 5 "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY, 8TH Ed., Lange Publishing, Los Altos, CA (1994).*

10 An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

15 Throughout this disclosure, results are expressed in terms of "IC₅₀'s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e., limiting HLA proteins and labeled peptide concentrations*), these values approximate K_D values. Assays for determining binding are described in detail, *e.g., in PCT publications WO 94/20127 and WO 94/03205.* It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g., HLA preparation, etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

25 Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide.

30 Binding may also be determined using other assay systems including those using: live cells (*e.g., Ceppellini et al., Nature 339:392, 1989; Christnick et al., Nature 352:67, 1991; Busch et al., Int. Immunol. 2:443, 1990; Hill et al., J. Immunol. 147:189, 1991; del Guercio et al., J. Immunol. 154:685, 1995*), cell free systems using detergent lysates (*e.g.,*

Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer
5 *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} , or K_D value, of 50 nM or less; "intermediate affinity" is binding
10 with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

The terms "identical" or percent "identity," in the context of two or more peptide
15 sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an
20 allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic peptide is derived.

25 The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

30 "Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion, covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses.

In humans, the MHC complex is also known as the HLA complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York, 1993.

5 The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

10 A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

15 A "non-native" sequence or "construct" refers to a sequence that is not found in nature, *i.e.*, is "non-naturally occurring". Such sequences include, *e.g.*, peptides that are lipidated or otherwise modified, and polypeptidic compositions that contain epitopes that are not contiguous in a native protein sequence.

20 The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, 25 more usually between about 12 and 25, and often between about 15 and 20 residues.

 "Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition.

30 A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor

residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table 1. For example, analog peptides can be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

"Promiscuous recognition" is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at "secondary anchor positions." A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A "subdominant epitope" is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

"Synthetic peptide" refers to a peptide that is man-made using such methods as
5 chemical synthesis or recombinant DNA technology.

As used herein, a "vaccine" is a composition that contains one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more epitopes of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides
10 or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or
15 polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be admixed with, or linked to, HLA class II-binding peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

20 The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal
25 end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter
30 designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are shown below.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

5 The mechanism by which T cells recognize antigens has been delineated during
the past ten years. Based on our understanding of the immune system we have developed
efficacious peptide epitope vaccine compositions that can induce a therapeutic or
prophylactic immune response to HIV in a broad population. For an understanding of the
value and efficacy of the claimed compositions, a brief review of immunology-related
10 technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand
recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P.

- et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (*see also, e.g.*, Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : <http://134.2.96.221/scripts.hlaserver.dll/home.htm>; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).
- Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA antigen(s).

- The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to

select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

- 1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.,*
5 Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the
10 peptide become activated during this time and are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells.
- 2) Immunization of HLA transgenic mice (*see, e.g.,* Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's
15 adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.
- 3) Demonstration of recall T cell responses from immune individuals who have effectively been vaccinated, recovered from infection, and/or from chronically infected patients (*see, e.g.,* Rehermann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997);
20 In applying this strategy, recall responses are detected by culturing PBL from subjects that have been naturally exposed to the antigen, for instance through infection, and thus have generated an immune response "naturally", or from patients who were vaccinated against the infection. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of
25 "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.
30

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

5 As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, 15 (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or 20 vaccines.

As disclosed herein, higher HLA binding affinity is correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a 25 response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides lead to more vigorous immunogenic 30 responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.,* 5 Sette, *et al.*, *J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute 10 hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the 15 shaping of T cell responses (*see, e.g.,* Schaeffer *et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.,* Southwood *et al. J. Immunology* 160:3363-3373, 1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to 20 define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was 25 associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC₅₀ of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

The binding affinity of peptides for HLA molecules can be determined as 30 described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues

required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.*, Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few

supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.*, Tables I-III), or if the presence of the motif corresponds to the ability to bind several
5 allele-specific HLA antigens, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with
10 the invention.

Examples of peptide epitopes bearing a respective supermotif or motif are included in Tables as designated in the description of each motif or supermotif below. The Tables include a binding affinity ratio listing for some of the peptide epitopes. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard
15 peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also
20 be used when performing binding studies.

To obtain the peptide epitope sequences listed in each Table, protein sequence data for all of the HIV-1 isolates present in the 1999 Los Alamos database (<http://hiv-web.lanl.gov>) were evaluated for the presence of the designated supermotif or motif. A listing of the strains is provided in Table XXVI. Nine HIV-1 structural and regulatory
25 proteins, gag, pol, env, nef, rev, tat, vif, vpr, and vpu, were included in the analysis. Peptide epitopes were additionally evaluated on the basis of their conservancy (*i.e.*, the amount of variance) among the available protein sequences for each HIV antigen. A criterion for conservancy used to generate the peptides set out in Tables VII-XX requires that the entire sequence of an HLA class I binding peptide be totally conserved in 15% of
30 the sequences available for a specific HIV antigen. Similarly, a criterion for conservancy requires that the entire 9-mer core region of an HLA class II binding peptide be totally conserved in 15% of the sequences available for a specific protein. The percent conservancy of the selected peptide epitopes is indicated on the Tables. The frequency, *i.e.* the number of sequences of the HIV protein antigen in which the totally conserved

peptide sequence was identified, is also shown. The "pos" (position) column in the Tables designates the amino acid position in the HIV protein that corresponds to the first amino acid residue of the epitope. The "number of amino acids" indicates the number of residues in the epitope sequence.

5

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

15

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope.

The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

20

25

Representative peptide epitopes that comprise the A1 supermotif are set forth in Table VII.

30

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and

cross-reactive binding among HLA-A2 and -A28 molecules have been described. (See, e.g., Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif, which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

10 The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific

15 HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A2 supermotif are set forth in Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

20

IV.D.3. HLA-A3 supermotif

The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see, e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA

25 molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

30

Representative peptide epitopes that comprise the A3 supermotif are set forth in Table IX.

IV.D.4. HLA-A24 supermotif

5 The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g., Sette and Sidney, Immunogenetics, in press, 1999*). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e., the A24*
10 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

15 Representative peptide epitopes that comprise the A24 supermotif are set forth in Table X.

IV.D.5. HLA-B7 supermotif

20 The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e., the HLA-B7 supertype*) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507,
25 B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g., Sidney, et al., J. Immunol. 154:247, 1995; Barber, et al., Curr. Biol. 5:179, 1995; Hill, et al., Nature 360:434, 1992; Rammensee, et al., Immunogenetics 41:178, 1995 for reviews of relevant data*). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in
30 Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth in Table XI.

IV.D.6. HLA-B27 supermotif

5 The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27
10 supermotif (*i.e.*, the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably
15 choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on Table XII.

IV.D.7. HLA-B44 supermotif

20 The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.*, the B44
25 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

30 IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in

press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table VI.

- 5 Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B58 supermotif are set forth on Table XIII.

10

IV.D.9. HLA-B62 supermotif

- The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

20

Representative peptide epitopes that comprise the B62 supermotif are set forth on Table XIV.

25

IV.D.10. HLA-A1 motif

- The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data).

30

Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif primary anchors.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g., Falk et al., Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g., Hunt et al., Science* 255:1261-1263, March 6, 1992; Parker *et al., J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kast et al., J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g., Del Guercio et al., J. Immunol.* 154:685-693, 1995; Ruppert *et al., Cell* 74:929-937, 1993; Sidney *et al., Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g., Ruppert et al., Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on Table VIII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (see, e.g., DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on Table XVI. Those peptide epitopes that also comprise the A3 supermotif are also listed in Table IX. The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or

secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (see, e.g., the review by Southwood *et al. J. Immunology* 160:3363-3373,1998).

Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA-DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Conserved 9-mer core regions (*i.e.*, sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis), comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue core, are set forth in Table XIXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in section "a" of the Table. Cross-reactive binding data for exemplary 15-residue supermotif-bearing peptides are shown in Table XIXb.

IV.D.16. HLA DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3A) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3B): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Conserved 9-mer core regions (*i.e.*, those sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) corresponding to a nine residue sequence comprising the DR3A submotif (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XXa. Table XXb shows binding data of exemplary DR3 submotif A-bearing peptides.

Conserved 9-mer core regions (*i.e.*, those that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) comprising the DR3B submotif and respective exemplary 15-mer peptides comprising the DR3 submotif-B epitope are set forth in Table XXc. Table XXd shows binding data of exemplary DR3 submotif B-bearing peptides.

Each of the HLA class I or class II peptide epitopes set out in the Tables herein are deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI lists the overall frequencies of the HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on the average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups. The incremental coverage obtained by the inclusion of A1-, A24-, and B44-supertypes to the A2, A3, and B7 coverage and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups..

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al.*, *Adv. Immunol.* 27:5159, 1979; Bennink, *et al.*, *J. Exp. Med.* 168:1935-1939, 1988; Rawle,

et al., *J. Immunol.* 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, *et al.*, *Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, *et al.*, *J. Immunol.* 131:1635, 1983); Rosenthal, *et al.*, *Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., *IMMUNOLOGY, THE SCIENCE OF SELF/NONSELF DISCRIMINATION*, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco, *et al.*, *Curr. Opin. Immunol.* 7:524-531, 1995). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC_{50} in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC_{50} of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette, *et al.*, *J. Immunol.*, 153:558-5592, 1994). In the cancer setting this phenomenon is probably due to elimination or functional inhibition of the CTL recognizing several of the highest binding peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic

response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare
5 analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide epitope-based vaccines and therapeutic agents.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of
10 peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.*, analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding
15 capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate
20 with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and
25 motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and
30 III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.*, Sidney, J. *et al.*, *Hu. Immunol.* 45:79, 1996). Thus, one

strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with
5 elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T
10 cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been either infected, or transfected with the appropriate genes, or, in the case of class II
15 epitopes only, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable
20 but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in,
25 *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of α -amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding
30 and crossbinding capability in certain instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999). Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide epitope, *i.e.* at either anchor or non-anchor positions.

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. For example, the target molecules considered herein include, without limitation, the gag, pol, env, nef, rev, tat, vif, vpr, and vpu proteins of HIV.

In cases where the sequence of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide, be conserved in a designated percentage, of the sequences evaluated for a specific protein antigen.

Because HIV rapidly mutates thereby resulting in the generation of virus strains that have divergent amino acid sequences, an alternative method of selecting epitopes for inclusion in a vaccine composition is employed herein. In order to target a broad population that may be infected with a number of different strains, it is preferable to include in vaccine compositions epitopes that are representative of HIV antigen sequences from different HIV strains. For example, by selecting 5 epitopes from the same region, each of which is 20% conserved among HIV strains, the combination of the epitopes achieves 100% coverage of that region. As appreciated by those in the art, lower or higher degrees of conservancy, such as the 15% conservancy used for identification of

the epitopes set out in Tables VII-XX, can be employed as appropriate for a given antigenic target.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (*see, e.g., Ruppert, J. et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al., J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (*see, e.g., Milik et al., Nature Biotechnology* 16:753, 1998; Altuvia *et al., Hum. Immunol.* 58:1, 1997; Altuvia *et al., J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al., Bioinformatics* 14:121-130, 1998; Parker *et al., J. Immunol.* 152:163, 1993; Meister *et al., Vaccine* 13:581, 1995; Hammer *et al., J. Exp. Med.* 180:2353, 1994; Sturniolo *et al., Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of

any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

5 In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

In accordance with the procedures described above, HIV peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules have been identified (Tables VII-XX).

IV.H. Preparation of Peptide Epitopes

20 Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

When possible, it may be desirable to optimize HLA class I binding peptide epitopes of the invention to a length of about 8 to about 13 amino acid residues, preferably 9 to 10. HLA class II binding peptide epitopes may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules.

In alternative embodiments, epitopes of the invention can be linked as a polyepitopic peptide, or as a minigene that encodes a polyepitopic peptide.

10 In another embodiment, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a nested or overlapping manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984*). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/super motifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can give rise to CTL populations capable of reacting with selected target cells associated with

a disease. Corresponding assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

Conventional assays utilized to detect T cell responses include proliferation
5 assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are
10 deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with
15 peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence
20 was derived.

More recently, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other relatively recent technical developments include staining
25 for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).

HTL activation may also be assessed using such techniques known to those in the
30 art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice

with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. Mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

Exemplary immunogenic peptide epitopes are set out in Table XXIII.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

HLA class I and class II binding peptides as described herein are used, in one embodiment of the invention, as reagents to evaluate an immune response. The immune response to be evaluated may be induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that may be used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (*see, e.g.*, Ogg *et al.*, *Science* 279:2103-2106, 1998; and Altman *et al.*, *Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells.

A tetramer reagent using a peptide of the invention can typically be generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the

tetramer can be used to stain antigen-specific cells. The cells may then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes.

Peptides of the invention are also used as reagents to evaluate immune recall responses. (see, *e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, patient PBMC samples from individuals infected with HIV may be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

The peptides are also used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed using, for example, either of the methods described above. The patient is HLA typed, and peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of HIV epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention are also used to make antibodies, using techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose HIV infection. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

IV.K. Vaccine Compositions

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more peptides as described herein are further embodiments of the invention. Once appropriately immunogenic epitopes have been defined, they can be sorted and delivered by various means, herein referred to as "vaccine" compositions. Such vaccine compositions can include, for example, lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, *e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, *e.g.*,

Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Faló, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the

immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors
5 useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Furthermore, vaccines in accordance with the invention encompass compositions
10 of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that
15 react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid,
20 polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials
25 well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS).

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other
30 suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An
5 alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PanDR molecule, *e.g.*, PADRE™ (Epimmune, San Diego, CA; described, *e.g.*, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine
10 compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*.

15 Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat chronic infections, or tumors in
20 patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate
25 immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

30 The vaccine compositions of the invention can also be used in combination with other treatments used for HIV infection, including use in combination with therapy regimens including protease inhibitors and other immune adjuvants such as IL-2.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polypeptidic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. Exemplary epitopes that may be utilized in a vaccine to treat or prevent HIV infection are set out in Tables XXXVII and XXXVIII. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition can be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen (*see e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450).

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise both HLA class I and HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence

in order to insure that it does not have pathological or other deleterious biological properties.

- 6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest.
- 5 This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the
- 10 immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may
- 15 lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

- 7.) In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire
- 20 sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

IV.K.1. Minigene Vaccines

- 25 A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention
- 30 uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822,

1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998.

For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE™ universal helper T cell (HTL)

5 epitope, and an endoplasmic reticulum-translocating signal sequence was engineered.

The immunogenicity of a multi-epitopic minigene can be tested in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested.

Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA

10 plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene)

for expression in human cells, the amino acid sequences of the epitopes may be reverse

15 translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that

when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in

20 the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In

addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the

25 scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides

that encode the plus and minus strands of the minigene. Overlapping oligonucleotides

(30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides

30 can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are

preferably included in the vector to ensure expression in the target cells. Several vector

elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune

response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, e.g., as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytotoxicity, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of

HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ⁵¹Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention, or analogs thereof, which have immunostimulatory activity may be modified to provide desired attributes, such as improved serum half life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction with CTL epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer.

When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic
5 peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of amino
10 acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 51484), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 51485), and *Streptococcus* 18kD protein at positions 116 (GAVDSILGGVATYGAA; SEQ ID NO: 51486). Other
15 examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are
20 designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type.
25 An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other
30 molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

III.K.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P₃CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P₃CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

CTL and/or HTL peptides can also be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C1-C20) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.K.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or
5 isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on
10 their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more HIV antigens of interest. Optionally, a helper T cell (HTL) peptide such as a PADRE family molecule, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention, preferably comprising
15 epitopes from multiple HIV antigens, is used to treat HIV infection.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are useful for administration to mammals, particularly
20 humans, to treat and/or prevent HIV infection. Vaccine compositions containing the peptides of the invention are administered to a patient infected with HIV or to an individual susceptible to, or otherwise at risk for, HIV infection to elicit an immune response against HIV antigens and thus enhance the patient's own immune response capabilities.

As discussed herein, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The peptides (or DNA encoding them) can be administered individually or as fusions of one or more peptide sequences. The manner in which the peptide is contacted with the CTL or HTL is
25 not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more
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peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

When the peptide is contacted *in vitro*, the vaccinating agent can comprise a population of cells, *e.g.*, peptide-pulsed dendritic cells, or HIV-specific CTLs, which have
5 been induced by pulsing antigen-presenting cells *in vitro* with the peptide or by transfecting antigen-presenting cells with a minigene of the invention. Such a cell population is subsequently administered to a patient in a therapeutically effective dose.

In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL
10 response to the virus antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the
15 judgment of the prescribing physician.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human
20 typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's
25 blood.

Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

For pharmaceutical compositions, the immunogenic peptides of the invention, or
30 DNA encoding them, are generally administered to an individual already infected with HIV. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. HIV-infected patients can be treated with the immunogenic peptides separately or in conjunction with other treatments as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of HIV infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or HIV antigen-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in some patients, a vaccine comprising HIV-specific CTL may be more efficacious in killing HIV-infected cells than alternative embodiments.

The peptide or other compositions used for the treatment or prophylaxis of HIV infection can be used, *e.g.*, in persons who have not manifested symptoms of disease but who act as a disease vector. In this context, it is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. Boosting doses may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

The peptides and compositions of the present invention may be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

Administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides

5 compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The

10 resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium

15 acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes,

20 viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see*,

25 *e.g.*, Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition.

30 Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic

compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

10

Summary

Epitopes in accordance with the present invention were successfully used to induce an immune response. Immune responses with these epitopes have been induced by administering the epitopes in various forms. The epitopes have been administered as peptides, as nucleic acids, and as viral vectors comprising nucleic acids that encode the epitope(s) of the invention. Upon administration of peptide-based epitope forms, immune responses have been induced by direct loading of an epitope onto an empty HLA molecule that is expressed on a cell, and via internalization of the epitope and processing via the HLA class I pathway; in either event, the HLA molecule expressing the epitope was then able to interact with and induce a CTL response. Peptides can be delivered directly or using such agents as liposomes. They can additionally be delivered using ballistic delivery, in which the peptides are typically in a crystalline form. When DNA is used to induce an immune response, it is administered either as naked DNA, generally in a dose range of approximately 1-5mg, or via the ballistic "gene gun" delivery, typically in a dose range of approximately 10-100 µg. The DNA can be delivered in a variety of conformations, *e.g.*, linear, circular *etc.* Various viral vectors have also successfully been used that comprise nucleic acids which encode epitopes in accordance with the invention.

Accordingly compositions in accordance with the invention exist in several forms. Embodiments of each of these composition forms in accordance with the invention have been successfully used to induce an immune response.

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One composition in accordance with the invention comprises a plurality of peptides. This plurality or cocktail of peptides is generally admixed with one or more pharmaceutically acceptable excipients. The peptide cocktail can comprise multiple

copies of the same peptide or can comprise a mixture of peptides. The peptides can be analogs of naturally occurring epitopes. The peptides can comprise artificial amino acids and/or chemical modifications such as addition of a surface active molecule, *e.g.*, lipidation; acetylation, glycosylation, biotinylation, phosphorylation etc. The peptides can be CTL or HTL epitopes. In a preferred embodiment the peptide cocktail comprises a plurality of different CTL epitopes and at least one HTL epitope. The HTL epitope can be naturally or non-naturally (*e.g.*, PADRE®, Epimmune Inc., San Diego, CA). The number of distinct epitopes in an embodiment of the invention is generally a whole unit integer from one through one hundred fifty (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150).

An additional embodiment of a composition in accordance with the invention comprises a polypeptide multi-epitope construct, *i.e.*, a polyepitopic peptide. Polyepitopic peptides in accordance with the invention are prepared by use of technologies well-known in the art. By use of these known technologies, epitopes in accordance with the invention are connected one to another. The polyepitopic peptides can be linear or non-linear, *e.g.*, multivalent. These polyepitopic constructs can comprise artificial amino acids, spacing or spacer amino acids, flanking amino acids, or chemical modifications between adjacent epitope units. The polyepitopic construct can be a heteropolymer or a homopolymer. The polyepitopic constructs generally comprise epitopes in a quantity of any whole unit integer between 2-150 (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, or 150). The polyepitopic construct can comprise CTL and/or HTL epitopes. One or more of the epitopes in the construct can be modified, *e.g.*, by addition of a surface active material, *e.g.* a lipid, or chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the multiepitopic construct can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds *etc.*

Alternatively, a composition in accordance with the invention comprises construct which comprises a series, sequence, stretch, *etc.*, of amino acids that have homology to (

i.e., corresponds to or is contiguous with) to a native sequence. This stretch of amino acids comprises at least one subsequence of amino acids that, if cleaved or isolated from the longer series of amino acids, functions as an HLA class I or HLA class II epitope in accordance with the invention. In this embodiment, the peptide sequence is modified, so as to become a construct as defined herein, by use of any number of techniques known or to be provided in the art. The polyepitopic constructs can contain homology to a native sequence in any whole unit integer increment from 70-100%, e.g., 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100 percent.

10 A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more epitopes in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the epitope of the invention by any means known or to be determined in the art. Such means include
15 pulsing of dendritic cells with one or more individual epitopes or with one or more peptides that comprise multiple epitopes, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

Further embodiments of compositions in accordance with the invention comprise
20 nucleic acids that encode one or more peptides of the invention, or nucleic acids which encode a polyepitopic peptide in accordance with the invention. As appreciated by one of ordinary skill in the art, various nucleic acids compositions will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acid compositions falls within the scope of the present invention. This embodiment of the invention comprises
25 DNA or RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any composition comprising nucleic acids that will encode a peptide in accordance with the invention or any other peptide based composition in accordance with the invention, falls within the scope of this invention.

It is to be appreciated that peptide-based forms of the invention (as well as the
30 nucleic acids that encode them) can comprise analogs of epitopes of the invention generated using principles already known, or to be known, in the art. Principles related to analoging are now known in the art, and are disclosed herein; moreover, analoging principles (heteroclitic analoging) are disclosed in co-pending application serial number

U.S.S.N. 09/226,775 filed 6 January 1999. Generally the compositions of the invention are isolated or purified.

The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

10 The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

15 The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)).

20 The cell lines used as sources of HLA molecules (Table XXIV) and the antibodies used for the extraction of the HLA molecules from the cell lysates (Table XXV) are also described in these publications.

Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were 25 cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50µM 2-ME, 100µg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).

Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka 30 Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein

- A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC
- 5 molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.
- 10 A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ¹²⁵I-radiolabeled
- 15 probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl
- 20 ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β₁) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).
- 25 Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β₁) assay makes separation of bound from unbound peaks more difficult under
- 30 these conditions, all DRB1*1501 (DR2w2β₁) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and

integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

Radiolabeled peptides were iodinated using the chloramine-T method.

Representative radiolabeled probe peptides utilized in each assay, and its assay specific
5 IC₅₀ nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

10 Since under these conditions [label]<[HLA] and IC₅₀≥[HLA], the measured IC₅₀ values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 µg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide
15 by dividing the IC₅₀ of a positive control for inhibition by the IC₅₀ for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC₅₀ nM values by dividing the IC₅₀ nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data
20 compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α-chain specific, β₁ molecules are not separated from β₃ (and/or β₄ and β₅) molecules. The β₁ specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2),
25 and DRB1*0803 (DR8w3), where no β₃ is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2β₁), DRB5*0101 (DR2w2β₂), DRB1*1601 (DR2w21β₁),
30 DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DRβ molecule specificity have been described previously (see, e.g., Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate

5 Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage was
10 performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in
15 Examples 2 and 5 employed the protein sequence data from HIV-1 clade B virus strains that were available in the 1994 Los Alamos database.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated HIV protein sequences were analyzed using a text string search software program, e.g., MotifSearch 1.4 (D. Brown, San Diego)
20 to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally. Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II
25 molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\text{"}\Delta G\text{"} = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

30 where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs

at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Complete protein sequences from nine HIV structural and regulatory proteins were aligned, then scanned, utilizing motif identification software, to identify conserved 9- and 10-mer sequences containing the HLA-A2-supermotif main anchor specificity. The analysis included all isolates in the 1994 Los Alamos database. The conservation criteria varied according to antigen: greater than 80% of clade B isolates for gag, pol, env; greater than 70% for nef, rev, tat, vif, vpr; great than 60% for vpu.)

A total of 233 conserved, HLA-A2 supermotif-positive sequences were identified. The peptides corresponding to the sequences were then synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule). Thirty peptides bound A*0201 with IC_{50} values ≤ 500 nM; of these 30, 5 bound with high binding affinities (IC_{50} values ≤ 50 nM) and 25 bound with intermediate binding affinities, in the 50-500 nM range (Table XXVII).

The thirty A*0201-binding peptides were subsequently tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). As

shown in Table XXVII, 20 of the 30 peptides were found to be A2-supertype cross-reactive binders, binding at least 3 of the 5 A2-supertype alleles tested.

Selection of HLA-A3 supermotif-bearing epitopes

5 The HIV protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. A total of 353 conserved 9- or 10-mer motif-containing sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. Sixty-six of the peptides were found to bind one of
10 the two alleles with binding affinities of ≤ 500 nM (Table XXVIII). These peptides were then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801). Twenty one of the peptides bound at least three of the five HLA-A3-supertype molecules tested (Table XXVIII). Table XXVIII also includes two 11-mer peptides that were not selected using the search criteria outlined above, but
15 have been shown to be A3-supertype cross-reactive binders.

Selection of HLA-B7 supermotif bearing epitopes

When the same HIV target antigen protein sequences were also analyzed for the presence of conserved 9- or 10-mer peptides with the HLA-B7-supermotif, 54 sequences
20 were identified. The corresponding peptides were synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Sixteen peptides bound B*0702 with IC_{50} of ≤ 500 nM (Table XXIX). These peptides were then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401). As shown in Table XXIX, eight of the sixteen peptides
25 were capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine constructs. An analysis of the protein sequence data from the
30 HIV target antigens utilized above is also performed to identify HLA-A1- and A24-motif-containing conserved sequences.

Five conserved HIV-derived peptides that bind to A*0101 with an IC_{50} of 500 nM or less (Table XXX) have been identified. Eleven conserved HLA-A*2402-binding HIV-

derived peptides have also been identified, five of which bind with an IC₅₀ of 100 nM or less (Table XXXI).

Example 3. Confirmation of Immunogenicity

5 *Evaluation of A*0201 immunogenicity*

It has been shown that CTL induced in A*0201/K^b transgenic mice exhibit specificity similar to CTL induced in the human system (*see, e.g., Vitiello et al., J. Exp. Med.* 173:1007-1015, 1991; *Wentworth et al., Eur. J. Immunol.* 26:97-101, 1996). Accordingly, these mice were used to evaluate the immunogenicity of 19 of the 20 A2-
10 supertype cross-reactive peptides identified in Example 2 above.

CTL induction in transgenic mice following peptide immunization has been described (*Vitiello et al., J. Exp. Med.* 173:1007-1015, 1991; *Alexander et al., J. Immunol.* 159:4753-4761, 1997). In these studies, mice were injected subcutaneously at the base of the tail with each peptide (50 µg/mouse) emulsified in IFA in the presence of
15 an excess of an IA^b-restricted helper peptide (140 µg/mouse) (HBV core 128-140, *Sette et al., J. Immunol.* 153:5586-5592, 1994). Eleven days after injection, splenocytes were incubated in the presence of peptide-loaded syngenic LPS blasts. After six days, cultures were assayed for cytotoxic activity using peptide-pulsed targets. The data, summarized in Table XXXII, indicate that eight peptides were capable of inducing primary CTL
20 responses in A*0201/K^b transgenic mice. (For these studies, a peptide was considered positive if it induced CTL (L.U. 30/10⁶ cells ≥2 in at least two transgenic animals (*Wentworth et al., Eur. J. Immunol.* 26:97-101, 1996).

The cross-reactive candidate CTL epitopes were also tested for the ability to stimulate recall CTL responses HIV-infected patients. Briefly, PBMC from patients
25 infected with HIV were cultured in the presence of 10 µg/ml of synthetic peptide. After 7 and 14 days, the cultures were restimulated with peptide. The cultures were assayed for cytolytic activity on day 21 using target cells pulsed with the specific peptide in a ⁵¹Cr release assay. These data are also summarized in Table XXXII. As shown, 15 of the 19 peptides analyzed were recognized in recall CTL responses using PBMC from HIV-
30 infected patients.

The set of peptides screened for immunogenicity contained two redundant peptides, 1261.14 and 1261.04, which differ in length by a single amino acid. While both peptides exhibit supertype degenerate binding, only the short of the two peptides

exhibited immunogenicity. One supertype peptide not tested, 1211.09, has been reported to be recognized by CTL lines isolated from HIV-infected patients.

In summary, 16 A2-supertype cross-reactive peptides have been identified that are immunogenic in humans; 53% of these peptides are also recognized in HLA-A2 transgenic mice. The sixteen peptides represent epitopes from five HIV antigens: env, gag, pol, vpr, and nef.

*Evaluation of A*03/A11 immunogenicity*

Twenty one of the A3-supertype cross-reactive peptides identified in Example 2 above were evaluated for immunogenicity (Table XXXIII). Peptides were screened using HLA-A11/K^b transgenic mice, using the protocol described above for HLA-A2 transgenic mice (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997) and using PBMC obtained from HIV-infected patients to test for the ability to stimulate CTL recall responses. Ten peptides that were capable of inducing CTL in HLA-A11 transgenic mice were identified.

Three peptides, 966.01, 940.03, and 1069.47, have been shown by collaborators to be immunogenic in HIV-infected patients. Peptides 966.01 and 1069.47 also induced CTL responses in transgenic mice, peptide 940.03 exhibited immunogenicity in patients only.

In summary, 11 of 23 A3-supertype cross-reactive binding peptides were found to be immunogenic in either HLA-A11 transgenic mice or HIV-infected patients. These peptides represent epitopes from three HIV antigens: pol, env, and nef.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 is used to evaluate immunogenicity using HLA-B7 transgenic mice and PBMC from HIV-infected patients in a manner analogous to the evaluation of A2-and A3-supermotif-bearing peptides. Three of these peptides have been reported as being immunogenic in HIV-infected patients.

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also

allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged, or "fixed" to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

As shown in Example 2, twenty HIV-derived, A2-supertype-restricted epitopes were identified. Peptide engineering strategies are implemented to further increase the cross-reactivity of the candidate epitopes identified above which bind 3/5 of the A2 supertype alleles tested. On the basis of the data disclosed, *e.g.*, in related and co-pending U.S.S.N 09/226,775; the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide can be tested for binding to one or all supertype members and then analogued to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

Similarly, analogs of HLA-A3 supermotif-bearing epitopes are also generated. For example, peptides binding to 3/5 of the A3-supertype molecules can be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Typically, those peptides that demonstrate ≤ 500 nM binding capacity are then tested for A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, B7 supermotif-bearing peptide are also analoged. For example, peptides binding 3 or more B7-supertype alleles are modulated to achieve increased cross-reactive binding. B7 supermotif-bearing peptides can, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at Secondary Anchor Residues

Secondary anchor residues defined for HLA motifs and/or supermotifs are also used to engineer peptide with modified binding activity, typically increased cross-reactive binding and/or increased affinity. For example, the binding capacity of a B7 supermotif-bearing peptide representing a discreet single amino acid substitution at position 1 is analyzed. A peptide such as Peptide 1261.01 (Table XXIX), can, for example, be analogued to substitute L for F at position 1 and subsequently be evaluated for modulated binding activity, *e.g.*, increased binding affinity/ and or increased cross-reactivity. This procedure identifies analoged peptides with modified binding properties.

Engineered analogs with improved binding capacity or cross-reactivity are tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. The analoged peptides are typically additionally tested for the ability to stimulate a recall response using PBMC from HIV-infected patients.

Thus, by the use of even single amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of HIV-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif are identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify HIV-derived, HLA class II HTL epitopes, the protein sequences from the same HIV antigens used for the identification of HLA Class I supermotif/motif sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences were selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (*i.e.*, at position 1 and position 6) within a 9-mer core, but additionally evaluates

sequences for the presence of secondary anchors. Using allele specific selection tables (see, e.g., Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule.

Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The HIV-derived peptides identified above were tested for their binding capacity for various common HLA-DR molecules. All peptides were initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules were then tested for binding to DR2w2 β 1, DR2w2 β 2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least 2 of the 4 secondary panel DR molecules, and thus cumulatively at least 4 of 7 different DR molecules, were screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least 7 of the 10 DR molecules comprising the primary, secondary, and tertiary screening assays were considered cross-reactive DR binders. The composition of these screening panels, and the phenotypic frequency of associated antigens, are shown in Table XXXIV.

Thirteen HIV-derived peptides were found to bind at least 7 of 10 common HLA-DR alleles. The sequence of these 13 peptides, and their binding capacity for each assay in the primary through tertiary panels, are shown in Table XXXV. This set of peptide epitopes is predominantly derived from pol, but also includes epitopes from gag and env.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is an important criterion in the selection of HTL epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al.*, *J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct from the specificity of most other DR alleles. For maximum efficiency in developing vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specificity of the

DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the nine target HIV antigens were analyzed for conserved sequences carrying one of the two DR3 specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides were then synthesized and tested for the ability to bind DR3 with an affinity of $1\mu\text{M}$ or better, *i.e.*, less than $1\mu\text{M}$. Five peptides were found that met this binding criterion (Table XXXVI), and thereby qualify as HLA class II high affinity binders. Of these five, four represent epitopes from pol, and one is from vpu.

DR3 binding epitopes can also be included in vaccine compositions.

Example 6. Immunogenicity of HIV-derived HTL epitopes

Immunogenicity of HTL epitopes is typically evaluated in a manner analogous to the determination of immunogenicity of CTL epitopes using appropriate transgenic mice models and/or assessing the ability to stimulate recall responses using PBMC isolated from HIV-infected individuals.

The immunogenicity of 11 of the 13 HLA class II DR-supermotif binding epitopes identified in Example 5 was evaluated in a study testing PBMC isolated from HIV-infected individuals for recall proliferative responses. All eleven of these peptides were found to stimulate DR-restricted proliferative responses (Table XXXVII).

DR3-motif bearing peptides are typically evaluated in a similar manner. Such studies demonstrate the immunogenicity of class II epitopes derived from HIV proteins.

Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae $gf=1-(\text{SQRT}(1-af))$ (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies were calculated, and the cumulative antigen frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the superotypes were included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., $\text{total} = A + B \cdot (1 - A)$). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-superotypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analagous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Summary of preferred HLA class I epitopes

In summary, on the basis of the data presented in the above examples, 47 immunogenic and/or cross-reactive binding preferred CTL peptide epitopes derived from HIV were identified (see, Table XXXVIII). Of these 47 eptiopes, 6 are derived from gag, 22 from pol, 10 from env, 3 from nef, and one epitope each from rev, vif, and vpr. This set of epitopes includes 16 HLA-A2 supermotif-bearing epitopes (two from gag, eight from pol, three from env, two from vpr, and one from nef), all of which are recognized in HIV-infected patients. The 10 HLA-A3 supermotif-bearing candidate epitopes include 6 pol-derived epitopes, two env-derived epitopes and one eptiope each from gag, vif, and

nef. With the exception of peptides 1273.08 and 1273.03, all of the epitopes are immunogenic in HLA transgenic mice. The two additional peptides are included to enhance antigen diversity.

The CTL epitope set also includes 8 B7-restricted peptides. Of these eight, 3
5 epitopes have been reported as immunogenic in patients. Five B7-supermotif-bearing peptides were included as candidates based on supertype binding. Immunogenicity studies in humans (*e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. Given
10 these results, and in view of the limited immunogenicity data available for B7 supermotif-bearing peptides, the use of B7-supertype binding affinity is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

Similarly, A1- and A24-restricted peptides were included on the basis of both
15 demonstrated immunogenicity of the candidate epitopes and on the basis of binding affinity. Five of the preferred epitopes have been reported to be recognized in recall CTL responses from HIV-infected patients. Because a high percentage of the peptides with binding affinities ≤ 100 nM are found to be immunogenic, four A24-restricted peptides were included as vaccine candidates. An additional five A24-restricted epitopes and four
20 A1-restricted epitopes that bound their respective alleles with an IC_{50} of ≤ 500 nM were also included to provide a greater degree of population coverage.

With these 47 CTL epitopes, an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. Using the game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and
25 Rubinstein, A. "A course in game theory" MIT Press, 1994), it is estimated that 90% of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize 7 or more of the vaccine epitopes described herein (Figure 1)

30 *Summary of preferred HLA class II epitopes*

A list of preferred HIV-derived HTL epitopes for vaccine compositions is summarized in Table XXXIX. The set of HTL epitopes includes 13 DR supermotif-bearing peptides and 5 DR3 motif-bearing peptides. The majority of the epitopes are

derived from pol, 3 are from gag, 2 are from env and one is derived from vpu. The total estimated population coverage represented by this panel of HTL epitopes is estimated to be greater than 91% in each of five major ethnic groups (Table XL).

5 Example 8. CTL Recognition Of Endogenous Processed Antigens After Priming

This example determines that CTL induced by native or analoged peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide
10 epitopes as in Example 3, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ⁵¹Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of
15 peptide, and also tested on ⁵¹Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that
20 is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

25

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The
30 peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXVI-XXIX, or an analog of that epitope. The HTL

epitope is, for example, selected from Table XXXII. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).

In vitro CTL activation: One week after priming, spleen cells (30×10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10×10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of 200 μ l of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 $\mu\text{g/ml}$. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of 200 μ l) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$.

To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio

of 50:1 (i.e., 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000) - (1/500,000)] \times 10^6 = 18 \text{ LU}$.

The results are analyzed to assess the magnitude of the CTL responses of animals
5 injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in Example 3. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is
10 induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 10. Selection of CTL and HTL epitopes for inclusion in an HIV-specific vaccine.

15 This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (i.e., minigene) that encodes peptide(s), or can be single and/or polyepitopic peptides.

The following principles are utilized when selecting an array of epitopes for
20 inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen,
25 then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection.
30 Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less.

Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating a polyepitopic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.

In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables XXVI-XXIX and Table XXXII. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables XXVI-XXIX and XXXII. HLA class I supermotif or

motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage.

Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and

- 5 HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

- Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more
- 10 HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

- This example illustrates the methods to be used for construction of a minigene-
- 15 bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

- The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also
- 20 include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

- Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as
- 25 appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C
- 30 for 1 min.

For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each

dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

10 The degree to which a plasmid construct, for example a plasmid constructed in accordance with Example 11, is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines “antigenicity” and allows the use of human APC. The assay determines the ability of the
15 epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.,* Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated
20 by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.,* Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

25 Alternatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.

30 For example, to assess the capacity of a DNA minigene construct (*e.g.*, a pMin minigene construct generated as described in U.S.S.N. 09/311,784) containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^3H -thymidine incorporation proliferation assay, (*see, e.g.,* Alexander et al. *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.,* Barnett *et al., Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.,* Hanke *et al., Vaccine* 16:439-445, 1998; Sedegah *et al., Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al., Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period

(ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

The use of prime boost protocols in humans is described in Example 20.

15 Example 13. Peptide Composition for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

5 Example 14. Polyepitopic Vaccine Compositions Derived from Native HIV Sequences

 A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify “relatively short” regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that
10 contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The “relatively short” peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in
15 length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic
20 purposes.

 The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the
25 epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

 The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune
30 response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need

to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Directed To Multiple Diseases

The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

Example 16. Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal

addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and
5 magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered
10 saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of
15 cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

20

Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected
25 with HIV, or who have been vaccinated with an HIV vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA
30 supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO

Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al.* *J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 µM, and labeled with 100 µCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 $\mu\text{g/ml}$ synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^3H -thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

5 The vaccine is found to be both safe and efficacious.

Example 19. Phase II Trials In Patients Infected With HIV

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to
10 determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:

15 The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

20 There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV
25 and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

30 Example 20. Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization is performed using an expression vector, such as that constructed in Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μ g) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

Example 21. Administration of Vaccine Compositions Using Dendritic Cells

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as ProgenipoietinTM (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although $2 \cdot 50 \times 10^6$

DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment
5 with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10} . Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoiectin™ mobilizes 2% DC in
10 the peripheral blood of a given patient, and that patient is to receive 5×10^6 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoiectin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

15 *Ex vivo activation of CTL/HTL responses*

Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days),
20 in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cells.

Example 22. Alternative Method of Identifying Motif-Bearing Peptides

25 Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic
30 acids that express the antigen of interest, *e.g.* HIV regulatory or structural proteins. Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

The peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, *e.g.*, by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	<i>TILVMS</i>		FWY
A2	<i>LIVMATQ</i>		<i>IVMATL</i>
A3	<i>VSMATLI</i>		RK
A24	<i>YFWIVLMT</i>		<i>FIYWLM</i>
B7	P		<i>VILFMWYA</i>
B27	RHK		<i>FYLWMIVA</i>
B44	ED		<i>FWYLIMVA</i>
B58	ATS		<i>FWYLIVMA</i>
B62	<i>QLIVMP</i>		<i>FWYMIVLA</i>
MOTIFS			
A1	TSM		Y
A1		DEAS	Y
A2.1	<i>LMVQIAT</i>		<i>VLIMAT</i>
A3	<i>LMVISATFCGD</i>		<i>KYRHFA</i>
A11	<i>VTMLISAGNCDF</i>		<i>KRYH</i>
A24	<i>YFWM</i>		<i>FLIW</i>
A*3101	<i>MVTALIS</i>		RK
A*3301	<i>MVALFIST</i>		RK
A*6801	<i>AVTMSLI</i>		RK
B*0702	P		<i>LMFWYAIIV</i>
B*3501	P		<i>LMFWYIVA</i>
B51	P		<i>LIVFWYAM</i>
B*5301	P		<i>IMFWYALV</i>
B*5401	P		<i>ATIVLMFWY</i>

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T <i>L</i> V <i>M</i> S		F <i>W</i> Y
A2	V <i>Q</i> A <i>T</i>		V <i>L</i> I <i>M</i> A <i>T</i>
A3	V <i>S</i> M <i>A</i> T <i>L</i> I		R K
A24	Y <i>F</i> W <i>I</i> V <i>L</i> M <i>T</i>		F <i>I</i> Y <i>W</i> L M
B7	P		V <i>IL<i>F</i>M<i>W</i>YA</i>
B27	R H K		F <i>Y</i> L <i>W</i> M <i>IVA</i>
B58	A T S		F <i>W</i> Y <i>L</i> I V M A
B62	Q <i>L</i> I V M P		F <i>W</i> Y <i>M</i> I V L A
MOTIFS			
A1	T S M		Y
A1		D E A S	Y
A2.1	V <i>Q</i> A <i>T</i> *		V <i>L</i> I <i>MA<i>T</i></i>
A3.2	L <i>M</i> V <i>S</i> A <i>T</i> F <i>CGD</i>		K <i>Y</i> R <i>H</i> F A
A11	V <i>T</i> M <i>L</i> I S <i>A</i> G N C D F		K <i>R</i> H Y
A24	Y F W		F L I W

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE II

	POSITION							
	1	2	3	4	5	6	7	8 C-terminus
<u>SUPERMOTIFS</u>								
A1		1° Anchor TLVMS						1° Anchor FWY
A2		1° Anchor LIVMATQ						1° Anchor LIVMAT
A3	preferred	1° Anchor VSMA7LI	YFW (4/5)		YFW (3/5)	YFW (4/5)	P (4/5)	1° Anchor RK
	deleterious	DE (3/5); P (5/5)	DE (4/5)					
A24		1° Anchor YFWIVLM T						1° Anchor FLYWLM
B7	preferred	FWY (5/5) LIVM (3/5)	1° Anchor P	FWY (4/5)			FWY (3/5)	1° Anchor VILFMWYA
	deleterious	DE (3/5); P (5/5); G (4/5); A (3/5); QN (3/5)			DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)
B27		1° Anchor RHK						1° Anchor FYLWMIVA
B44		1° Anchor ED						1° Anchor FWYLIMVA
B58		1° Anchor ATS						1° Anchor FWYLIYMA
B62		1° Anchor QLIVMP						1° Anchor FWYMIYLA

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
		1	2	3	4	5	6	7	8	C-terminus
MOTIFS										
A1 preferred 9-mer	GFYW	1°Anchor STM	DEA	YFW	P	DEQN	YFW	1°Anchor Y		
deleterious	DE		RHKLIVM P	A	G	A				
A1 preferred 9-mer	GRHK	ASTCLIV M	1°Anchor DEAS	GSTC	ASTC	LIVM	DE	1°Anchor Y		
deleterious	A	RHKDEPY FW	DE	PQN	RHK	PG	GP			

MOTIFS

A1 9-mer	preferred	GFYW
-------------	-----------	------

deleterious DE

Al preferred GRHK
9-mer

deleterious A

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
A1 preferred 10-mer	YFW	<u>1°Anchor</u> STM	DEAQN	A	YFWQN		PASTC	GDE	P <u>1°Anchor</u> Y
deleterious	GP		RHKGLIV M	DE	RHK	QNA	RHKYFW	RHK	A
A1 preferred 10-mer	YFW	STCLIVM	<u>1°Anchor</u> DEAS	A	YFW		PG	G	YFW <u>1°Anchor</u> Y
deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN
A2.1 preferred 9-mer	YFW	<u>1°Anchor</u> LMIVQAT	YFW	STC	YFW		A	P	<u>1°Anchor</u> VLIMAT
deleterious	DEP		DERKH			RKH	DERKH		
A2.1 preferred 10-mer	AYFW	<u>1°Anchor</u> LMIVQAT	LVIM	G		G		FYWL VIM	<u>1°Anchor</u> VLIMAT
deleterious	DEP		DE	RKHA	P		RKH	DERK H	RKH

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
A3 preferred	RHK	<u>1°Anchor</u> LMVISAT FCGD	YFW	PRHKYFW	A	YFW		P	<u>1°Anchor</u> KYRHF4
deleterious	DEP		DE						
A11 preferred	A	<u>1°Anchor</u> VTLMISA GNCDF	YFW	YFW	A	YFW	YFW	P	<u>1°Anchor</u> KRYH
deleterious	DEP						A	G	
A24 preferred 9-mer	YFWRHK	<u>1°Anchor</u> YFW/M		STC			YFW	YFW	<u>1°Anchor</u> FLIW
deleterious	DEG		DE	G	QNP	DERHK	G	AQN	
A24 preferred 10-mer		<u>1°Anchor</u> YFW/M		P	YFWP		P		<u>1°Anchor</u> FLIW
deleterious			GDE	QN	RHK	DE	A	QN	DEA

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
A3101 preferred	RHK	<u>1°Anchor</u> MVTALIS	YFW	P		YFW	YFW	AP	<u>1°Anchor</u> RK
deleterious	DEP		DE		ADE	DE	DE	DE	
A3301 preferred		<u>1°Anchor</u> MVALFIS T	YFW				AYFW		<u>1°Anchor</u> RK
deleterious	GP		DE						
A6801 preferred	YFWSTC	<u>1°Anchor</u> AVTMSLI			YFWLIV M		YFW	P	<u>1°Anchor</u> RK
deleterious	GP		DEG		RHK			A	
B0702 preferred	RHKFWY	<u>1°Anchor</u> P	RHK		RHK	RHK	RHK	PA	<u>1°Anchor</u> LMFWYIV
deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE	
B3501 preferred	FWYLIVM	<u>1°Anchor</u> P	FWY				FWY		<u>1°Anchor</u> LMFWYIV
deleterious	AGP				G	G			

POSITION									
	1	2	3	4	5	6	7	8	9 or C-terminus
B51	preferred	LIVMF ^{1°Anchor} WY	FWY	STC	FWY	FWY	G	FWY	^{1°Anchor} LIVFWYAM
	deleterious	AGPDERHKSTC			DE	G	DEQN	GDE	
B5301	preferred	LIVMF ^{1°Anchor} WY	FWY	STC	FWY		LIVMF ^{1°Anchor} WY	FWY	IMFWYALY
	deleterious	AGPQN				G	RHKQN	DE	
B5401	preferred	FWY	^{1°Anchor} P	FWYLIVM	LIVM	FWYAP	ALIVM	FWYAP	^{1°Anchor} ATIVLMFWY
	deleterious	GPQNDE		GDESTC	RHKDE	DE	QNDGE	DE	

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.

TABLE III

MOTIFS		POSITION								
		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred deleterious	FMYLIVW	M	T	W	I	VSTCPALIM	MH R	MH	MH WDE
DR1	preferred deleterious	MFLIVWY	C	CH	PAMQ FD	CWD	VMATSPLIC	M GDE	D	AVM
DR7	preferred deleterious	MFLIVWY	M C	W	A G		IVMSACTPL	M GRD	N	IV G
DR Supermotif		MFLIVWY					VMSTACPLI			
DR3 MOTIFS		1° anchor 1	2	3	1° anchor 4	5	1° anchor 6			
motif a preferred		LIVMFY			D					
motif b preferred		LIVMFAY			DNQUEST		KRH			

Italicized residues indicate less preferred or "tolerated" residues.

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1141.02	FTQAGYPAL	40
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVVR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTL VYLL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VI

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*8002, A*8901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6001	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7001	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3001, B*3901, B*3902, B*7201	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4001, B*4002, B*1510, B*1518, B*1503
B44	B*1001, B*1002, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B50	B*5701, B*5702, B*5001, B*5002, B*1516, B*1517	
D62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

a. Verified alleles includes alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO
ENV	KLWVTYY	44	8	11	17		1
ENV	NLWVTYY	44	8	35	56		2
ENV	DTEVINW	75	8	19	30		3
ENV	VTENFMW	102	8	34	53		4
ENV	RIGPGQIF	357	8	11	17		5
ENV	GIGPGQIF	360	8	01	33		6
ENV	SIGSGQAF	360	8	01	33		7
ENV	KLREIRQF	405	8	01	25		8
ENV	STNGTETF	537	8	01	17		9
ENV	AVGIGAVE	595	8	11	17		10
ENV	ILLKLTW	630	8	13	20		11
ENV	ILLQLTVW	630	8	34	53		12
ENV	IIMQLTVW	650	8	10	16		13
ENV	RVLAVERY	665	8	33	52		14
ENV	NVPWNSSW	693	8	13	20		15
ENV	EIWDNMW	716	8	21	33		16
ENV	DLALDKW	754	8	20	31		17
ENV	ELLELDKW	754	8	10	16		18
ENV	DIITNWLWY	769	8	50	78		19
ENV	WLWYKIF	773	8	16	25		20
ENV	LIGLRIF	787	8	29	45		21
ENV	SIRLVNGF	787	8	13	20		22
ENV	SIRLVSGF	842	8	13	20		23
ENV	DLRNLCLF	856	8	17	27		24
ENV	DLRSLCLF	856	8	38	59		25
ENV	RSLLCLFY	858	8	35	55		26
ENV	ELLGRRW	881	8	31	37		27
ENV	TVYYGVVW	48	9	55	86		28
ENV	NYTFNFMW	101	9	34	53		29
ENV	DSSNSTGN	218	9	01	20		30
ENV	ILKCNKKF	271	9	12	19		31
ENV	RIGPGQIF	357	9	11	17		32
ENV	GIGPGQIF	360	9	01	33		33
ENV	SIGSGQAF	360	9	01	33		34
ENV	DLETTISF	428	9	36	56		35
ENV	IISFNCGGF	434	9	16	25		36
ENV	IISFNCRGF	434	9	30	47		37
ENV	RIKQINMW	488	9	12	19		38
ENV	RIKQINMW	488	9	02	18		39
ENV	GSENGTET	538	9	11	18		40
ENV	GIGAVFLG	598	9	04	18		41
ENV	MLGAMFLG	599	9	03	36		42
ENV	TIGAMFLG	599	9	04	27		43
ENV	LICTTAVPW	688	9	19	30		44
ENV	LICTTNVPW	688	9	17	27		45
ENV	LICTTVPW	688	9	12	19		46
ENV	ALDKWASLW	757	9	13	33		47
ENV							48

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO
ENV	GLICLRIVF	786	9	29	45		51
ENV	IVNRVRQGY	799	9	38	59		52
ENV	RSIRLVNGF	841	9	12	19		53
ENV	RSIRLVSGF	841	9	13	20		54
ENV	VSGFLALAW	846	9	16	25		55
ENV	FSYIRLRDF	863	9	18	28		56
ENV	SLKGLRLGW	889	9	11	39		57
ENV	SLRGLQRGW	889	9	05	18		58
ENV	RLGWEGLY	894	9	09	29		59
ENV	VTVYGVVW	47	10	55	86		60
ENV	QMIHDIISLW	116	10	29	45		61
ENV	ITQACPVSF	245	10	29	45		62
ENV	VSEFPIHLY	253	10	28	44		63
ENV	PIIYCATAGF	260	10	27	42		64
ENV	PIIYCTPAGF	260	10	10	16		65
ENV	AILKCNDRKF	270	10	12	19		66
ENV	NTSPSRVAY	376	10	01	33		67
ENV	ISFNCGGFF	434	10	35	55		68
ENV	ISFNCRGFF	434	10	16	25		69
ENV	NTFNKTIEF	537	10	01	17		70
ENV	NTGNITIEF	537	10	01	17		71
ENV	KLICTTAVPW	687	10	19	30		72
ENV	KLICTTNVPW	687	10	17	27		73
ENV	KLICTTVPW	687	10	12	19		74
ENV	TTNVPWSS	691	10	11	17		75
ENV	SIVNRVRQGY	798	10	36	56		76
ENV	LVSGFLALAW	845	10	16	25		77
ENV	DLRNLCLFSY	856	10	16	25		78
ENV	DLRNLCLFSY	856	10	35	55		79
ENV	IVELLGIRGW	879	10	22	34		80
ENV	SSLKGLRLGW	886	10	10	16		81
ENV	WVTYVYGVVW	46	11	55	86		82
ENV	PWKKEATTL	54	11	22	34		83
ENV	TLFCASDAKA	64	11	40	63		84
ENV	VITQACPKVSF	244	11	14	22		85
ENV	KVSFPIHLY	252	11	28	44		86
ENV	GTAGNSSRAA	375	11	01	33		87
ENV	TTIISFNCGE	432	11	16	25		88
ENV	TTIISFNCGE	432	11	12	19		89
ENV	VMISFNCGGE	432	11	13	20		90
ENV	ISFNCGGFF	434	11	35	55		91
ENV	ISFNCRGFF	434	11	16	25		92
ENV	NMWQEVGKA	494	11	15	23		93
ENV	DMRDNIWRIEL	552	11	37	58		94
ENV	AVGIGAVFLGF	595	11	11	17		95
ENV	YLRDQQLGI	672	11	27	42		96
ENV	YLRDQQLGI	672	11	18	28		97
ENV	CTTNVPWSS	690	11	11	17		98
ENV	WMEWERIDN	723	11	10	16		99
ENV	LLALDKWASL	755	11	11	17		100

Table VII
HIV Δ01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO
ENV	LLELDKWASL	755	11	18	28		101
ENV	ALDKWASLW	757	11	16	16		102
ENV	ELDKWASLW	757	11	16	25		103
ENV	ISNWLWYIKIF	770	11	12	17		104
ENV	ITKWLWYIKIF	770	11	12	19		105
ENV	ITNWLWYIKIF	770	11	14	22		106
ENV	LSVNRVRQGY	797	11	34	53		107
ENV	KVRQGYSPLSF	802	11	47	73		108
ENV	RLVSGFLALA	844	11	16	25		109
ENV	CLFSYIURLRDF	861	11	18	28		110
ENV	RIVELGRRG	878	11	22	34		111
ENV	RLGLWEGGLK	892	11	09	29		112
ENV	RLGWEGGLKYL	894	11	07	23		113
GAG	ASRELERF	38	8	46	72		114
GAG	SSQVSONY	145	8	15	31		115
GAG	KVIEKAF	178	8	24	38		116
GAG	KVIEKAF	178	8	28	44		117
GAG	TLQEQIAW	263	8	12	19		118
GAG	TLQEQIGW	263	8	27	42		119
GAG	PIPVGDIY	279	8	11	17		120
GAG	PIPVGEIY	279	8	35	55		121
GAG	ASQEVKNW	333	8	11	17		122
GAG	ATQDVKNW	333	8	15	23		123
GAG	ATQEVKNW	333	8	18	28		124
GAG	IMMQRSNF	408	8	11	17		125
GAG	IMMQRCNF	408	8	27	42		126
GAG	CTERQANF	459	8	55	87		127
GAG	ETIDKDIY	537	8	01	25		128
GAG	LTSLKSLF	549	8	13	20		129
GAG	LTSLKSLF	549	8	12	19		130
GAG	LSGKLDIAW	8	9	16	25		131
GAG	GSEELRSY	73	9	12	19		132
GAG	NSSQVSONY	144	9	14	31		133
GAG	ISPTLNAY	168	9	36	56		134
GAG	LSPTLNAY	168	9	17	27		135
GAG	ESPEVPMF	185	9	54	84		136
GAG	TINEAAEW	225	9	53	83		137
GAG	STLQEQIAW	262	9	12	19		138
GAG	STLQEQIGW	262	9	27	42		139
GAG	PVGDIYKRW	281	9	40	63		140
GAG	PVGDIYKRW	281	9	60	94	0.0017	141
GAG	GLNKIVRMV	293	9	10	17		142
GAG	NIMMORCNF	407	9	13	22		143
GAG	TIMMORCNF	407	9	13	22		144
GAG	SSKGRICNF	476	9	20	31		145
GAG	PTAPPAESF	495	9	15	23		146
GAG	PTAPPAESF	495	9	02	67		147
GAG	PTAPPAESF	507	9	01	33		148
GAG	PTAPPAESF	507	9	01	33		149
GAG	PLASKSLF	548	9	15	23		150

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SiQ ID NO
GAG	PLTSLKSLF	548	9	12	19		151
GAG	PLTSLRSF	548	9	12	19		152
GAG	VLSGGKLDAA	7	10	15	23		153
GAG	RLRIGGKKY	20	10	34	53		154
GAG	SLFNTVATLY	79	10	15	23		155
GAG	SLYNTVATLY	79	10	22	34		156
GAG	ALSPRTLNAW	167	10	29	45		157
GAG	ALSPRTLNAW	167	10	10	16		158
GAG	WVKVIEKAF	176	10	24	38		159
GAG	WVKVVEKAF	176	10	28	44		160
GAG	DTINEEAAEW	224	10	31	48		161
GAG	ETINEEAAEW	224	10	22	34		162
GAG	TSTLQEQAW	261	10	12	19		163
GAG	TSTLQEQAW	261	10	27	42		164
GAG	DIRQGPKEF	308	10	19	30		165
GAG	DIRQGPKEF	308	10	41	64		166
GAG	ATIMMQIGNF	406	10	11	28		167
GAG	PSIKGRPGNF	475	10	23	36		168
GAG	PSNKGRPGNF	475	10	14	22		169
GAG	PSSKGRPGNF	475	10	11	17		170
GAG	SVLSGGKLDAA	6	11	15	23		171
GAG	IYWASRELER	35	11	19	30		172
GAG	LWVASRELER	35	11	25	39		173
GAG	RSLYNTVATL	78	11	15	24		174
GAG	TSTLQEQIA	260	11	11	17		175
GAG	TSTLQEQIG	260	11	34	43		176
GAG	PIPVGEIKRW	279	11	33	53		177
GAG	ILGLNKIVRMV	291	11	57	89		178
GAG	ASAOQDLKGG	392	11	01	50		179
GAG	ATAQDLKGG	392	11	01	50		180
GAG	PTATPAESFGF	495	11	10	16		181
GAG	PTATPAESFRF	495	11	14	22		182
GAG	PTATPAESFRF	507	11	02	67		183
GAG	PTATPAESFRF	507	11	01	33		184
NEF	ATNAIDCAW	71	8	12	22		185
NEF	PMYKCAF	105	8	12	19		186
NEF	DLDLWVY	185	8	20	31		187
NEF	EILDWVY	185	8	33	52		188
NEF	WVYHTQGF	191	8	13	20		189
NEF	WVYHTQGY	191	8	21	33		190
NEF	GIRYPLTF	213	8	13	20		191
NEF	GIRYPLTF	213	8	43	67		192
NEF	PLTFQWCF	219	8	20	31		193
NEF	WSKSSIVGW	5	9	10	16		194
NEF	QVPLRPMTF	100	9	46	72		195
NEF	QVPLRPMTY	100	9	13	20		196
NEF	WVYHTQGF	191	9	21	33		197
NEF	WVYHTQGYF	191	9	14	22		198
NEF	IITQGFPDW	194	9	25	39		199
NEF	IITQGYFPDW	194	9				200

0.0008

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
NEF	NTQGYFDW	194	9	12	19		201
NEF	YTPGCIKY	207	9	17	27		202
NEF	YTPGCIKE	207	9	13	20		203
NEF	DLWVYHTQGF	188	10	13	20		204
NEF	DLWVYHTQGY	188	10	21	33		205
NEF	GIRYPLTFGW	213	10	13	20		206
NEF	GTRFPLTFGW	213	10	12	19		207
NEF	IMARELIHPEY	320	10	10	16		208
NEF	IMARELIHPEY	68	11	12	19		209
NEF	NTAATNAUCA	102	11	12	19		210
NEF	PLRPMTYKGA	188	11	13	30		211
NEF	DLWVYHTQGF	188	11	21	33		212
NEF	DLWVYHTQGY	320	11	10	16		213
NEF	IMARELIHPEY	122	8	13	20		214
POL	DINLPCKW	122	8	12	19		215
POL	EINLPCKW	133	8	62	97		216
POL	MIGIGIGF	179	8	41	64		217
POL	QIGCTLNF	179	8	16	25		218
POL	QLGCTLNF	238	8	51	80		219
POL	KICPENPY	238	8	11	17		220
POL	RICPENPY	297	8	60	94		221
POL	VLDVGDAY	306	8	18	28		222
POL	SVPLDKDF	353	8	44	69		223
POL	MTKILEPF	434	8	13	20		224
POL	QLPEKDSW	434	8	13	20		225
POL	VLPKDSW	448	8	62	97		226
POL	KLYCKLNW	568	8	19	30		227
POL	ATESIVIV	591	8	10	16		228
POL	ETWWTIDYW	625	8	28	44		229
POL	IVGAEIFY	626	8	28	44		230
POL	IVGAEIFY	668	8	12	19		231
POL	KTELOAIY	686	8	62	97		232
POL	NIYTDQY	717	8	35	55		233
POL	LIKKEKYY	828	8	59	92		234
POL	AVIIVASGY	844	8	59	92		235
POL	ETQQTETAY	853	8	34	53		236
POL	ILKLAGRW	853	8	25	39		237
POL	LLKLAGRW	866	8	51	80		238
POL	ITDNGSNF	876	8	15	23		239
POL	TTVKAACW	877	8	32	50		240
POL	AVKAACW	877	8	24	38		241
POL	TVKAACW	968	8	12	19		242
POL	QITKIONF	968	8	35	55		243
POL	KIONFERVY	971	8	52	81		244
POL	PTRRELQVW	30	9	13	20		245
POL	FSPQITLW	85	9	14	22		246
POL	KMIGIGGF	132	9	62	97		247
POL	ELNKRTOGF	268	9	57	89		248
POL	TVLDVGDAY	296	9	57	89	0.0180	249
POL	VLDVGDAYF	297	9	60	94		250

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SFQ ID NO
POL	FSVPLDKDF	305	9	18	28		251
POL	PLDKDFKY	308	9	19	30		252
POL	ETPIGRYQY	327	9	52	81	0.0052	253
POL	SMTKILEPF	352	9	43	67		254
POL	ELREIILLKW	393	9	17	27		255
POL	ELRQIILLRW	393	9	15	23		256
POL	IVLPEKUSW	433	9	13	20		257
POL	KLNWASQIY	452	9	60	94	0.0070	258
POL	VIWGTKPKF	573	9	47	73		259
POL	KLPIQKETW	582	9	20	31		260
POL	RLPIQKETW	582	9	26	41		261
POL	WTDYWQATW	594	9	14	22		262
POL	WTEYWQATW	594	9	24	38		263
POL	ATWIPWEEF	609	9	52	81		264
POL	NTPLPLKLV	610	9	57	89		265
POL	PVCAETHY	625	9	28	44	0.0007	266
POL	ETKLOKAGY	641	9	35	55	0.0010	267
POL	QLIKKEKVV	716	9	28	44	0.0007	268
POL	SSGIKKVLF	745	9	26	41		269
POL	QVDCSNGIW	805	9	57	89		270
POL	ETGOETAYF	844	9	57	89		271
POL	FILKLGRW	852	9	32	50		272
POL	FLKLGRW	852	9	25	39		273
POL	STTVKAACW	875	9	15	23		274
POL	TTVKAACW	875	9	15	23		275
POL	KTAVQMAVF	925	9	57	89		276
POL	QMAVFUINF	929	9	60	94	0.0056	277
POL	KIONFRVY	971	9	52	81		278
POL	LTQGCITLNF	177	10	41	64		279
POL	LTQLGCTLNF	177	10	15	23		280
POL	GMXGPKVKQ	201	10	51	80	0.0130	281
POL	ISKIGHENIY	236	10	42	66		282
POL	ISKIGHENIY	236	10	11	17		283
POL	AIKKKIDSTKW	251	10	57	89		284
POL	STRWRKLVDF	257	10	58	91		285
POL	ELNKRITQDFW	268	10	57	89	0.2800	286
POL	VTLDVGDAY	295	10	56	88		287
POL	TVLDVGDAYF	296	10	57	89		288
POL	SSMTKILEPF	351	10	33	52		289
POL	VIVQYMDLLY	368	10	51	80	0.2500	290
POL	PIQLPERDSW	432	10	13	20		291
POL	PVLPEKDSW	432	10	13	20		292
POL	ILKEPIVIGVY	498	10	40	63	0.0017	293
POL	EIOKQGQDQW	520	10	13	20		294
POL	EIOKQGQDQW	520	10	15	23		295
POL	WTYQYQEPF	529	10	42	66		296
POL	KIATESIVIV	566	10	14	22		297
POL	IVIWGTKPKF	572	10	47	73		298
POL	PIQKETWEAW	584	10	15	23		299
POL	PIQKETWEW	584	10	27	42		300

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	ETWETWTD	588	10	10	16		301
POL	ETWETWTE	588	10	10	16		302
POL	NTPLVKLWY	610	10	57	89	0.0041	303
POL	EVNIVDSQY	684	10	59	92	0.0530	304
POL	VSAGIRKVL	744	10	15	23		305
POL	VSSGIRKVL	744	10	26	41		306
POL	LVAVIIVASGY	826	10	53	83	0.0390	307
POL	THIIDNGSNF	864	10	14	22		308
POL	VIIIDNGSNF	864	10	24	38		309
POL	TSAAVKAACW	874	10	27	42		310
POL	TSTVKAACW	874	10	14	22		311
POL	TSTVKAACW	875	10	15	23		312
POL	GIKQEEGIRY	886	10	22	34	0.0010	313
POL	GIKQEEGIRY	886	10	11	17		314
POL	IKIQNFRVY	969	10	12	19		315
POL	IKIQNFRVY	969	10	36	57	0.0010	316
POL	NSPTRELVQ	28	11	12	19		317
POL	VSFSFQITLW	78	11	07	15		318
POL	GTTLNFQITF	79	11	01	17		319
POL	PSLSFQITLW	79	11	02	33		320
POL	GTLNCPQITL	80	11	01	33		321
POL	PTENFQITLW	80	11	01	33		322
POL	SSFSFQITLW	82	11	03	30		323
POL	VLEDINLPCKW	119	11	13	20		324
POL	VLEENLPCKW	119	11	12	19		325
POL	GIGGFKVRQY	136	11	53	83		326
POL	LLTQIGCTLNF	176	11	21	33		327
POL	MLTQIGCTLNF	176	11	17	27		328
POL	MLTQIGCTLN	176	11	10	16		329
POL	KISKIGPENPY	235	11	41	64		330
POL	KISKIGPENPY	235	11	11	17		331
POL	DSTKWRKLVLD	256	11	58	91		332
POL	SVTLVLDVDA	294	11	56	88		333
POL	VTVLVGVDA	294	11	56	88		334
POL	SVPLDKDFRK	306	11	18	28		335
POL	SINNETVIGIRY	323	11	32	50		336
POL	STNNETVIGIRY	323	11	11	17		337
POL	QSSMTKILEFF	350	11	33	52		338
POL	IVYQYMDL	367	11	42	66		339
POL	ELREILLKWG	393	11	14	22		340
POL	ELRQILLRWG	393	11	12	19		341
POL	WMGYELIPDK	418	11	60	94		342
POL	DIQKLVCKLN	445	11	62	97		343
POL	EILKEIVIGVY	497	11	40	63		344
POL	ILKEPVIQVY	498	11	38	59		345
POL	SIVIWGKTPKF	571	11	41	64		346
POL	PIQKETWEAW	584	11	15	23		347
POL	PIQKETWETW	584	11	27	42		348
POL	ETWETWTD	588	11	16	26		349
POL	FVNTPPLVKL	608	11	54	86		350

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*9101	SEQ ID NO
POL	LIKKEKVVLA	717	11	20	31		351
POL	LIKKEKVVLSW	717	11	13	20		352
POL	LVSAQIRKVLV	743	11	15	23		353
POL	LVSSGIRKVLV	743	11	26	41		354
POL	ISMWRAMAS	768	11	32	50		355
POL	ILVAIVIVASGY	825	11	53	83		356
POL	KVIITDNGSNF	863	11	21	33		357
POL	FTSAAVKAAC	873	11	27	42		358
POL	FTSTIVKAAC	873	11	14	22		359
POL	TSAAVKAACW	874	11	27	42		360
POL	TSTIVKAACW	874	11	14	22		361
POL	ILKTAVQMAV	923	11	57	89		362
POL	AVQMAVEIIN	927	11	60	94		363
POL	QIKIQNFRVY	968	11	12	19		364
POL	QITKIQNFRVY	968	11	35	55		365
POL	ITKIQNFRVY	969	11	12	19		366
POL	PIWKGPAKLL	985	11	36	57		367
POL	PLWKGPAKLL	985	11	35	55		368
REV	ILYQSNPY	23	8	18	28	0.0110	369
REV	AVRIKILY	17	9	27	42		370
REV	KILYQSNPY	22	9	13	20		371
REV	IKILYQSNPY	20	11	26	41		372
TAT	PVDINLEPW	3	9	18	28		373
TAT	PVDPRLEPW	3	9	20	31		374
TAT	FLNKGGLISY	41	10	14	22		375
VIF	SLVKIILIMY	23	8	14	22		376
VIF	RLVITTYW	65	8	44	69		377
VIF	QLIHLYYF	110	8	12	19		378
VIF	QLIIMIIYF	110	8	14	22		379
VIF	ILYYFDCF	113	8	16	25		380
VIF	IMIIYFDCF	113	8	15	23		381
VIF	IVSPRCFY	133	8	14	22		382
VIF	KSLVKIILIMY	22	9	18	28		383
VIF	NSLVKIIIMY	22	9	24	38		384
VIF	GLITGERDW	73	9	22	34		385
VIF	GLQTGERDW	73	9	12	19		386
VIF	SIEWRLRLY	89	9	11	17		387
VIF	QVDRMKIRTW	12	10	12	19		388
VIF	QVDRMRINTW	12	10	16	25		389
VIF	QVDRMRIRTW	12	10	31	48		390
VIF	ILGIIGVSIW	83	10	25	39		391
VIF	ILGQGVSIW	83	10	26	41		392
VIF	VSIEWRLRLY	88	10	11	17		393
VIF	LIHLYYFDCF	111	10	16	25		394
VIF	LIHIIYFDCF	111	10	15	23		395
VIF	SVKKLTEDRW	174	10	13	20		396
VIF	GVSIEWRLRR	87	11	10	16		397
VIF	GLADQLIHMH	106	11	11	17		398
VIF	QLIILYYFDCF	110	11	13	20		399
							400

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
VIF	QLIIMIIYDCF	110	11	14	22		401
VIF	PSVKKLIEDR	173	11	13	20		402
VPR	KSEAVRIIF	27	8	15	23		403
VPR	WLIIGLQY	38	8	11	17		404
VPR	RILQQLF	62	8	45	70		405
VPR	AVRIIFRIW	30	9	14	22		406
VPR	AVRIIFRPW	30	9	34	53		407
VPR	ELKNEAVRIIF	25	10	17	27		408
VPR	ELKSEAVRIIF	25	10	15	23		409
VPR	WLIIGLQIIF	38	10	20	31		410
VPR	IHYETYGDTW	45	10	17	27		411
VPR	IHYNTYGDTW	45	10	14	22		412
VPR	YIYETYGDTW	45	10	14	22		413
VPR	IIRILQQLF	60	10	41	64		414
VPR	ILOQLLFIF	63	10	35	55		415
VPR	AIRILQQLF	59	11	38	59		416
VPR	RILQQLHIF	62	11	34	53		417
VPU	LIAIVVW	26	8	10	16		418
VPU	IVVWTIVF	30	8	15	23		419
VPU	WTIVFIEY	34	8	12	19		420
VPU	EMGHIAFW	89	8	11	17		421
VPU	AVVWTIVF	29	9	14	22		422
VPU	VVWTIVFIEY	31	10	12	19		423
VPU	GVEMGHIAFW	91	10	01	50		424
VPU	KVDYRIVIVAF	7	11	01	33		425
VPU	IVVWTIVFIEY	30	11	12	19		426
VPU	RIKEIRDSIDY	64	11	01	50		427
VPU	RIRIIRDSIDY	64	11	01	50		428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SI:Q ID NO
ENV	LILGLVII	21	8	09	15						429
ENV	GLVICS	28	8	10	16						430
ENV	GMLMCSA	28	8	12	19						431
ENV	QLYATVYA	34	8	01	50						432
ENV	WVTVYGV	46	8	58	91						433
ENV	TVVYGVV	48	8	55	86						434
ENV	GVPVWKEA	52	8	34	53						435
ENV	PVWKEATT	54	8	22	34						436
ENV	ATTLFCA	59	8	24	38						437
ENV	TLFCASDA	64	8	54	84						438
ENV	EVHNVWAT	77	8	36	56						439
ENV	ATHACVPT	83	8	36	88						440
ENV	NVTENFNM	101	8	34	53						441
ENV	NMWRNDMV	107	8	12	19						442
ENV	NMWRNNMV	107	8	34	53						443
ENV	EQMIEDII	115	8	24	38						444
ENV	DQSLKPCV	126	8	50	78						445
ENV	SLKPCVKL	128	8	55	86						446
ENV	KLTPLCVT	134	8	53	83						447
ENV	LTPLCVTL	135	8	34	84						448
ENV	VTSIGNSA	161	8	01	20						449
ENV	ALFYKLDV	202	8	10	16						450
ENV	ALFYRLDV	202	8	12	19						451
ENV	NISPKNNT	217	8	01	33						452
ENV	LINCNTSA	237	8	17	27						453
ENV	NTSALTQA	241	8	14	22						454
ENV	NTSVITQA	241	8	13	20						455
ENV	ITQACIKV	245	8	37	58						456
ENV	PIHIYCT	258	8	40	63						457
ENV	PIHIYCTA	258	8	18	28						458
ENV	PIHIYCTPA	260	8	37	58						459
ENV	CAPAGFAI	260	8	18	28						460
ENV	CTPAGFAI	264	8	29	45						461
ENV	GTGPKKNV	264	8	10	16						462
ENV	NVSTVQCT	281	8	17	27						463
ENV	TVQCTHGI	287	8	51	80						464
ENV	CTHIGIKIV	290	8	51	80						465
ENV	CTHIGIRPV	294	8	33	52						466
ENV	GKPVVST	297	8	26	41						467
ENV	GIRPVVST	297	8	33	52						468
ENV	PVSTQLL	300	8	26	41						469
ENV	VVSTQLLL	301	8	60	94						470
ENV	QLLLNGSL	305	8	60	94						471
ENV	LLLLNGSL	306	8	57	89						472
ENV	SLAEFVVI	311	8	55	86						473
ENV	LAEEFVVI	312	8	14	22						474
ENV	IRSENLT	319	8	13	20						475
ENV	CTRPNNNT	345	8	10	16						476
ENV	NTRLSIRI	351	8	29	45						477
ENV				10	16						478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NTSPKSRV	376	8	01	33						479
ENV	TAGNSSRA	376	8	01	33						480
ENV	IGDIHQQA	377	8	30	49						481
ENV	MQNGTNT	458	8	01	17						482
ENV	ITIEGNITL	478	8	01	50						483
ENV	NITLPCR	482	8	11	17						484
ENV	ITTLPCR	482	8	14	22						485
ENV	RIKQIIM	488	8	30	47						486
ENV	RIKQVNM	488	8	12	19						487
ENV	IINMVOEV	492	8	17	27						488
ENV	WQEVGKAM	496	8	18	28						489
ENV	WQVVGQAM	496	8	11	17						490
ENV	EVGKAMYA	498	8	18	28						491
ENV	RVGQAMYA	498	8	10	16						492
ENV	KAMYAPPI	502	8	23	36						493
ENV	RAMYAPPI	502	8	14	22						494
ENV	QIRCSSNI	512	8	12	19						495
ENV	NITGLIT	519	8	11	17						496
ENV	NITGLLT	519	8	35	55						497
ENV	ELYKYKVV	560	8	56	89						498
ENV	KVYKIEPL	565	8	25	39						499
ENV	KIEPLGVA	568	8	23	37						500
ENV	PTKAKRRV	576	8	22	34						501
ENV	VVEREKRA	588	8	32	50						502
ENV	VQREKRA	588	8	17	27						503
ENV	VQREKRAV	589	8	17	27						504
ENV	RAVGIGAV	594	8	12	19						505
ENV	GALFLGFL	601	8	12	19						506
ENV	GAMFLGFL	601	8	13	20						507
ENV	GAVFLGFL	601	8	22	34						508
ENV	FLGFLGAA	604	8	48	75						509
ENV	FLGAAGST	608	8	55	86						510
ENV	AAGSTMGA	611	8	58	91						511
ENV	TMGAASIT	614	8	39	61						512
ENV	GAASITLT	615	8	39	61						513
ENV	AASITLV	617	8	39	61						514
ENV	SITLTVQA	618	8	36	56						515
ENV	LTVQARQL	620	8	32	50						516
ENV	TVQARQLL	623	8	38	59						517
ENV	ROLLSGIV	624	8	36	56						518
ENV	IVQQNNL	628	8	49	77						519
ENV	IVQQJNL	634	8	26	41						520
ENV	VQQNNLL	634	8	32	50						521
ENV	VQQNNLL	635	8	26	41						522
ENV	VQQNNLL	635	8	32	50						523
ENV	QNNLLRA	637	8	32	50						524
ENV	QSNLLRA	637	8	26	41						525
ENV	NLLRAIEA	640	8	26	41						526
ENV	ALIAQQIL	644	8	51	80						527
ENV			8	49	77						528

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
ENV	AQHIILKL	647	8	13	20						529
ENV	AQHILLQL	647	8	35	55						530
ENV	AQHIMLQL	647	8	10	16						531
ENV	QHIILKLT	648	8	13	20						532
ENV	QHIILQLT	648	8	34	53						533
ENV	QHIIMLQLT	648	8	10	16						534
ENV	LQLTVWGI	652	8	44	69						535
ENV	TVWGIKQL	655	8	59	92						536
ENV	KQOARVL	660	8	41	64						537
ENV	QLOARVLA	661	8	41	64						538
ENV	LQARVLAV	662	8	33	52						539
ENV	VLAVERYL	666	8	34	53						540
ENV	YLRDQQLL	672	8	31	48	0.0001					541
ENV	YLRDQQLL	672	8	18	28						542
ENV	KLICITAV	687	8	19	30						543
ENV	KLICITNV	687	8	17	27						544
ENV	KLICITTV	687	8	12	19						545
ENV	WMWERHEI	723	8	12	19						546
ENV	LLALDKWA	723	8	19	30						547
ENV	LLLELDKWA	725	8	21	33						548
ENV	ALDKWASL	757	8	11	17						549
ENV	FLDKWASL	757	8	18	28						550
ENV	SLWNWFDI	763	8	17	27						551
ENV	ITKWLWYI	770	8	16	25						552
ENV	ITNWLWYI	770	8	19	30						553
ENV	YKIFIMI	776	8	43	67						554
ENV	FIMVGGIL	780	8	44	69						555
ENV	IMVGGILI	781	8	35	56						556
ENV	IVGGLIGL	783	8	42	66						557
ENV	IVGGLVGL	783	8	10	16						558
ENV	GLIGLRII	786	8	15	23						559
ENV	GLIGLRIV	786	8	32	50						560
ENV	GLRIEAV	789	8	18	28						561
ENV	GLRIEAV	789	8	29	45						562
ENV	IFAVLSI	792	8	15	23						563
ENV	IVFAVLSI	792	8	20	31						564
ENV	VLSVNRV	796	8	38	59						565
ENV	PLSFQITL	809	8	10	16						566
ENV	PLSFQITL	809	8	13	20						567
ENV	GLDRPGT	823	8	01	33						568
ENV	RLVNGFLA	844	8	13	20						569
ENV	LVNGFLAL	844	8	20	31						570
ENV	LVSGFLAL	845	8	14	22						571
ENV	LALAWDDL	845	8	19	30						572
ENV	CLFSYIIRL	850	8	25	39						573
ENV	RLRDLILI	861	8	42	66						574
ENV	IAARTVEL	874	8	13	20	0.0001					575
ENV	AARTVELL	876	8	12	19						576
ENV	ELLGISSL	881	8	11	17						577
ENV				09	15						578

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0306	A*6802	SEQ ID NO
ENV	LQYWSQEL	907	8	16	25						579
ENV	QDELKNSA	911	8	12	19						580
ENV	QDELKNSA	911	8	12	19						581
ENV	SAVSLNNA	917	8	11	17						582
ENV	AVSLNAT	918	8	11	17						583
ENV	SLLNATAI	920	8	14	22						584
ENV	LLNATAIA	921	8	15	23						585
ENV	DTIAIAVA	923	8	10	16						586
ENV	NATAIAVA	923	8	14	22						587
ENV	AIATAEGT	926	8	32	50						588
ENV	VAECTDRI	929	8	19	30						589
ENV	VAEGTDRV	929	8	16	25						590
ENV	GTDRIEIV	932	8	11	17						591
ENV	ILIHPRRI	947	8	13	20						592
ENV	PTRIHQGL	951	8	12	19						593
ENV	ROGLERAL	955	8	35	55	0.0003					594
ENV	VTVYTGVPV	47	9	55	86	0.0002					595
ENV	GVVVKKEAT	52	9	22	34	0.0002					596
ENV	PVWKEATT	54	9	22	34	0.0002					597
ENV	EATTLFCA	58	9	24	38	0.0002					598
ENV	TLFLCASDA	61	9	52	81	0.0002					599
ENV	DAKAYDTEV	70	9	17	27	0.0001					600
ENV	DTEVINVVA	75	9	18	28	0.0001					601
ENV	NVWATIACV	80	9	49	77	0.0002					602
ENV	WATIACVPT	82	9	56	88	0.0002					603
ENV	PTDRHQEL	80	9	25	39	0.0002					604
ENV	PTDRHQEV	80	9	21	33	0.0002					605
ENV	MVEQMIEDI	113	9	23	36	0.0002					606
ENV	QMIEDIISL	116	9	29	45	0.0023					607
ENV	ISLWDQSL	121	9	38	59	0.0180					608
ENV	VISLWDQSL	121	9	10	16						609
ENV	SLKPCVKLT	128	9	55	86	0.0001					610
ENV	CVKLTPLCV	132	9	55	86	0.0002					611
ENV	KLTLPLCVTL	134	9	52	81	0.0002					612
ENV	PLCVTLNCT	137	9	22	34	0.0005					613
ENV	EIKNCSFNI	181	9	13	20						614
ENV	ALFYRLDVV	202	9	11	17						615
ENV	VONNHSNT	218	9	01	20						616
ENV	RLNCHTSAI	236	9	17	27						617
ENV	LINCHTSAI	237	9	15	23						618
ENV	ATQACPKV	244	9	13	20						619
ENV	VITQACPKV	244	9	15	23						620
ENV	KVSFERIH	252	9	30	47						621
ENV	CAPAFUAIL	264	9	29	45	0.0001					622
ENV	STVQCTHIGI	289	9	51	80	0.0001					623
ENV	CTHIGIKPVV	294	9	32	50						624
ENV	CTHIGIRPVV	294	9	26	41	0.0001					625
ENV	PVVS1QLLL	300	9	60	94	0.0001					626
ENV	TQLLNGSL	304	9	57	89	0.0001					627
ENV	QLLNGSLA	305	9	55	86	0.0001					628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6002	SEQ ID NO
ENV	SLAGEVVI	311	9	13	20	0.0020					629
ENV	NAKTIIVQL	329	9	14	22						630
ENV	ATGDHIGDI	369	9	12	19						631
ENV	DIHGDHQA	372	9	12	19						632
ENV	EHGDHQA	372	9	10	15						633
ENV	GTAGNSSRA	375	9	01	33						634
ENV	NTSPRSVA	376	9	01	33						635
ENV	TAGNSRAA	376	9	01	33						636
ENV	DIQQAICNI	380	9	15	23						637
ENV	DIQQAICNV	380	9	10	16						638
ENV	TLPCNIKQI	484	9	26	41						639
ENV	QINMWQEV	491	9	17	27	0.0026					640
ENV	NMWQEVGKA	494	9	15	23	0.0022					641
ENV	QAMVYAPPI	501	9	14	22						642
ENV	QIRCSSNI	511	9	11	17						643
ENV	QIRCSSNI	512	9	11	17	0.0001					644
ENV	NTETNKIET	537	9	01	17						645
ENV	NTETNKIET	537	9	01	17						646
ENV	VVKIPLGV	566	9	23	36						647
ENV	PLGVAPTKA	571	9	23	36	0.0001					648
ENV	PLKAKRRV	576	9	22	34	0.0001					649
ENV	RVVEREKRA	587	9	32	50						650
ENV	RVVQREKRA	587	9	17	27	0.0001					651
ENV	VVEREKRAV	588	9	25	39						652
ENV	VVQREKRAV	588	9	16	25						653
ENV	AVGIGAVFL	595	9	11	17	0.0950					654
ENV	ALFLGFLGA	602	9	11	17						655
ENV	AMFLGFLGA	602	9	12	19						656
ENV	AVFLGFLGA	602	9	19	30						657
ENV	FLGAGSTM	608	9	55	86						658
ENV	GAGSTMGA	610	9	55	86	0.0190					659
ENV	AAGSTMGA	611	9	45	70	0.0009					660
ENV	STMGAASIT	614	9	39	61	0.0001					661
ENV	TMGAASITL	615	9	39	61						662
ENV	GAASITLV	617	9	36	56						663
ENV	TLTVQARQL	622	9	37	58						664
ENV	LVQARQL	623	9	36	56						665
ENV	QARQLLSGI	626	9	38	59						666
ENV	GIVQQQNNL	633	9	26	41						667
ENV	GIVQQQNNL	633	9	32	50	0.0001					668
ENV	IVQQQNNL	634	9	26	41						669
ENV	IVQQQNNL	634	9	32	50	0.0001					670
ENV	QQQNNLLRA	636	9	25	39						671
ENV	QQQNNLLRA	636	9	26	41						672
ENV	QQNNLLRAI	637	9	26	41						673
ENV	QQNNLLRAI	637	9	26	41						674
ENV	RAIEAQQIIL	643	9	45	70						675
ENV	RAIEAQQIIL	643	9	48	75						676
ENV	EAQQIILLKL	646	9	12	19						677
ENV	EAQQIILLKL	646	9	35	56						678

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
ENV	AQHIILKLT	647	9	13	20						679
ENV	AQHILKLT	647	9	34	53						680
ENV	AQHIMLQLT	647	9	10	16						681
ENV	QQHILKLT	648	9	13	20						682
ENV	QQHILKLT	648	9	34	53						683
ENV	LLKLTWGI	651	9	13	20						684
ENV	LLQLTWGI	651	9	34	53						685
ENV	MLQLTWGI	651	9	10	16	0.5100	0.0200	0.2300	0.1500	0.0620	686
ENV	LTWGIKQL	654	9	59	92	0.2500					687
ENV	GIKQLQARV	658	9	40	63	0.0001					688
ENV	KQLQARVLA	660	9	41	64	0.0001					689
ENV	QLQARVLAV	661	9	33	52	0.0085					690
ENV	RLVAYERYL	665	9	33	52	0.0009					691
ENV	GIWCCSGKL	680	9	48	75	0.0011					692
ENV	QQEKHEQDL	747	9	16	25						693
ENV	QQEKHEQEL	747	9	18	28						694
ENV	DLLALDKWA	754	9	15	23						695
ENV	ELLELDKWA	754	9	18	28	0.0002					696
ENV	LALDKWASL	756	9	11	17						697
ENV	SLWNWFDIT	763	9	13	20						698
ENV	DIINWLYYI	769	9	10	16						699
ENV	WLWYIKIFI	773	9	49	77	0.0360					700
ENV	YIKFIMIV	776	9	39	61	0.0001					701
ENV	FIMVGGILI	780	9	35	55						702
ENV	MIVGGILGL	782	9	36	56						703
ENV	LIGLRIFA	787	9	16	25						704
ENV	LIGLRIFA	787	9	21	33						705
ENV	GLRIIFAVL	789	9	17	27						706
ENV	GLRIIFAVL	789	9	28	43	0.0009					707
ENV	RIFAVLSI	791	9	14	22						708
ENV	RIFAVLSI	791	9	19	30	0.0002					709
ENV	IIFAVLSIV	792	9	15	23						710
ENV	IVFAVLSIV	792	9	18	28	0.0012					711
ENV	AVLSIVNIRV	795	9	31	48	0.0130					712
ENV	AVRQCYSP	802	9	55	86	0.0005					713
ENV	SIRLVNGL	842	9	11	17						714
ENV	SIRLVNGL	842	9	13	20						715
ENV	RLVNGFLAL	844	9	12	19						716
ENV	RLVNGFLAL	844	9	19	30						717
ENV	LVSGFLALA	845	9	16	25						718
ENV	FLALAWDDL	849	9	25	39						719
ENV	LAWDILRSL	852	9	20	31						720
ENV	LIAARTVEL	873	9	12	19						721
ENV	IAARTVELL	874	9	11	17						722
ENV	LLGRRGWEA	882	9	10	16						723
ENV	GLRLGWEG	892	9	10	16						724
ENV	LLQTYWSQEL	906	9	16	25	0.0270					725
ENV	QQLKNSAI	911	9	12	19						726
ENV	SQLKNSAV	911	9	10	16						727
ENV	ELKNNAINL	913	9	10	16						728

Table VIII
 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6R02	SEQ ID NO
ENV	ELKNSAISL	913	9	10	16						729
ENV	ELKNSAVSL	913	9	12	19						730
ENV	SAVSLNAT	917	9	11	17	0.0001					731
ENV	AVSLLNATA	918	9	11	17						732
ENV	SLLNATAIA	920	9	14	22						733
ENV	LLNATAIAV	921	9	15	23						734
ENV	IAIAVAEGT	925	9	10	16						735
ENV	TAIAVAEGT	925	9	22	34						736
ENV	AVAEGTDRI	928	9	16	25						737
ENV	AVAEGTDIRV	928	9	14	22	0.0008					738
ENV	VAEGTDRI	929	9	18	28						739
ENV	VAEGTDRVI	929	9	16	25	0.0001					740
ENV	AIHIIIPRI	946	9	12	19						741
ENV	RIRQLERA	953	9	34	53	0.0003					742
ENV	RQGLERALL	955	9	34	53						743
ENV	ILGLVICS	26	10	10	16						744
ENV	LLGLMICA	26	10	10	16						745
ENV	QLYATVYAGV	34	10	01	50	0.0150					746
ENV	KLWVTYYGV	44	10	11	17	0.0160					747
ENV	NLWVTYYGV	44	10	34	54	0.0009					748
ENV	WTVVYGVIV	46	10	55	86						749
ENV	GVPVWKEATT	52	10	22	34	0.0001					750
ENV	PVWKEATTL	54	10	22	34	0.0001					751
ENV	KTLTFCASDA	60	10	12	19						752
ENV	TLTFCASDA	60	10	24	38	0.0001					753
ENV	TLFCA3IDAKA	64	10	46	72	0.0006					754
ENV	CASDAKAYDT	67	10	19	30	0.0001					755
ENV	KAYDTEVINV	72	10	17	27	0.0013					756
ENV	DTEVIRVWAT	75	10	18	28	0.0001					757
ENV	EVINVWATHA	77	10	35	55	0.0001					758
ENV	PTDIPNIQEVV	89	10	13	20						759
ENV	NMVEQMIEDI	112	10	20	31	0.0001					760
ENV	MVEQMIEDH	113	10	23	36	0.0001					761
ENV	EQMIHDIISL	115	10	22	34						762
ENV	DIISLWDQSL	120	10	38	59	0.0001					763
ENV	DVISLWDQSL	120	10	10	16						764
ENV	DQSLKPCVKL	126	10	47	73						765
ENV	CVKLTPLCVT	132	10	53	83						766
ENV	STSNSSNST	159	10	01	50	0.0001					767
ENV	VISTGNSAGT	161	10	01	20						768
ENV	EIKNCSFNT	181	10	12	19						769
ENV	SVQNNNSNT	217	10	01	33						770
ENV	RLINCNTSAI	236	10	15	24						771
ENV	LINCNTSAIT	237	10	14	22						772
ENV	SAITQACPKV	243	10	13	20						773
ENV	SVITQACPKV	243	10	13	23						774
ENV	PIPIHYCAPA	258	10	36	56	0.0002					775
ENV	PIPIHYCTPA	258	10	18	28						776
ENV	GTGFCINVST	281	10	12	19						777
ENV	CTNVSTVQCT	285	10	13	20						778

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	Site ID NO
ENV	VQCTIIGIKIV	292	10	32	50						779
ENV	VQCTIIGIRIV	292	10	23	39						780
ENV	GIRPVSTOL	297	10	33	52						781
ENV	GIRPVSTQL	297	10	26	41	0.0002					782
ENV	STOLLNGSL	303	10	57	89	0.0001					783
ENV	TOLLNGSLA	304	10	55	86						784
ENV	RIGPGQIFYA	357	10	10	16						785
ENV	RIGPGQIFYA	357	10	10	16						786
ENV	SIGSGQAFYV	360	10	01	33						787
ENV	SIGSGQAFYV	360	10	01	33						788
ENV	YATGDHIGDI	368	10	11	17						789
ENV	GTAGNSSRAA	375	10	01	33						790
ENV	MONGTNTIST	438	10	01	17						791
ENV	NANTIRIRI	478	10	01	50						792
ENV	ITLPCRIRKI	483	10	23	39						793
ENV	ITLPCRIRKI	484	10	15	23						794
ENV	TLPCRIRKQIV	484	10	10	16						795
ENV	KQIINAIWQIV	490	10	17	27						796
ENV	NMIQEVGKAM	494	10	15	23	0.0004					797
ENV	WQEVGKAMIA	496	10	18	28						798
ENV	WQEVGKAMIA	496	10	10	16						799
ENV	GQIRCSNIT	511	10	11	17						800
ENV	EIFRPGGDDM	544	10	17	27	0.0001					801
ENV	EIFRPGGDDM	544	10	21	33						802
ENV	DMRDNRWSEL	552	10	37	58	0.0001					803
ENV	ELYKYKAVEI	560	10	13	21						804
ENV	ELYKYKVKI	560	10	29	46						805
ENV	KVKIEPLGV	565	10	23	36						806
ENV	VVKIEPLGVA	566	10	23	36						807
ENV	KIEPLGVAPT	568	10	23	37						808
ENV	VAPTKAKRRV	574	10	17	27						809
ENV	STRTIUREKRA	586	10	01	50	0.0001					810
ENV	RVEREKRAV	587	10	25	39						811
ENV	RVVQREKRAV	587	10	16	25						812
ENV	RAVGIGAVFL	594	10	11	17						813
ENV	GIGAVFLGFL	598	10	11	18						814
ENV	MUGAMFLGFL	599	10	04	36						815
ENV	TIGAMFLGFL	599	10	03	27						816
ENV	GALFLGFLGA	601	10	11	17	0.0003					817
ENV	GAMFLGFLGA	601	10	12	19						818
ENV	GAVFLGFLGA	601	10	19	30						819
ENV	ALFLGFLGAA	602	10	11	17	0.5000					820
ENV	AMFLGFLGAA	602	10	12	19						821
ENV	AVFLGFLGAA	602	10	19	30						822
ENV	GAASTMGAA	610	10	42	66	0.0004					823
ENV	STMGAASITL	614	10	39	61						824
ENV	TMGAAASITL	615	10	39	61						825
ENV	AASITLTVQA	618	10	28	44						826
ENV	ITLTVOARQL	621	10	27	42						827
ENV	TLTVQARQL	622	10	35	55						828
ENV	VQARQLLSGI	625	10	36	56						

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SEQ ID NO
ENV	QARQLLSGIV	626	10	38	59						829
ENV	GIVQQSNLL	633	10	26	41	0.0002					830
ENV	VQQQSNLLRA	635	10	32	50						831
ENV	VQQQSNLLRA	635	10	25	39						832
ENV	VQQQSNLLRA	635	10	26	41						833
ENV	VQQQSNLLRAI	636	10	25	39						834
ENV	QOQSNLLRAI	636	10	26	41						835
ENV	RAIEAQHILL	643	10	44	69						836
ENV	EAQQHILLKLT	646	10	12	19						837
ENV	EAQQHILLQLT	646	10	34	54						838
ENV	AQQHILLKLT	647	10	13	20						839
ENV	AQQHILLQLT	647	10	34	53						840
ENV	ILLKLTIVWGI	650	10	13	20						841
ENV	ILLQLTIVWGI	650	10	34	53						842
ENV	KLTVWGIKQL	653	10	13	20						843
ENV	QLTVWGIKQL	653	10	44	69	0.0015					844
ENV	TVWGIKQLQA	655	10	49	77	0.0150					845
ENV	GKQLQARVL	658	10	40	63	0.0002					846
ENV	KQLQARVLAV	660	10	33	52						847
ENV	YLRDQQLLGI	672	10	27	42						848
ENV	YLRDQQLLGI	672	10	18	28						849
ENV	GIWGLSGKLI	680	10	48	75	0.0004					850
ENV	MTWMEWEREI	721	10	12	19						851
ENV	NQEKNEQDL	746	10	13	20						852
ENV	NQEKNEQDL	746	10	15	23						853
ENV	QKEKNEQDL	747	10	16	25						854
ENV	QKEKNEQDL	747	10	18	28						855
ENV	LLALDKWASL	755	10	11	17						856
ENV	LLALDKWASL	755	10	18	28	0.0024					857
ENV	WASLWVWFI	761	10	17	27						858
ENV	ITKWLWYIKI	770	10	15	23						859
ENV	ITNWLWYIKI	770	10	14	22	0.0002					860
ENV	WLWYIKIFIM	773	10	43	67	0.0001					861
ENV	KIFIMVIGGL	778	10	38	59	0.0003					862
ENV	IMVIGGLKLI	781	10	34	54						863
ENV	IVGGLIGLRI	783	10	42	66						864
ENV	GLIGLRIFA	786	10	15	23						865
ENV	GLIGLRIFA	786	10	21	33						866
ENV	LIGLRIFAV	787	10	16	25						867
ENV	LIGLRIFAV	787	10	21	33						868
ENV	RIFAVLSIV	791	10	14	22						869
ENV	RIFAVLSIV	791	10	17	27	0.0007					870
ENV	FAVLVSINRV	794	10	31	48	0.0002					871
ENV	SIRLVSGFLA	842	10	12	19						872
ENV	RLVSGFLA	844	10	16	25						873
ENV	ALAWIDLRLS	851	10	19	30						874
ENV	NLCFLSYHRL	859	10	11	17						875
ENV	SLCLFSYHRL	859	10	31	48						876
ENV	LIAARTVELL	873	10	11	17						877
ENV	ELLGRSGWEA	881	10	10	16						878

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 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LLGRRGWEAL	882	10	09	15						879
ENV	RLQWEGLYL	894	10	09	29						880
ENV	NLQYWSQEL	905	10	16	25	0.0059					881
ENV	ELKNSAVSL	913	10	10	16						882
ENV	SAVSLNATA	917	10	11	17						883
ENV	AVSLNATAI	918	10	11	17						884
ENV	SLNATAIIV	920	10	14	22	0.0650	0.0074	0.0390	0.0680	0.0390	885
ENV	LNATAIAGA	921	10	14	22	0.0740					886
ENV	ATAIAVAEGT	924	10	14	22						887
ENV	IAVAEGTDRI	927	10	16	25						888
ENV	IAVAEGTDRI	927	10	14	22	0.0001					889
ENV	AVAEGTDRII	928	10	15	23						890
ENV	AVAEGTDRII	928	10	14	22	0.0014					891
ENV	RAILHPRRI	945	10	12	19						892
ENV	IIPRRIRQGL	949	10	13	21						893
ENV	NIPRRIRQGL	949	10	11	17						894
ENV	RURQGLERAL	953	10	34	53	0.0001					895
ENV	LILGLVILCSA	21	11	09	15						896
ENV	KQLYATVYSGV	34	11	01	50						897
ENV	GVFWKEATT	52	11	22	34						898
ENV	ATTLFCASDA	59	11	23	36						899
ENV	TLFCASDAKA	61	11	44	69						900
ENV	NVWATHIACVIT	80	11	48	75						901
ENV	CVPTDINPQEI	87	11	25	39						902
ENV	CVPTDINPQEV	87	11	21	33						903
ENV	PTDINPQEV	89	11	12	19						904
ENV	NWKNMNMVEOM	107	11	30	47						905
ENV	NWVEQMHEIDII	112	11	20	31						906
ENV	SLWDQSLKPCV	123	11	47	75						907
ENV	DQSLKPCVKLT	126	11	47	73						908
ENV	SLKPCVKRLTPL	128	11	54	84						909
ENV	CVKRLTLCVIL	132	11	52	81						910
ENV	LTPLCVTLNCT	135	11	22	34						911
ENV	EIKNCSFNIT	181	11	11	17						912
ENV	RLNCHTSAT	236	11	14	22						913
ENV	QACPVSSEPI	248	11	30	47						914
ENV	PIIYCTPAGFA	260	11	27	42						915
ENV	GTGFCRNVSTV	281	11	10	16						916
ENV	NVSTVQCTIIGI	287	11	12	19						917
ENV	TVQCTIIGIKPV	290	11	51	80						918
ENV	VQCTHIGIKPV	290	11	28	44						919
ENV	VQCTHIGIKPVV	292	11	22	34						920
ENV	CTHIGIKPVST	292	11	31	48						921
ENV	CTHIGIKPVST	294	11	25	39						922
ENV	CTHIGIKPVST	294	11	32	50						923
ENV	GIRPVVSTQLL	297	11	26	41						924
ENV	GIRPVVSTQLL	297	11	33	52						925
ENV	STQLLLNGSLA	303	11	26	41						926
ENV	LLNGSLAEEV	307	11	55	86						927
ENV			11	16	25						928

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0701	A*0202	A*0203	A*0206	A*8802	SEQ ID NO
ENV	EINCRPNNT	342	11	10	16						929
ENV	RICPGQTFYAT	357	11	10	16						930
ENV	GIGGQTFYAT	360	11	01	33						931
ENV	SIGSGQAFYVT	360	11	01	33						932
ENV	EMIITNYSNDT	438	11	01	17						933
ENV	NITLPCRKIOI	482	11	11	17						934
ENV	TITLPCRKIOI	482	11	13	20						935
ENV	ITLPCRKIOI	483	11	15	23						936
ENV	IINMWQEVGKA	492	11	12	19						937
ENV	EVGKAMYAPPI	498	11	18	28						938
ENV	RVGQAMYAPPI	498	11	10	16						939
ENV	QIRCCSNITGL	512	11	11	17						940
ENV	KVKIEPLGVA	565	11	23	36						941
ENV	GVPTKAKRRV	573	11	17	27						942
ENV	VATPKAKRRV	574	11	17	27						943
ENV	NIITPIREKRA	586	11	01	50						944
ENV	STRTIIEKRAV	586	11	01	50						945
ENV	VVEREKRAVGH	588	11	11	17						946
ENV	GALFLGFLGAA	601	11	11	17						947
ENV	GAMFLGFLGAA	601	11	12	19						948
ENV	GAFLGFLGAA	601	11	19	30						949
ENV	FLGFLGAAAGST	604	11	48	75						950
ENV	FLGAAGSTMGA	608	11	55	86						951
ENV	AAGSTMGAASI	611	11	34	53						952
ENV	STMGAASITLT	614	11	39	61						953
ENV	TMGAAASITLT	615	11	36	56						954
ENV	GAASITLTVOA	617	11	28	44						955
ENV	SITLTVOARQL	620	11	27	42						956
ENV	ITLTVOARQL	621	11	27	42						957
ENV	TVOARQLLSGI	624	11	36	56						958
ENV	VQARQLLSGI	625	11	36	56						959
ENV	IVQQQINLLRA	634	11	25	39						960
ENV	IVQQQNLLRA	634	11	26	41						961
ENV	VQQQNLLRAI	635	11	25	39						962
ENV	VQQQNLLRAI	635	11	26	41						963
ENV	QQNLLRAIEA	637	11	26	41						964
ENV	QSNLLRAIEA	637	11	23	36						965
ENV	LLIAEAQHIL	641	11	45	70						966
ENV	ALIAEAQHIL	644	11	12	19						967
ENV	ALIAEAQHIL	644	11	35	55						968
ENV	EAQIHLKLT	646	11	12	19						969
ENV	EAQIHLKLT	646	11	34	54						970
ENV	LQITVIGIKQL	652	11	44	69						971
ENV	LTWGIKQLQA	654	11	49	77						972
ENV	GKQLQARVLA	658	11	40	63						973
ENV	QARVLAVERYL	663	11	33	52						974
ENV	AVERYLKDQQL	668	11	23	36						975
ENV	AVERYLRDQQL	668	11	11	17						976
ENV	LLGIWGCCKL	678	11	46	72						977
ENV	NMTWMEWEREI	720	11	12	19						978

Table VIII
 HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NQKEKNEQDL	746	11	13	20						979
ENV	NQKEKNEQELL	746	11	13	23						980
ENV	QOEKNEQDLA	747	11	16	25						981
ENV	EQDLALDKWA	752	11	12	19						982
ENV	EQELLEDKWA	752	11	11	17						983
ENV	ELLELDKWASL	754	11	15	23						984
ENV	WASLWNWFDIT	761	11	13	20						985
ENV	WLWYKIFIMI	773	11	43	67						986
ENV	KIFIMVGGLI	778	11	31	48						987
ENV	FIMIVGGGLI	780	11	34	53						988
ENV	FIMVGGGLIRI	782	11	36	56						989
ENV	IVGGGLIGLRII	783	11	12	19						990
ENV	IVGGGLIGLRIV	783	11	30	47						991
ENV	GLIGLRIFAV	786	11	15	23						992
ENV	GLIGLRIFAV	786	11	21	33						993
ENV	LIGLRIFAVL	787	11	15	23						994
ENV	LIGLRIFAVL	787	11	20	31						995
ENV	GLRIFAVLSI	789	11	14	22						996
ENV	GLRIFAVLSI	789	11	19	30						997
ENV	RQGYSPLSFQT	804	11	45	70						998
ENV	SIRLVSGFLAL	842	11	11	17						999
ENV	LALAWDDLRLSL	850	11	19	30						1000
ENV	LAWDDLRLSL	852	11	20	31						1001
ENV	CLFSYIIRLRL	861	11	20	31						1002
ENV	ELLGREGWEAL	881	11	09	15						1003
ENV	SOELKNSAVSL	911	11	10	16						1004
ENV	SAVSLNATAI	917	11	11	17						1005
ENV	AVSLNATAIA	918	11	11	17						1006
ENV	SLNATAIAVA	920	11	13	20	0.2700					1007
ENV	NATAIAVAEGT	923	11	13	20						1008
ENV	AIAVAEGTDRI	926	11	16	25						1009
ENV	AIAVAEGTDRV	926	11	14	22						1010
ENV	IAVAEGTDRII	927	11	15	23						1011
ENV	IAVAEGTDRVI	927	11	14	22						1012
ENV	PIRROGLERA	951	11	11	17						1013
ENV	RIROGLERALL	953	11	33	52						1014
GAG	SVLSGGEL	6	8	11	17						1015
GAG	SVLSGGKL	6	8	28	44						1016
GAG	KLDWWEKI	12	8	18	28						1017
GAG	KLDKWEKI	12	8	10	16						1018
GAG	DAWEKIRL	14	8	17	27						1019
GAG	KLKHIWVA	31	8	13	20						1020
GAG	RLKHIWVA	31	8	17	27						1021
GAG	IWVASREL	35	8	21	33						1022
GAG	LWVASREL	35	8	36	56						1023
GAG	FALNPGLL	46	8	22	34						1024
GAG	FAVNPGLL	46	8	16	25						1025
GAG	QLQPALQT	65	8	17	27						1026
GAG	QLQPSLQT	65	8	15	23						1027
GAG	LQTGSEEL	70	8	17	27						1028

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	GTEELRSL	73	8	12	19						1029
GAG	ELRSLYNT	76	8	17	27						1030
GAG	SLFNIVAT	79	8	16	25						1031
GAG	SLYNTIVAT	79	8	22	34						1032
GAG	TVATLYCV	83	8	41	64						1033
GAG	DVKITKEA	95	8	11	17						1034
GAG	EVKDTKEA	95	8	22	34						1035
GAG	AQQAADT	132	8	10	16						1036
GAG	AQQAADT	132	8	01	33						1037
GAG	KVSGNYPI	148	8	15	27						1038
GAG	QVSGNYPI	148	8	27	48						1039
GAG	VQNAQQQM	156	8	21	33						1040
GAG	VQNLQGM	156	8	29	45						1041
GAG	GQNVIIQAI	161	8	28	44						1042
GAG	IIQAISPT	165	8	29	45						1043
GAG	IIQAISPT	165	8	11	17						1044
GAG	QAISPTIL	166	8	29	45						1045
GAG	QAISPTIL	166	8	11	17						1046
GAG	TLNAWVKV	172	8	61	95						1047
GAG	KAFSEPI	183	8	50	78						1048
GAG	EVIPMFSA	188	8	46	72						1049
GAG	EVIPMFSA	188	8	14	22						1050
GAG	VIIPMFSA	189	8	46	72						1051
GAG	VIIPMFSA	189	8	14	22						1052
GAG	FTALSEGA	193	8	15	23						1053
GAG	SALSEGA	194	8	44	69						1054
GAG	TALSEGA	194	8	15	23						1055
GAG	ATPQDLNM	200	8	12	19						1056
GAG	ATPQDLNT	200	8	42	66						1057
GAG	PQDLNML	202	8	12	19						1058
GAG	PQDLNML	202	8	43	67						1059
GAG	DLNMLNI	204	8	12	19						1060
GAG	DLNTVLNT	204	8	44	69						1061
GAG	NIVGGIQA	210	8	12	19						1062
GAG	NTVGGIQA	210	8	47	73						1063
GAG	TVGGIQA	211	8	12	19						1064
GAG	TVGGIQA	211	8	47	73						1065
GAG	HQAAMQML	215	8	61	95						1066
GAG	AMQNLKDT	218	8	33	52						1067
GAG	AMQNLKET	218	8	26	41						1068
GAG	MQMLKDTI	219	8	33	52						1069
GAG	MQMLKETI	219	8	26	41						1070
GAG	DTINSEAA	224	8	33	52						1071
GAG	ETINSEAA	224	8	22	34						1072
GAG	EAAEWDRV	229	8	39	61						1073
GAG	EAAEWDRV	229	8	15	23						1074
GAG	PVHAGPIA	238	8	55	86						1075
GAG	DIAGTTST	256	8	55	86						1076
GAG	IAGTTSTL	257	8	48	75						1077
GAG	STLQEQA	262	8	12	19						1078

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
GAG	LQEQIAWM	264	8	14	22						1079
GAG	LQEQIGWM	264	8	29	45						1080
GAG	WMTNPPH	270	8	20	31						1081
GAG	WMTSNPPH	270	8	16	25						1082
GAG	DIYKRWH	284	8	17	27						1083
GAG	EYKRWH	284	8	39	61						1084
GAG	ILGLNKI	290	8	57	89						1085
GAG	ILGLNKIV	291	8	58	91						1086
GAG	GLNKLIVRM	293	8	60	94						1087
GAG	IVRMYSPT	297	8	15	23						1088
GAG	IVRMYSPT	297	8	42	66						1089
GAG	RMYSPTSI	299	8	14	22						1090
GAG	RMYSPTSI	299	8	40	63						1091
GAG	YVDNFKT	320	8	28	44						1092
GAG	YVDNFKT	320	8	28	44						1093
GAG	YVDNFKT	326	8	54	84						1094
GAG	YVDNFKT	327	8	35	55						1095
GAG	YVDNFKT	334	8	11	17						1096
GAG	YVDNFKT	334	8	15	23						1097
GAG	YVDNFKT	334	8	18	28						1098
GAG	YVDNFKT	340	8	22	34						1099
GAG	YVDNFKT	340	8	37	58						1100
GAG	YVDNFKT	343	8	22	34						1101
GAG	YVDNFKT	343	8	37	58						1102
GAG	YVDNFKT	349	8	45	70						1103
GAG	YVDNFKT	357	8	16	25						1104
GAG	YVDNFKT	359	8	16	25						1105
GAG	YVDNFKT	360	8	16	25						1106
GAG	YVDNFKT	360	8	18	28						1107
GAG	YVDNFKT	363	8	16	25						1108
GAG	YVDNFKT	364	8	16	25						1109
GAG	YVDNFKT	364	8	10	16						1110
GAG	YVDNFKT	364	8	29	45						1111
GAG	YVDNFKT	365	8	46	72						1112
GAG	YVDNFKT	366	8	11	17						1113
GAG	YVDNFKT	366	8	46	72						1114
GAG	YVDNFKT	370	8	60	94						1115
GAG	YVDNFKT	383	8	57	89						1116
GAG	YVDNFKT	387	8	17	27						1117
GAG	YVDNFKT	387	8	36	57						1118
GAG	YVDNFKT	394	8	10	16						1119
GAG	YVDNFKT	433	8	18	28						1120
GAG	YVDNFKT	433	8	13	20						1121
GAG	YVDNFKT	433	8	21	33						1122
GAG	YVDNFKT	466	8	57	89						1123
GAG	YVDNFKT	480	8	02	100						1124
GAG	YVDNFKT	487	8	10	16						1125
GAG	YVDNFKT	487	8	28	44						1126
GAG	YVDNFKT	543	8	14	22						1127
GAG	YVDNFKT	543	8	11	17						1128

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	PLASLKSL	548	8	15	23						1129
GAG	PLTSLKSL	548	8	12	19						1130
GAG	PLTSLRSL	548	8	12	19						1131
GAG	SLFGNDPL	554	8	12	19						1132
GAG	SLFGSDPL	554	8	11	17						1133
GAG	VLGGKSLDA	7	9	15	23						1134
GAG	HLVWASREL	34	9	21	33						1135
GAG	HLVWASREL	34	9	36	56						1136
GAG	ALNPILLET	47	9	19	30						1137
GAG	AVNPILLET	47	9	14	22						1138
GAG	ETSEGRQRI	54	9	16	25						1139
GAG	ILGQLQPSL	62	9	11	17						1140
GAG	QQLQPSLOT	64	9	11	17						1141
GAG	LQALQTGT	66	9	14	22						1142
GAG	SLOTISEEL	69	9	14	22						1143
GAG	ELRSLYNIV	76	9	15	23						1144
GAG	SLNTIVATL	79	9	16	25	0.0037					1145
GAG	SLNTIVATL	79	9	22	34	0.0053				0.0004	1146
GAG	NIVATLYCV	82	9	41	64						1147
GAG	TLVCYIIQRI	86	9	12	19						1148
GAG	TLVCYIIQRI	86	9	15	23						1149
GAG	IIORIEVKDT	91	9	10	16						1150
GAG	DVKDTKEAL	95	9	11	17						1151
GAG	EVKDTKEAL	95	9	20	31						1152
GAG	DTKEALDKI	98	9	32	50						1153
GAG	DTKEALEKI	98	9	10	16						1154
GAG	EQNKSKKKA	109	9	17	27						1155
GAG	KAQQAADT	118	9	10	16						1156
GAG	SQVSQNYPI	146	9	22	44						1157
GAG	KVSQNYPIV	148	9	15	27						1158
GAG	QVSQNYPIV	148	9	27	48						1159
GAG	IVQNAQGM	155	9	21	33	0.0001					1160
GAG	VQNLAQGM	155	9	29	45						1161
GAG	VQNAQGMV	156	9	14	22						1162
GAG	VQNLAQGMV	156	9	29	45						1163
GAG	AQGMVVIQA	159	9	12	19						1164
GAG	LOQMVIQIA	159	9	21	33						1165
GAG	IIQALSPRTL	165	9	29	45						1166
GAG	IIQALSPRTL	165	9	11	17						1167
GAG	ALSPRTLNA	167	9	29	45						1168
GAG	ALSPRTLNA	167	9	10	16						1169
GAG	RTLNWVKV	171	9	61	95						1170
GAG	TLNAWVKV	171	9	30	47						1171
GAG	TLNAWVKV	172	9	31	48	0.0012					1172
GAG	WVKVVEKA	172	9	25	39	0.0032					1173
GAG	WVKVVEKA	176	9	28	44	0.0005					1174
GAG	EVIPMFAL	188	9	46	72						1175
GAG	EVIPMFAL	188	9	14	22	0.0001					1176
GAG	FTALSEGAT	193	9	15	23						1177
GAG	GATPQDLNM	199	9	12	19						1178

Table VIII
HIV A12 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
GAG	GATPQDLNT	199	9	42	66						1179
GAG	ATPQDLNMM	200	9	12	19						1180
GAG	ATPQDLNTM	200	9	42	66						1181
GAG	DLNMMNLIV	204	9	12	19						1182
GAG	DLNTMLNTV	204	9	42	66	0.0001					1183
GAG	NIVGGHIQAA	210	9	12	19						1184
GAG	NTVGGHIQAA	210	9	47	73						1185
GAG	IVGGHIQAA	211	9	12	19						1186
GAG	TVGGHIQAA	211	9	47	73						1187
GAG	AAMQMLKDT	217	9	33	52						1188
GAG	AAMQMLKET	217	9	26	41						1189
GAG	AMQMLKDTI	218	9	33	52						1190
GAG	AMQMLKETI	218	9	26	41						1191
GAG	DIAGTTSTL	256	9	48	75	0.0001					1192
GAG	TTSTLQEQI	260	9	45	71						1193
GAG	TLQEQIAWM	263	9	12	19						1194
GAG	TLQEQIGWM	263	9	27	42						1195
GAG	LQEQIAWMT	264	9	14	22						1196
GAG	LQEQIGWMT	264	9	29	45						1197
GAG	MTNPPPIV	271	9	20	31	0.0300	0.0006	0.3000	0.0023	3.3000	1198
GAG	MTSNPPPIV	271	9	16	25						1199
GAG	DIYKRWHIL	284	9	17	27						1200
GAG	WILGLNKL	289	9	37	58	0.0001					1201
GAG	WILGLNKL	289	9	57	89	0.0091					1202
GAG	ILGLNKLIV	290	9	57	89	0.0003					1203
GAG	KIVRMYSPT	296	9	15	23						1204
GAG	KIVRMYSPIV	296	9	41	64						1205
GAG	RMYSPTSIL	299	9	14	22	0.0007					1206
GAG	RMYSPIVSI	299	9	40	63						1207
GAG	YVDRFETL	320	9	27	42						1208
GAG	YVDRFYKTL	320	9	28	44						1209
GAG	KTLRAEQAT	326	9	34	53	0.0010					1210
GAG	RAEQASQEV	329	9	12	19						1211
GAG	RAEQATQDV	329	9	15	23						1212
GAG	RAEQATQEV	329	9	27	42						1213
GAG	ATQDVKNWM	333	9	15	23						1214
GAG	ATQEVKNWM	333	9	18	28						1215
GAG	SQEVKNWMT	334	9	11	17						1216
GAG	TQEVKNWMT	334	9	15	23						1217
GAG	TQEVKNWMT	334	9	18	28						1218
GAG	DVKNWMTDT	336	9	12	19						1219
GAG	DVKNWMTET	336	9	12	19						1220
GAG	NANPDCKSI	349	9	25	39						1221
GAG	NANPDCKTI	349	9	11	17						1222
GAG	TILKALGPA	356	9	45	70						1223
GAG	ILKALGPAA	357	9	16	25	0.0001					1224
GAG	ILKALGPAA	357	9	16	25						1225
GAG	KALGPAATL	359	9	18	28						1226
GAG	KALGPAATL	359	9	16	25	0.0001					1227
GAG	PAATLEEMM	363	9	16	25						1228

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
GAG	ATLEEMMT	364	9	16	25						1229
GAG	GASLEEMMT	364	9	10	16						1230
GAG	ATLEEMMT	364	9	28	44						1231
GAG	ATLEEMMTA	365	9	46	72						1232
GAG	EMMTACQGV	369	9	59	92	0.0006					1233
GAG	GVGGPGHKA	376	9	37	58						1234
GAG	GVGGPSIKA	376	9	23	36						1235
GAG	KARVLAEAM	383	9	57	89						1236
GAG	VLAELMSQA	386	9	16	25						1237
GAG	VLAELMSQV	386	9	33	52						1238
GAG	LAEAMSOVT	387	9	23	37	0.1100					1239
GAG	AMSOVTNSA	390	9	11	17						1240
GAG	CTERQANFL	459	9	55	87						1241
GAG	RQANFLGKI	465	9	56	88						1242
GAG	FLOKRPET	486	9	10	16						1243
GAG	FLOSRPMT	486	9	28	44						1244
GAG	LQNRPTA	487	9	10	16	0.0004		0.3100	0.0002	0.0130	1245
GAG	LQNRPTA	487	9	10	16						1246
GAG	PAETPTA	492	9	28	44						1247
GAG	KQEPIDKEL	531	9	01	50						1248
GAG	PIDKFLYPL	534	9	12	19						1249
GAG	KQEPIDKEL	535	9	01	19						1250
GAG	KQETIDKDL	535	9	01	25						1251
GAG	MDKELYP	538	9	01	25						1252
GAG	TIDKILYPL	538	9	01	25						1253
GAG	RASVLSGGEL	4	10	11	17						1254
GAG	RASVLSGGKL	6	10	28	44						1255
GAG	SVLSGGKLD	6	10	15	23						1256
GAG	KLDKWEKRL	12	10	16	25						1257
GAG	KLDKWEKRL	12	10	10	16						1258
GAG	WASRELERPA	37	10	44	69						1259
GAG	FALNPGLLLET	46	10	18	28						1260
GAG	FALNPGLLLET	46	10	14	22						1261
GAG	ETSEGCROIL	54	10	14	22						1262
GAG	QILGQLQPSL	61	10	11	17						1263
GAG	QLQPALQIGT	65	10	14	22						1264
GAG	QTGSEELRSL	71	10	12	19						1265
GAG	ELRSLYNTVA	76	10	15	23						1266
GAG	ATLYCVIIOKI	85	10	12	19						1267
GAG	ATLYCVIIOKI	85	10	15	23						1268
GAG	RIEVKDTKEA	93	10	13	20						1269
GAG	GAAATDSNI	123	10	01	50						1270
GAG	AAGTGNSSQV	130	10	01	50						1271
GAG	SONYPIVON	146	10	22	44						1272
GAG	SONYPIVON	150	10	22	34						1273
GAG	SONYPIVONL	150	10	30	47						1274
GAG	PIVQNAQQGM	154	10	21	33						1275
GAG	PIVQNAQQGM	154	10	29	45						1276
GAG	IVQNLQGMV	155	10	14	22						1277
GAG	IVQNLQGMV	155	10	29	45						1278

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
GAG	NAQGQMVIHQ	158	10	12	19						1279
GAG	NLGGQMVIIQA	158	10	21	33						1280
GAG	LQGMVYIQA	159	10	15	23						1281
GAG	MVHQVISPRT	163	10	27	42						1282
GAG	QALSPRTINA	166	10	29	45						1283
GAG	QALSPRTINA	166	10	10	16						1284
GAG	RTLNAWVKVI	171	10	30	47						1285
GAG	RTLNAWVKV	171	10	31	48						1286
GAG	KAFSEVIVM	183	10	50	78	0.0003					1287
GAG	PMFSALSEGA	191	10	45	70						1288
GAG	PMFTALSEGA	191	10	15	23						1289
GAG	GATPQDLNMM	199	10	12	19						1290
GAG	GATPQDLNMM	199	10	42	66						1291
GAG	ATPQDLNMM	200	10	12	19						1292
GAG	ATPQDLNMM	200	10	42	66						1293
GAG	PQDLNMMMLN	202	10	11	17						1294
GAG	PQDLNMMMLN	202	10	43	67						1295
GAG	MLNIVGGIIQA	208	10	12	19						1296
GAG	MLNIVGGIIQA	208	10	47	73	0.0022					1297
GAG	NIVGGIIQAAM	210	10	12	19						1298
GAG	NTVGGIIQAAM	210	10	47	73						1299
GAG	QAAMQMLKDT	216	10	33	52						1300
GAG	QAAMQMLKET	216	10	26	41						1301
GAG	AAMQMLKDTI	217	10	33	52						1302
GAG	AAMQMLKETI	217	10	26	41						1303
GAG	MLKDTINEEA	221	10	32	50						1304
GAG	MLKDTINEEA	221	10	22	34						1305
GAG	AAEWDRLIIPV	230	10	34	53						1306
GAG	AAEWDRVIIPV	230	10	14	22						1307
GAG	RLIIPVIAQPI	235	10	22	34						1308
GAG	RLIIPVIAQPI	235	10	14	22						1309
GAG	IIAGPIAPGQM	240	10	18	28						1310
GAG	IIAGPIPGQM	240	10	17	27						1311
GAG	QMRPGSDI	248	10	44	69						1312
GAG	GTSTLQEQI	259	10	45	70						1313
GAG	TTSTLQEQIA	260	10	11	17						1314
GAG	STLQEQIAWM	262	10	12	19						1315
GAG	STLQEQIAWM	262	10	27	42						1316
GAG	TLQEQIAWMT	263	10	12	19						1317
GAG	TLQEQIAWMT	263	10	27	42						1318
GAG	WMTNHPPIPV	270	10	20	31						1319
GAG	WMTNHPPIPV	270	10	16	25						1320
GAG	GANSIPVQDI	276	10	01	50						1321
GAG	PVGDITKRWI	281	10	17	27						1322
GAG	PVGEIARRWI	281	10	40	63						1323
GAG	WIILGLNKIV	289	10	57	89						1324
GAG	ILGLNKIVRM	291	10	57	89	0.0009					1325
GAG	IVRMYSPTSI	297	10	14	22	0.0010					1326
GAG	IVRMYSPTSI	297	10	40	63						1327
GAG	QASQEVKNWM	332	10	11	17						1328

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*GR02	SEQ ID NO
GAG	QATQDVKNWM	332	10	15	23						1329
GAG	QATQEVKNWM	332	10	18	28						1330
GAG	ATQDVKNWMT	333	10	15	23						1331
GAG	ATQEVKNWMT	333	10	18	28						1332
GAG	DVKNWMTDTL	336	10	12	19						1333
GAG	DVKNWMTETL	336	10	11	17						1334
GAG	EVKNWMTETL	336	10	25	39						1335
GAG	MTDTLLVQNA	341	10	22	34						1336
GAG	MTETLLVQNA	341	10	36	56						1337
GAG	VQNAIPDCKT	347	10	45	70						1338
GAG	NANPICKSIL	349	10	11	17						1339
GAG	NANPECKTIL	349	10	45	70						1340
GAG	KTILKALGPA	355	10	16	25						1341
GAG	TILKALGPA	356	10	16	25						1342
GAG	TILRALGPGA	356	10	13	20						1343
GAG	ILKALGPAAT	357	10	16	25						1344
GAG	PAATLEHMIT	363	10	16	25						1345
GAG	AATLEHMITA	364	10	16	25						1346
GAG	GASLEHMITA	364	10	10	16						1347
GAG	GATLEHMITA	364	10	28	44						1348
GAG	RVLAEMSQA	385	10	16	25						1349
GAG	RVLAEMSQT	385	10	33	52	0.0058					1350
GAG	VLAEMSQT	386	10	20	31						1351
GAG	EAMSVTNSA	389	10	11	17						1352
GAG	AMSVTNSAT	390	10	10	16						1353
GAG	QMKDCTERQA	455	10	49	77						1354
GAG	FQNRPEPTA	486	10	10	16						1355
GAG	FQSRPEPTA	486	10	28	44						1356
GAG	PAESFEET	511	10	02	67						1357
GAG	TTHSQKQET	522	10	09	45	0.0013					1358
GAG	ETDKDLYPL	537	10	01	25						1359
GAG	PIDKELYPL	538	10	01	25						1360
GAG	RTENSLYPL	538	10	01	25						1361
GAG	TIDKLYPLA	538	10	01	25						1362
GAG	WASRELERFAL	37	11	22	34						1363
GAG	WASRELERFV	37	11	17	27						1364
GAG	ELERFALNPGL	42	11	14	22						1365
GAG	ELERFVNPGL	42	11	15	23						1366
GAG	LLETSEGCRQI	52	11	16	25						1367
GAG	ROIIGQLOPSL	60	11	11	17						1368
GAG	LQTGSIELNSL	70	11	11	17						1369
GAG	ELRSLYNTVAT	76	11	13	20						1370
GAG	VATLYCVIIQKI	84	11	12	19						1371
GAG	VATLYCVIIQRI	84	11	15	23						1372
GAG	RIEVKETKEAL	93	11	12	19						1373
GAG	PIVQNAQQGMV	154	11	14	22						1374
GAG	PIVQNLQQGMV	154	11	29	45						1375
GAG	NLQGMVHIQAI	158	11	15	23						1376
GAG	QMVIIQAIISPT	162	11	27	42						1377
GAG	MVHIQAIISPTL	163	11	27	42						1378

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SHQ ID NO
GAG	IIQISPRTLNA	165	11	29	45						1379
GAG	IIQALSPRTLNA	165	11	10	16						1380
GAG	ALSPRTLNAWV	167	11	29	45						1381
GAG	ALSPRTLNAWV	167	11	10	16						1382
GAG	NAWVKVVEEKA	174	11	25	39						1383
GAG	NAWVKVVEEKA	174	11	27	42						1384
GAG	VIEEKAFSPREV	179	11	20	31						1385
GAG	VVEEKAFSPREV	179	11	28	44						1386
GAG	PMFSALSEGAT	191	11	44	69						1387
GAG	PMFTALSEGAT	191	11	15	23						1388
GAG	ALSEGATIQDL	195	11	58	91						1389
GAG	GATPQDLNML	199	11	12	19						1390
GAG	GATPQDLNML	199	11	42	66						1391
GAG	PQDLNMLNIV	202	11	11	17						1392
GAG	PQDLNMLNIV	202	11	41	64						1393
GAG	MMLNIVGGIIQA	207	11	12	19						1394
GAG	TMLNTVGGIIQA	207	11	43	67						1395
GAG	MLNIVGGIIQA	208	11	12	19						1396
GAG	MLNIVGGIIQA	208	11	47	73						1397
GAG	IVGGIIQAAMQM	211	11	11	17						1398
GAG	TVGGIIQAAMQM	211	11	47	73						1399
GAG	IIQAAMQMLKDT	215	11	33	52						1400
GAG	IIQAAMQMLKET	215	11	26	41						1401
GAG	QAAMQMLKETI	216	11	33	52						1402
GAG	QAAMQMLKETI	216	11	26	41						1403
GAG	QMLKDTINEEA	220	11	32	50						1404
GAG	QMLKETINEEA	220	11	22	34						1405
GAG	MLKDTINEEA	221	11	32	50						1406
GAG	MLKETINEEA	221	11	22	34						1407
GAG	EAAEWIRLIIPV	229	11	34	53						1408
GAG	EAAEWIRLIIPV	229	11	14	22						1409
GAG	RLHIPVIAAGPIA	235	11	15	23						1410
GAG	QOMREPRGSDI	247	11	44	69						1411
GAG	QMRPRIGSDIA	248	11	44	69						1412
GAG	GTISTLQIQIA	259	11	11	17						1413
GAG	STLQEQIAWMT	262	11	12	19						1414
GAG	STLQEQIGWMT	262	11	27	42						1415
GAG	QIGWMTNPPH	267	11	18	29						1416
GAG	QIGWMTSNPPI	267	11	10	16						1417
GAG	PVGDII'KRWII	281	11	17	27						1418
GAG	PVGEIYKRWII	281	11	39	61						1419
GAG	DIYKRWIIIGL	284	11	17	27						1420
GAG	EYKRWIIIGL	284	11	37	58						1421
GAG	IILGLNKIVRM	290	11	56	88						1422
GAG	KIVRMYSPTSI	296	11	14	22						1423
GAG	KIVRMYSPTSI	296	11	39	61						1424
GAG	IVRMYSPTSIL	297	11	14	22						1425
GAG	IVRMYSPTSIL	297	11	40	63						1426
GAG	RMYSPTSILDI	299	11	13	20						1427
GAG	RMYSPTSILDI	299	11	38	59						1428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6R02	SEQ ID NO
GAG	YVDRFFKTLRA	320	11	27	42						1429
GAG	YVDRFYKTLRA	320	11	28	44						1430
GAG	TLRAEQASQEV	327	11	12	19						1431
GAG	TLRAEQATQDV	327	11	11	17						1432
GAG	TLRAEQATQEV	327	11	24	38						1433
GAG	EQASQEVKNWM	331	11	11	17						1434
GAG	EQATQDVKNWM	331	11	15	23						1435
GAG	EQATQEVKNWM	331	11	18	28						1436
GAG	QASQEVKNWMT	332	11	11	17						1437
GAG	QATQDVKNWMT	332	11	15	23						1438
GAG	QATQEVKNWMT	332	11	18	28						1439
GAG	QEVKNWMTET	334	11	11	17						1440
GAG	TQDVKNWMTDT	334	11	11	17						1441
GAG	TQEVKNWMTET	334	11	14	22						1442
GAG	QVKNWMTDTLL	336	11	12	19						1443
GAG	QVKNWMTETLL	336	11	11	17						1444
GAG	EVKNWMTETLL	336	11	25	39						1445
GAG	WMTDTLLVQNA	340	11	22	34						1446
GAG	WMTETLLVQNA	340	11	35	55						1447
GAG	LVQNAVPDCKT	346	11	45	70						1448
GAG	VQNAVPDCKSI	347	11	10	16						1449
GAG	VQNAVPDCKTI	347	11	45	70						1450
GAG	KTILKALGPA	355	11	16	25						1451
GAG	KTILKALGGA	355	11	13	20						1452
GAG	TLKALGPAAT	356	11	16	25						1453
GAG	ILKALGPAATL	357	11	16	25						1454
GAG	ALGPAATLEEM	360	11	16	25						1455
GAG	ALGPAATLEEM	360	11	17	27						1456
GAG	PAATLEEMMTA	363	11	16	25						1457
GAG	QGVGGPGHIKA	374	11	36	56						1458
GAG	QGVGGPGSIKA	374	11	23	36						1459
GAG	GVGGPGHIKARV	376	11	36	56						1460
GAG	GVGGPGHIKARV	376	11	19	30						1461
GAG	RVLAEAMSOVT	385	11	20	31						1462
GAG	EAMSOVTRSAT	389	11	10	16						1463
GAG	SAQQDLKGGYT	393	11	01	50						1464
GAG	TAQQDLKGGYT	393	11	01	50						1465
GAG	HQMKDCTERQA	454	11	49	77						1466
GAG	PAEPTAPPAEI	492	11	01	50						1467
GAG	PAESFRFEET	511	11	02	67						1468
GAG	SQKQENDKEL	529	11	09	15						1469
GAG	ETIDKILYPLA	537	11	01	25						1470
GAG	RTENSILYPLT	538	11	01	25						1471
GAG	SLKSLFGNDPL	551	11	12	19						1472
NEF	RAQAEPA	32	8	01	17						1473
NEF	AAQAEPA	33	8	01	17						1474
NEF	PAADGVGA	41	8	15	23						1475
NEF	PAAGVGGA	41	8	21	33						1476
NEF	AADGVGAV	42	8	11	18						1477
NEF	AAEGVGAA	42	8	10	16						1478

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
NEF	AIEGVGAV	42	8	17	28						1479
NEF	DLEKIIGAI	57	8	14	22						1480
NEF	GAITSNT	62	8	32	50						1481
NEF	GALTSSNT	62	8	10	16						1482
NEF	AITSSNTA	63	8	27	42						1483
NEF	ITSSNTAA	64	8	15	23						1484
NEF	AAINADCA	70	8	12	22						1485
NEF	EAQEEVEV	82	8	16	25						1486
NEF	PVRPQVPL	95	8	48	75						1487
NEF	QVPLRPM	99	8	56	88						1488
NEF	QVPLRPM	100	8	57	89	0.0001					1489
NEF	ALDLSHFL	111	8	11	17						1490
NEF	AVDLSHFL	111	8	15	23						1491
NEF	FLKEKGGL	117	8	56	88						1492
NEF	SQKRQDIL	177	8	12	19						1493
NEF	QTEPAAGV	32	9	01	17						1494
NEF	RAEPAAGV	32	9	01	17						1495
NEF	RAQAEPA	32	9	01	17						1496
NEF	RTEPAAGV	32	9	01	17						1497
NEF	QAEPAAGV	33	9	01	17						1498
NEF	QAETAAGV	34	9	01	33						1499
NEF	QAEPAAGV	41	9	11	17						1500
NEF	PAADGVGAV	41	9	12	19						1501
NEF	PAEGVGAV	41	9	12	19						1502
NEF	GVGAASQDL	45	9	11	17						1503
NEF	GVGAVSQDL	45	9	21	33	0.0001					1504
NEF	GVGAVSRDL	45	9	17	27						1505
NEF	DLEKIIGAIT	57	9	14	22						1506
NEF	GAITSNTA	62	9	27	42						1507
NEF	AITSSNTA	63	9	14	22						1508
NEF	ITSSNTAAT	64	9	13	20						1509
NEF	TAATNADCA	69	9	12	19						1510
NEF	ATNALCAWL	71	9	12	22						1511
NEF	NADCAWLEA	73	9	17	27						1512
NEF	POVPLRPM	99	9	56	88						1513
NEF	PLRPMTYKA	102	9	21	33						1514
NEF	MTYKGAHIL	106	9	12	19						1515
NEF	GAFDLSHFL	110	9	10	16						1516
NEF	RQILDILWV	182	9	20	31						1517
NEF	RQILDILWV	182	9	35	55						1518
NEF	ILDLWVYIT	186	9	34	53						1519
NEF	ILDLWVYIT	186	9	19	30						1520
NEF	LTFGACFKL	221	9	39	61						1521
NEF	LVPVDPREV	239	9	11	17						1522
NEF	KQAEPAAGV	32	10	01	17						1523
NEF	RQAEPAAGV	32	10	01	17						1524
NEF	QAETAAAGV	33	10	01	17						1525
NEF	GAITSNTAA	62	10	14	22						1526
NEF	AITSSNTAAT	63	10	13	20						1527
NEF	NTAATNADCA	68	10	12	19						1528

Table VIII
 HIV-1 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
NEF	AATNADCAWL	70	10	12	22						1529
NEF	WLEAQEEVEV	79	10	15	24						1530
NEF	EVGFVRPQV	91	10	40	63						1531
NEF	PLRMITYKAA	102	10	20	31						1532
NEF	PLRMITYKGA	102	10	25	39						1533
NEF	PMYKGAFDL	105	10	12	19						1534
NEF	LIYSKKRQEI	174	10	18	28						1535
NEF	SOKRQDILD	177	10	12	19						1536
NEF	DILDWVYIT	185	10	12	19						1537
NEF	EILDWVYIT	185	10	22	34						1538
NEF	EILDWVYNT	185	10	11	17						1539
NEF	WQNYTRGCI	204	10	18	29						1540
NEF	WQNYTRGCI	204	10	21	33						1541
NEF	WQNYTRGCI	204	10	11	17						1542
NEF	PLTEGWCHL	219	10	39	61	0.0150	0.0038	0.0021	0.0010	0.8400	1543
NEF	LTGWCWFKLV	221	10	35	55	0.0170	0.0880	0.0560	0.0640	6.5000	1544
NEF	KLVPVDPHEV	228	10	11	17						1545
NEF	LLIIPICQIGM	257	10	10	16						1546
NEF	LLIIPMSQIGM	257	10	12	19						1547
NEF	QTEPAAGVGA	32	11	01	17						1548
NEF	RAEPAADGVGA	32	11	01	17						1549
NEF	RAQAEPAAGV	32	11	01	17						1550
NEF	RTEPAAGVGA	32	11	01	17						1551
NEF	QAEPAAGVGA	33	11	01	17						1552
NEF	QAFTAAGVGA	33	11	01	17						1553
NEF	QAEPAAGVGA	34	11	01	33						1554
NEF	AVSRDLEKIGA	48	11	11	17						1555
NEF	GAITSSNTAAT	62	11	13	20						1556
NEF	ITSSNTAATNA	64	11	12	19						1557
NEF	TAATNADCAWL	69	11	12	19						1558
NEF	ATNADCAWLEA	71	11	12	22						1559
NEF	AQEEVEGEPV	83	11	17	27						1560
NEF	PVRPQVPLRPM	95	11	47	73						1561
NEF	QVPLRPMITYKA	100	11	20	31						1562
NEF	FLKEKGGLDGL	117	11	26	41						1563
NEF	FLKEKGGLGL	117	11	29	45						1564
NEF	GLYSKKRQEI	173	11	18	28						1565
NEF	LYSKKRQEI	174	11	18	28						1566
NEF	YTPGGRIRYL	207	11	16	25						1567
NEF	YTPGGRIRFL	207	11	13	20						1568
NEF	PLTFGWCFKL	219	11	35	55						1569
NEF	CLLIIPMSQIGM	256	11	10	16						1570
POL	LAFPGGEA	6	8	12	19						1571
POL	LAFPGKA	6	8	12	19						1572
POL	LAFQGEA	6	8	16	25						1573
POL	QTRANSPT	21	8	28	45						1574
POL	PTRELSQV	30	8	14	22						1575
POL	QTRANSPT	35	8	01	33						1576
POL	PTRELSQV	36	8	01	33						1577
POL	GADRQGV	70	8	01	20						1578

Table VIII
HIV A12 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GTLNCPQI	80	8	01	33						1579
POL	PTFNFPQI	80	8	01	33						1580
POL	ITLWQRPL	90	8	47	73						1581
POL	TLWQRPLV	91	8	49	77						1582
POL	WQRPLVTI	93	8	21	33						1583
POL	WQRPLVTV	93	8	19	30						1584
POL	TIKIGQOL	99	8	17	27						1585
POL	TVKIGGOL	99	8	11	17						1586
POL	GQLEALL	104	8	10	16						1587
POL	GQLKEALL	104	8	34	53						1588
POL	LIEALLDT	106	8	10	16						1589
POL	EALLDTGA	108	8	61	95						1590
POL	DTGADDTV	112	8	63	98						1591
POL	TVLEEDNL	118	8	13	20						1592
POL	TVLEEDNL	118	8	13	20						1593
POL	GIGGFIV	136	8	64	100						1594
POL	KVRCYDDI	142	8	41	64						1595
POL	RQYDQILI	144	8	20	31						1596
POL	RQYDQIMI	144	8	13	20						1597
POL	EICGHKAI	152	8	19	30						1598
POL	EICGKKAI	152	8	24	38						1599
POL	KAIGTVLV	157	8	48	75						1600
POL	VLVGFTPV	160	8	60	94						1601
POL	NIIGRNLL	170	8	53	83						1602
POL	NIIGRNML	170	8	26	41						1603
POL	IIGRNLLT	171	8	31	48						1604
POL	IIGRNMLT	171	8	26	41						1605
POL	LLTQIGCT	176	8	30	47						1606
POL	MLTQIGCT	176	8	21	33						1607
POL	MLTQIGCT	176	8	18	28						1608
POL	LTQIGCTL	177	8	10	16						1609
POL	LTQIGCTL	177	8	42	66						1610
POL	PSMETV	187	8	15	23						1611
POL	PVKLKIGIM	195	8	57	89						1612
POL	KVKQWPLT	207	8	36	58						1613
POL	LTEEKIKA	213	8	49	77						1614
POL	KIKALTEI	217	8	56	88						1615
POL	KIKALVEI	217	8	28	44						1616
POL	KALTEICT	219	8	15	23						1617
POL	KALVEICT	219	8	12	19						1618
POL	LVEICTEM	221	8	15	24						1619
POL	EMENEGKI	229	8	42	66						1620
POL	AIKKKDDT	251	8	59	92						1622
POL	STRWRKLV	257	8	59	92						1623
POL	KLVDFFEL	262	8	63	98						1624
POL	RTQDFWEV	272	8	55	86						1625
POL	QLGHPHPA	280	8	56	89						1626
POL	GIPIIPAGI	282	8	56	89						1627
POL	GLKKKKSV	288	8	52	81						1628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6K02	SEQ ID NO
POL	TVLDSGDA	296	8	58	91						1629
POL	DAYTSVPL	302	8	55	86						1630
POL	TAFTIPSI	317	8	37	58						1631
POL	TAFTIPST	317	8	13	20						1632
POL	GIRYQYNY	330	8	52	81						1633
POL	PAIFQSSM	346	8	42	66						1634
POL	AIQSSMT	347	8	39	61						1635
POL	FQSSMTKI	349	8	38	59						1636
POL	KONPDIVI	362	8	14	22						1637
POL	DIVIVQYM	366	8	18	28						1638
POL	EIVIVQYM	366	8	24	38						1639
POL	DLYVGSOL	375	8	63	98						1640
POL	YVGSDEI	377	8	58	91						1641
POL	HLLKWGFT	397	8	22	34						1642
POL	HLLRWGFT	397	8	25	39						1643
POL	LLKWGFTT	398	8	23	36						1644
POL	LLRWGFTT	398	8	24	38						1645
POL	IQKEPPL	410	8	62	97						1646
POL	FLWMGYEL	416	8	62	100						1647
POL	ELIPIKWT	422	8	64	94						1648
POL	WTQVQIVL	428	8	60	94						1649
POL	WTQVQIVL	428	8	28	44						1650
POL	TVNDIQKL	442	8	62	97						1651
POL	IQKLVGKL	446	8	62	97						1652
POL	LVGKLNWA	449	8	61	95						1653
POL	KLNWASOI	452	8	61	95						1654
POL	QIYAGIKV	458	8	27	43						1655
POL	QIYAGIKV	458	8	27	43						1656
POL	KVKQLCKL	464	8	29	45						1657
POL	KVRQLCKL	464	8	19	30						1658
POL	KLRLGAKA	470	8	25	40						1659
POL	KLRLGTKA	470	8	24	38						1660
POL	LLRGAKAL	471	8	30	47						1661
POL	LLRGTKAL	471	8	24	38						1662
POL	GAKALTDI	474	8	25	39						1663
POL	GTKALTEV	474	8	19	30						1664
POL	ALTDIVPL	477	8	21	33						1665
POL	ALTEVIPL	477	8	16	25						1666
POL	LTIDIVPLT	478	8	23	36						1667
POL	LTEVIPLT	478	8	16	25						1668
POL	IVPLTEEA	481	8	13	20						1669
POL	VIPLTEEA	481	8	11	17						1670
POL	PLTEEAEL	483	8	30	47						1671
POL	ELAENREI	491	8	57	89						1672
POL	LAENREIL	492	8	57	89						1673
POL	KQGQDQWT	523	8	15	23						1674
POL	KQGQGWWT	523	8	25	39						1675
POL	YQEPFKNL	534	8	43	67						1676
POL	NLKTGKYA	540	8	58	92						1677
POL	KTGKYAKM	542	8	19	30						1678

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	KTGRYARM	542	8	13	21						1679
POL	RTAHINDV	550	8	11	17						1680
POL	ITINDVKQL	553	8	49	77						1681
POL	DKVKQLTEA	556	8	33	52						1682
POL	LTEAVQKI	560	8	34	53						1683
POL	EAVQKIAT	562	8	11	17						1684
POL	KIATESIV	566	8	14	22						1685
POL	IATESIVI	567	8	14	22						1686
POL	SIVWIGKT	571	8	42	66						1687
POL	KLPQKET	582	8	20	31						1688
POL	RLPQKET	582	8	26	41						1689
POL	IQKETWEA	585	8	15	23						1690
POL	IQKETWET	585	8	27	42						1691
POL	ETWEAWWT	588	8	11	17						1692
POL	ETWETWWT	588	8	22	34						1693
POL	WTDYWQAT	594	8	15	23						1694
POL	WTIEYWQAT	594	8	24	38						1695
POL	WIPEWFEV	602	8	52	84						1696
POL	FVNTPLV	608	8	54	86						1697
POL	NTPLVLKL	610	8	57	89						1698
POL	LVKLWYQL	614	8	58	91						1699
POL	KLWYQLET	616	8	12	19						1700
POL	YQLEKDPH	619	8	14	22						1701
POL	YQLEKEPI	619	8	31	48						1702
POL	YQLETEPI	619	8	11	17						1703
POL	QLEKEPIV	620	8	16	25						1704
POL	ETFYVDGA	630	8	55	86						1705
POL	AANRETKL	637	8	30	47						1706
POL	KLGRKAGYV	643	8	36	56						1707
POL	RQKVVSILT	655	8	19	30						1708
POL	KVVSILTET	657	8	11	17						1709
POL	VVSLIDIT	658	8	10	16						1710
POL	VVSLTET	658	8	11	17						1711
POL	TINQKTEL	664	8	55	86						1712
POL	NQKTELIIA	666	8	12	19						1713
POL	NQKTELOA	666	8	42	66						1714
POL	ELQAIILA	670	8	16	25						1715
POL	ELQAIYLA	670	8	12	19						1716
POL	LQAIHIAL	671	8	16	25						1717
POL	LQAIYLAL	671	8	12	19						1718
POL	LALQDSGL	676	8	27	42						1719
POL	LQDSGLEV	678	8	27	42						1720
POL	LQDSGSEV	678	8	25	39						1721
POL	GLEVNIIVT	682	8	26	41						1722
POL	IVTDSQYA	687	8	61	95						1723
POL	VTDSSQYAL	688	8	59	92						1724
POL	SQYALGII	691	8	59	92						1725
POL	YALGIIQA	693	8	58	91						1726
POL	NQIEQLI	711	8	24	38						1727
POL	SQIEQLI	711	8	20	31						1728

Table VIII
 HIV Δ92 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	QLIKKEKV	716	8	28	44						1729
POL	WVPAIKGI	727	8	63	98						1730
POL	GIGNEQV	733	8	59	92						1731
POL	QVDRKLSA	739	8	16	25						1732
POL	SAGIRKVL	745	8	15	23						1733
POL	GIRKVLFL	747	8	51	80						1734
POL	KVLFLDGI	750	8	50	78						1735
POL	FLGDIDKA	753	8	55	86						1736
POL	AMASDFNL	773	8	45	70						1737
POL	IVAKEIV	782	8	26	41						1738
POL	PVVAKEIV	782	8	28	44						1739
POL	IVAKEIVA	783	8	26	41						1740
POL	VVAKEIVA	783	8	31	48						1741
POL	COLKGEAM	795	8	53	83						1742
POL	QVDCSTGI	805	8	57	89						1743
POL	GIWQLDCT	811	8	59	92						1744
POL	WQLDCTHL	813	8	61	95						1745
POL	CTHILEGKI	817	8	35	55						1746
POL	CTHILEGKV	817	8	26	41						1747
POL	ILLEKIL	819	8	31	48						1748
POL	ILLEGKVL	819	8	23	36						1749
POL	ILVAVIIV	824	8	30	47						1750
POL	VILVAVIIV	824	8	24	38						1751
POL	ILVAVIIVA	825	8	54	84						1752
POL	VASGYIEA	831	8	52	81						1753
POL	PAETCOIT	842	8	58	91						1754
POL	GQETAYFI	846	8	31	48						1755
POL	GQETAYFL	846	8	26	41						1756
POL	TAYIILKL	849	8	32	50						1757
POL	TAYFLKL	849	8	27	42						1758
POL	KLGRWIV	855	8	59	92						1759
POL	FTSAAVKA	873	8	28	44						1760
POL	FTSTTVKA	873	8	14	22						1761
POL	AACW-WAGI	880	8	32	50						1762
POL	GKQCEFGI	886	8	22	34						1763
POL	GKQCEFGI	886	8	11	17						1764
POL	SQGVVISM	899	8	53	83						1765
POL	DQAEHLKT	919	8	46	72						1766
POL	QAEHLKT	919	8	13	20						1767
POL	QAEHLKTA	920	8	59	92						1768
POL	IILKTAVQM	923	8	57	89						1769
POL	KTAVQMAV	925	8	57	89						1770
POL	AVQNAVFI	927	8	60	94						1771
POL	RIDDIAT	931	8	29	45						1772
POL	RIVDIAT	931	8	12	19						1773
POL	IISDIQT	955	8	15	23						1774
POL	IATDIQT	955	8	41	64						1775
POL	LQKHKI	965	8	13	20						1776
POL	LQKHKI	965	8	36	56						1777
POL	LLWKGECA	993	8	62	97						1778

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	VIQINSDI	1003	8	37	58						1779
POL	VIQINSEI	1003	8	12	19						1780
POL	KVIFRRKA	1011	8	52	81						1781
POL	KVIFRRKV	1011	8	11	17						1782
POL	OMAGIDCV	1027	8	44	69						1783
POL	MAGHDCVA	1028	8	44	69						1784
POL	NLAFFQGEA	5	9	10	16						1785
POL	NLAFFQGEA	5	9	16	25						1786
POL	EQTRANSPT	20	9	26	41						1787
POL	EQTRANSPT	34	9	01	33						1788
POL	OTRANSPTI	35	9	01	33						1789
POL	EAGADROGT	64	9	10	16						1790
POL	GQRQGTVSL	69	9	01	17						1791
POL	GTLNFPQI	79	9	01	17						1792
POL	ASL3LPQI	80	9	01	33						1793
POL	GTLNCPQIT	80	9	01	33						1794
POL	PTFNFPQIT	80	9	01	33						1795
POL	QITLWQRL	89	9	47	73						1796
POL	ITLWQRLPLV	90	9	47	73						1797
POL	TLWQRLPLV	91	9	39	61						1798
POL	VTIKIGGOL	98	9	17	27						1799
POL	VTIKIGGOL	98	9	11	17	0.0185	0.0002	0.0040	0.0002	0.0140	1800
POL	KIGGQLKEA	101	9	23	36						1801
POL	QLKEALLDT	105	9	10	16						1802
POL	QLKEALLDT	105	9	34	53						1803
POL	LLDTGADDT	110	9	63	98						1804
POL	DTGADDTVL	112	9	61	95						1805
POL	DTVLEBIL	117	9	13	20						1806
POL	DTVLEBIL	117	9	14	22						1807
POL	MIGGIGGFI	133	9	62	97						1808
POL	KVRQYDQIL	142	9	21	33	0.0025					1809
POL	LIEICGHKA	150	9	10	16	0.0001					1810
POL	LIEICGHKA	150	9	13	20						1811
POL	TVLVSTPVP	161	9	53	83						1812
POL	LVGPTFVNI	163	9	54	84	0.0047	0.0280	0.5200	0.0013	0.5900	1813
POL	PVNIIGRNL	168	9	26	41	0.0110					1814
POL	PVNIIGRNL	168	9	24	38	0.0001					1815
POL	NIIGRNMLT	170	9	26	41						1816
POL	NIIGRNMLT	170	9	30	47						1817
POL	NLLTQIGCT	175	9	21	33						1818
POL	NMLTQIGCT	175	9	18	28						1819
POL	NMLTQIGCT	175	9	10	16						1820
POL	LLTQIGCTL	176	9	21	33						1821
POL	MLTQIGCTL	176	9	18	28						1822
POL	MLTQIGCTL	176	9	10	16						1823
POL	TLNFPISH	183	9	61	97						1824
POL	PIETVPVKL	190	9	53	83	0.0660	0.0029	9.3000	0.0019	0.7000	1825
POL	PLTEEKIKAL	212	9	54	84	0.0001					1826
POL	LTEEKIKAL	213	9	56	88						1827
POL	ALVEICTEM	220	9	15	23	0.0230	0.0230	0.0710	0.0140	0.0140	1828

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*0202	Seq ID NO
POL	FAIKKKDST	250	9	59	92						1829
POL	TQDFVEVOL	273	9	55	86						1830
POL	VQLGRIIPA	279	9	54	84						1831
POL	GLKKKKSVT	288	9	49	77						1832
POL	VTVLIVGDA	295	9	57	89						1833
POL	DVGDAYFSV	299	9	54	84						1834
POL	YTAFTIPSI	316	9	37	58	0.1005	0.7100	1.1000	0.5300	2.4000	1835
POL	YTAFTIPST	316	9	13	20	0.1900					1836
POL	TIPSNNET	320	9	37	58						1837
POL	TIPSNNET	320	9	14	22						1838
POL	SINNETPGI	323	9	32	50						1839
POL	STNNETPGI	323	9	11	17						1840
POL	GIRYQYNVL	330	9	52	81	0.0001					1841
POL	PQGAKGSPA	339	9	59	92						1842
POL	PAIFQSSMT	346	9	39	61						1843
POL	FOSSMTKIL	349	9	38	59						1844
POL	VIVQYMDDL	368	9	51	80	0.0004					1845
POL	YQYMDILYV	370	9	61	95						1846
POL	DLEIGQIRA	381	9	28	44						1847
POL	DLEIGQIRT	381	9	21	33						1848
POL	EIGQIRAKI	383	9	26	41						1849
POL	EIGQIRTKI	383	9	21	33						1850
POL	KHEELREHL	390	9	19	30						1851
POL	KHEELROHL	390	9	17	27	0.0001					1852
POL	HLLKVGFTT	397	9	22	34						1853
POL	HLLRWGFTT	397	9	24	38						1854
POL	ELHFDKWTV	422	9	60	94	0.0001					1855
POL	QLPEKDSWT	434	9	13	20						1856
POL	VLEPKDSWT	434	9	13	20						1857
POL	WTNDIQKL	441	9	62	97						1858
POL	TVNDIQKL	442	9	61	95	0.0001					1859
POL	DIQKLVGKL	445	9	62	97	0.0001					1860
POL	KLVGELNWA	448	9	61	95	0.0001	0.3400	1.7000	0.0930	0.0130	1861
POL	WASCIYAGI	455	9	27	42	0.0040					1862
POL	WASCIYPGI	455	9	29	45	0.0020					1863
POL	SOIYAGIKV	457	9	27	42						1864
POL	SOIYAGIKV	457	9	27	42						1865
POL	YAGIRVKQL	460	9	18	28						1866
POL	KVKQLCKLL	464	9	28	44						1867
POL	KVRQCKLL	464	9	19	30						1868
POL	QLCKLLRGA	467	9	25	39						1869
POL	QLCKLLRGT	467	9	21	33						1870
POL	KLLRGAKAL	470	9	25	40						1871
POL	KLLRGAKAL	470	9	24	38						1872
POL	LLRGAKALT	471	9	30	47						1873
POL	LLRGAKALT	471	9	24	38						1874
POL	GAKALTDIV	474	9	24	38						1875
POL	GKALTEVI	474	9	11	17						1876
POL	KALTEVPL	476	9	21	33	0.1069					1877
POL	KALTEVIPL	476	9	16	25						1878

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	ALTDIVPLT	477	9	21	33						1879
POL	ALTEVPLT	477	9	16	25						1880
POL	DIVPLTEEA	480	9	13	20						1881
POL	EVPLTEEA	480	9	11	17						1882
POL	LTEEALEEL	484	9	37	58						1883
POL	ELAEAREIL	491	9	57	89	0.0001					1884
POL	ILKEPVIHV	498	9	41	64	0.0055					1885
POL	GDQWYQI	525	9	13	20						1886
POL	GKQWYQI	525	9	25	39						1887
POL	YAKMRTAIT	546	9	10	16						1888
POL	YAMRGAIT	546	9	13	20						1889
POL	HTNDVRLT	553	9	43	67						1890
POL	DVKQLTEAV	556	9	33	52	0.0001					1891
POL	QLTEAVOKI	559	9	34	53	0.0007					1892
POL	LTEAVOKIA	560	9	26	41						1893
POL	VQKATIESI	564	9	14	22						1894
POL	KIATESIVI	566	9	14	22						1895
POL	KTPKRLPI	577	9	17	27						1896
POL	KTPKRLPI	577	9	29	45						1897
POL	PIQKETVEA	584	9	15	23						1898
POL	PIQKETWET	584	9	27	42						1899
POL	PLVRLWYQL	613	9	54	84	0.0002					1900
POL	YQLEKEPIV	619	9	16	25						1901
POL	IVGAETFYV	626	9	28	44	0.0099					1902
POL	ETFYVVDGAA	630	9	51	80						1903
POL	GAANRETKL	636	9	30	47	0.0002					1904
POL	KLKGAGYVT	643	9	36	56						1905
POL	VTDROQRKV	650	9	30	47						1906
POL	KVSLTETT	657	9	11	17						1907
POL	LTDTTNQKT	661	9	19	30						1908
POL	LTETTNQKT	661	9	25	39						1909
POL	DTTNQKT	663	9	26	41						1910
POL	ETTNQKT	663	9	29	45						1911
POL	NQKTELIAI	666	9	12	19						1912
POL	NQKTELQAI	666	9	42	66	0.0001					1913
POL	KTELQAIHL	668	9	15	23	0.0005					1914
POL	KTELQAIYL	668	9	12	19	0.0083					1915
POL	ELQAIHLAL	670	9	16	25						1916
POL	ELQAIYLLAL	670	9	12	19						1917
POL	ILALQDSGL	675	9	15	23	0.0005					1918
POL	ALQDSGLEV	677	9	27	42	0.0083					1919
POL	ALQDSGSEV	677	9	25	39						1920
POL	NIVTDSQYA	686	9	61	95	0.0024					1921
POL	IVTDSQYAL	687	9	59	92						1922
POL	LVNQHIEQL	709	9	19	30						1923
POL	LVNQHIEQL	709	9	19	30						1924
POL	EQLKKEKV	715	9	28	44						1925
POL	LIKKEKVYL	717	9	35	55	0.0001					1926
POL	KVYLAWVPA	722	9	20	32						1927
POL	KVYLAWVPA	722	9	23	37						1928

Table VIII
 IIIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0812	SEQ ID NO
POL	EQVDKLVS	738	9	16	25						1929
POL	LYSAGIRKV	743	9	15	23	0.0001					1930
POL	LYSSGIRKV	743	9	26	41						1931
POL	RAMASDFNL	772	9	41	64	0.0230	0.0370	0.0004	0.0710	0.0130	1932
POL	PVVAKEIVA	782	9	25	39						1933
POL	PVVAKEIVA	782	9	28	44						1934
POL	VASCDKCOL	789	9	43	67						1935
POL	QVYCSFGI	804	9	57	89						1936
POL	CTHLEGGKII	817	9	35	55						1937
POL	CTHLEGGKII	817	9	26	41						1938
POL	IILEGKVILV	819	9	31	48	0.0010					1939
POL	KILVAVHIV	823	9	23	36	0.0006					1940
POL	KILVAVHIV	823	9	30	47	0.0007					1941
POL	KILVAVHIV	823	9	23	36	0.0001					1942
POL	ILVAVHIVA	824	9	30	47						1943
POL	VILVAVHIVA	824	9	23	36						1944
POL	AVHVASGYI	828	9	53	83						1945
POL	AVHVASGYI	830	9	52	81						1946
POL	YIEAEVIPA	835	9	53	83						1947
POL	FAETVPAET	837	9	62	98						1948
POL	PAETQETA	842	9	58	91						1949
POL	GOETAYFIL	846	9	31	48						1950
POL	GOETAYFLL	846	9	26	41						1951
POL	ETAYFILKL	848	9	31	48						1952
POL	ETAYFILKL	848	9	27	42						1953
POL	TAYFILKLA	849	9	32	50						1954
POL	TAYFILKLA	849	9	27	42						1955
POL	LAGRWPKVT	856	9	14	22						1956
POL	LAGRWPKVT	856	9	30	47						1957
POL	ITDNGSNFT	866	9	49	77						1958
POL	FTSAAVKAA	873	9	27	42						1959
POL	FTSTTVKAA	873	9	14	22						1960
POL	AVKAAACWAA	877	9	32	50						1961
POL	TVKAAACWAA	877	9	23	36	0.0180	0.0040	0.1200	0.0230	0.0150	1962
POL	KAACVWAGI	879	9	31	49						1963
POL	VVESMKNEL	902	9	48	75						1964
POL	SMKNELKKT	905	9	53	83						1965
POL	ELKKIIGQV	909	9	57	89	0.0001					1966
POL	IIGQVRDQA	913	9	44	69						1967
POL	IIGQVREQA	913	9	13	20						1968
POL	QVRDQAEHL	916	9	48	75	0.0001					1969
POL	QVRDQAEHL	916	9	13	20						1970
POL	DQAEHLKTA	919	9	46	72						1971
POL	QAEHLKTA	920	9	13	20						1972
POL	QAEHLKTA	920	9	59	92						1973
POL	ILKTAVQMA	923	9	57	89						1974
POL	TAVQMAVFI	926	9	59	92	0.0033					1975
POL	SAGERIIDI	947	9	41	64						1976
POL	SAGERIIDI	947	9	22	34						1977
POL	IIDIIASDI	952	9	12	19						1978

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	IIDIIATDI	952	9	29	45						1979
POL	IVDIIATDI	952	9	12	19						1980
POL	DIIASDIQT	954	9	15	23						1981
POL	DIIATDIQT	954	9	40	63						1982
POL	ATDIQTKEI	957	9	35	55						1983
POL	OTKEIQKQI	961	9	46	72						1984
POL	ELQKQIKI	964	9	13	21						1985
POL	ELQKQIKI	964	9	34	54						1986
POL	IIKIQNFRV	969	9	12	19						1987
POL	ITKIQNFRV	969	9	36	57						1988
POL	PIWKGPAPL	985	9	36	56						1989
POL	PLWKGPAPL	985	9	19	30						1990
POL	LLWKGEQGA	992	9	60	94	0.0002					1991
POL	LLWKGEQGA	993	9	62	97	0.0230					1992
POL	VVIQDINSII	1002	9	37	58	0.0001					1993
POL	VVIQDINSII	1002	9	12	19						1994
POL	IQDINSIIK	1004	9	38	59						1995
POL	IQDINSIIK	1004	9	12	19						1996
POL	VVPIRIKAKI	1012	9	51	80						1997
POL	VVPIRIKAKI	1012	9	11	17						1998
POL	IKDYGGKQM	1020	9	11	17						1999
POL	IKDYGGKQM	1020	9	50	78						2000
POL	KOMAGIDICV	1026	9	44	69						2001
POL	QMGAGIDICV	1027	9	44	69	0.0001					2002
POL	KAREFSQET	12	10	10	16						2003
POL	RANSPTREL	26	10	16	25						2004
POL	RANSPTREL	26	10	10	16						2005
POL	STNSPTSREL	32	10	01	33						2006
POL	SQTRANSPTT	34	10	01	33						2007
POL	RANSPSSHEL	35	10	01	33						2008
POL	RANSPTREL	37	10	01	50						2009
POL	GAISLSLPQI	79	10	01	17						2010
POL	GTTLNFPQT	80	10	01	33						2011
POL	AISLSLPQIT	80	10	01	33						2012
POL	GTILNCPQITL	80	10	01	33						2013
POL	PTENFPQITL	80	10	01	33						2014
POL	PQITLWQRPL	88	10	47	73						2015
POL	QITLWQRPLV	89	10	47	73						2016
POL	ITLWQRPLVT	90	10	37	58						2017
POL	TLWQRPLVTI	91	10	21	33						2018
POL	TLWQRPLVTI	91	10	18	28						2019
POL	WORPLVTIKI	93	10	14	22						2020
POL	WORPLVTIKI	93	10	12	19						2021
POL	LVTIKIGGQL	97	10	13	20						2022
POL	KIGGQLKEAL	101	10	23	36						2023
POL	GQKEALLDT	104	10	10	16						2024
POL	GQKEALLDT	104	10	34	53						2025
POL	LIEALLDTGA	106	10	10	16						2026
POL	ALLDTGADDT	109	10	61	95						2027
POL	LLDTGADDTV	110	10	63	98	0.0005					2028

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	GADDTVLEDI	114	10	15	23						2029
POL	GADDTVLEEI	114	10	18	28						2030
POL	GADDTVLEEM	114	10	11	17						2031
POL	NLIQKWKPKM	124	10	35	55						2032
POL	KMIGSIGGFI	132	10	62	97	0.0290	0.0790	2.1000	0.0048	0.0120	2033
POL	FKVRQYDQI	140	10	41	64						2034
POL	KVRQYDQILI	142	10	20	31						2035
POL	KVRQYDQIPI	142	10	13	20						2036
POL	ROYDOILIEI	144	10	20	31						2037
POL	ROYDOIPIEI	144	10	12	19						2038
POL	ILIEICGKKA	149	10	13	20						2039
POL	LIEICGJIKAI	150	10	10	16						2040
POL	LIEICGKKAI	150	10	13	20						2041
POL	EICGIIKAIGT	152	10	19	30						2042
POL	EICGKKAIGT	152	10	24	38						2043
POL	AGTVLVGPT	158	10	52	81						2044
POL	GTVLVGTPV	160	10	53	83	0.0025					2045
POL	VLVGPVTVNI	162	10	53	83	0.0015					2046
POL	LVGPTPVNII	163	10	52	81	0.0002					2047
POL	PVNIIGRNLL	168	10	26	41						2048
POL	PVNIIGRNML	168	10	24	38						2049
POL	IIGRNLLTQI	171	10	21	33						2050
POL	IIGRNMLTQI	171	10	18	28						2051
POL	IIGRNMLTQL	171	10	11	17	0.0007					2052
POL	NLLTQIGCTL	175	10	21	33						2053
POL	NMLTQIGCTL	175	10	18	28						2054
POL	NMLTQLGCTL	175	10	10	16						2055
POL	QIGCTLNFI	179	10	41	64	0.0025					2056
POL	QLGCTLNFI	179	10	16	25						2057
POL	CTLNFIPI	182	10	60	94	0.0340	0.1800	0.3300	0.4400	0.4000	2058
POL	PISPIETVPV	187	10	56	88	0.0002					2059
POL	TPVVKLKPGM	193	10	54	84						2060
POL	KQWPLTHEKI	209	10	56	88						2061
POL	PLTEEKIKAL	212	10	54	84	0.0002					2062
POL	LTEEKIKALT	213	10	37	58						2063
POL	LTEEKIKALV	213	10	15	23						2064
POL	KIKALTEICT	217	10	12	19						2065
POL	KIKALVEICT	217	10	15	23						2066
POL	KALVEICTEM	219	10	15	24						2067
POL	CTEMKEGKI	225	10	27	42						2068
POL	KIGPENPYNT	238	10	50	78						2069
POL	RIGPENPYNT	238	10	10	16						2070
POL	RTQDFWEVOL	272	10	53	83						2071
POL	EVOLGIPHPA	278	10	54	84						2072
POL	QLGIPHPAGL	280	10	56	89	0.0002					2073
POL	PAGLKKKKSIV	286	10	50	78						2074
POL	GLKKKKSIVT	288	10	49	77	0.0002					2075
POL	SVTVLDVGDA	294	10	57	89						2076
POL	PLDKDFRKYT	308	10	19	30						2077
POL	FTIPSINNET	319	10	37	58						2078

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	Seq ID NO
POL	FTIPSTNNIET	319	10	13	20						2079
POL	POGWKGSPI	339	10	59	92						2080
POL	IVFQSMTKI	347	10	36	56						2081
POL	IVYQSMDDL	367	10	42	66						2082
POL	DLVYGSDEI	375	10	58	91	0.0007					2083
POL	GQIRAKIEEL	385	10	25	39	0.0001					2084
POL	GQIRTKIEEL	385	10	20	31						2085
POL	KIEELREIILL	390	10	19	30						2086
POL	KIEELRQIILL	390	10	17	27	0.0002					2087
POL	IRQIILLRWGFT	395	10	12	19						2088
POL	HOKEPFLWM	410	10	62	97						2089
POL	IQLPEKDSWT	433	10	13	20						2090
POL	IVLPEKDSWT	433	10	13	20						2091
POL	QLPEKDSWT	434	10	13	20						2092
POL	VLPEKDSWT	434	10	13	20						2093
POL	WTVNIHQKLV	441	10	61	95	0.0056					2094
POL	KLNWSQIYA	452	10	27	42	0.0001					2095
POL	GKVKQLCKL	462	10	28	44	0.0230					2096
POL	GKVRQLCKL	462	10	18	28						2097
POL	KQLCKLLRGA	466	10	12	19						2098
POL	KQLCKLLRGT	466	10	14	22						2099
POL	ROLCKLLRGA	466	10	13	21						2100
POL	KLLRGAKALT	470	10	25	40						2101
POL	KLLRGTKALT	470	10	24	38						2102
POL	KALTDHVPIT	476	10	21	33						2103
POL	KALTEVPILT	476	10	16	25						2104
POL	IVPLTEAEAL	481	10	13	20						2105
POL	VIPLTEAEAL	481	10	11	17						2106
POL	PLTEAEAEAL	483	10	30	47						2107
POL	LTEAEAELEA	484	10	36	56						2108
POL	ELELAENREI	489	10	53	83						2109
POL	EILKEPVIGV	497	10	41	64						2110
POL	GYYIYIUSKDL	508	10	38	59	0.0007					2111
POL	IQKQGGQDQWT	521	10	12	19						2112
POL	IQKQGGQDQWT	521	10	15	23						2113
POL	QIYQEPFKNL	532	10	40	63						2114
POL	YQEPFKNLKT	534	10	43	67	0.0002					2115
POL	NLKTGKYAKM	540	10	18	29						2116
POL	NLKTGKYARM	540	10	13	21						2117
POL	KTGKYAKMRT	542	10	10	16						2118
POL	RMRGAIITNDV	548	10	12	19						2119
POL	GAITNDVKQL	551	10	19	30						2120
POL	SAITNDVKQL	551	10	16	25						2121
POL	TAITNDVKQL	551	10	11	17						2122
POL	KQLTEAVQKI	558	10	32	51						2123
POL	QLTEAVQKIA	559	10	26	41						2124
POL	LTEAVQKIAT	560	10	11	17						2125
POL	AVQKIATESI	563	10	10	16						2126
POL	VQKIATESIV	564	10	14	22						212

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0303	Δ*0206	Δ*6802	SEQ ID NO
POL	WTDYWQATWI	594	10	14	22						2129
POL	WTEYWQATWI	594	10	24	38						2130
POL	ATWIPEWFEV	600	10	51	80	0.0013					2131
POL	WIPEWFEVNT	602	10	50	81						2132
POL	FVNTPLVKL	608	10	54	86	0.0002					2133
POL	LVKLWYQLET	614	10	11	17						2134
POL	QLEKEPIVGA	620	10	16	25						2135
POL	PIVGAETFYV	625	10	28	44	0.0002					2136
POL	GAETFFYVDA	628	10	48	75						2137
POL	YVDGAANRET	633	10	45	70						2138
POL	ETKLGKAGYV	641	10	35	55						2139
POL	YVTDGRGRQV	649	10	29	45						2140
POL	VTDRGRQKVV	650	10	28	44	0.0002					2141
POL	ROKVSLSLET	655	10	10	16						2142
POL	SLTDTTNQKT	660	10	11	17						2143
POL	SLTETTNQKT	660	10	19	30						2144
POL	TTNQKTELHA	664	10	12	19						2145
POL	TTNQKTELQA	664	10	42	66						2146
POL	KTELOAIHLA	668	10	15	23						2147
POL	KTELOAIHLA	668	10	12	19						2148
POL	LALQDSGLEV	676	10	27	42	0.0006					2149
POL	LALQDSGSEV	676	10	25	39						2150
POL	LQDSGLEVNI	678	10	27	42						2151
POL	LQDSGSEVNI	678	10	25	39						2152
POL	NIVTDSQYAL	686	10	59	92	0.0004					2153
POL	VTDSQYALGI	688	10	58	91						2154
POL	SOYALGHQIA	691	10	58	91						2155
POL	AQPDKSESEL	700	10	36	56						2156
POL	ELVNHQIEQL	708	10	18	28						2157
POL	ELVSHQIEQL	708	10	19	30						2158
POL	LVNQHIEQLI	709	10	19	30						2159
POL	LVSQHEQLI	709	10	19	30	0.0006					2160
POL	QLIKKEKYYL	716	10	28	44						2161
POL	LIKKEKYYLA	717	10	31	41						2162
POL	LAWVPPIIKGI	725	10	20	31						2163
POL	QVDKLVSAIGI	739	10	15	23						2164
POL	QVDKLVSSGI	739	10	15	23						2165
POL	KLVSAIGIRKV	742	10	29	45	0.0074					2166
POL	KLVSSGIRKV	742	10	15	23						2167
POL	LVSAGIRKVL	743	10	15	23	0.0002					2168
POL	LVSSGIRKVL	743	10	26	41						2169
POL	SAGIRKVLFL	745	10	15	23						2170
POL	VLFLDGIDKA	751	10	51	80	0.0007					2171
POL	MASDINLPPI	774	10	22	34						2172
POL	MASDINLPPI	774	10	25	39	0.0006	0.1900	0.1800	0.1100	2.2000	2173
POL	NLPPVIAKEI	779	10	26	41						2174
POL	IVASCIVAKEL	779	10	27	42	0.0007					2175
POL	IVASCIVAKEL	788	10	43	67	0.0006					2176
POL	GIWQLDCTHL	811	10	43	67	0.0003					2177
POL	CTHILEGKIIL	817	10	31	48						2178

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SI:Q ID NO
POL	CTHLECKVIL	817	10	23	36						2179
POL	HLEGGKILVA	819	10	31	48						2180
POL	HLEGGKILVA	819	10	23	36						2181
POL	KILVAVIIVA	823	10	30	47						2182
POL	KVILVAVIIVA	823	10	22	34						2183
POL	VAVILVAVSGYI	827	10	53	83						2184
POL	VASGYIEAEV	831	10	52	81						2185
POL	VIPAETGQET	840	10	58	91						2186
POL	ETGQETAYFI	844	10	31	48						2187
POL	ETGQETAYFL	844	10	26	41						2188
POL	ETAYFILKLA	848	10	31	48						2189
POL	ETAYFLLKLA	848	10	27	42						2190
POL	ILKLAGRWPV	853	10	34	53						2191
POL	LLKLAGRWPV	853	10	25	39	0.0004					2192
POL	KLGRWPVKV	855	10	14	22						2193
POL	KLGRWPVKV	855	10	30	47						2194
POL	LAGRWVPKTI	856	10	13	20						2195
POL	LAGRWVPKVI	856	10	22	34						2196
POL	AAYKAAACVWA	876	10	28	44						2197
POL	TTVKAACVWA	876	10	14	22						2198
POL	WAGRIQEFGI	884	10	21	33						2199
POL	WAGRIQEFGI	884	10	11	17						2200
POL	POSQGVVFSM	897	10	53	83						2201
POL	GVVFSMNKEL	901	10	48	75						2202
POL	SMNKLKKT	905	10	53	83						2203
POL	KIGQVVDQA	912	10	43	67						2204
POL	KIGQVREQA	912	10	13	20						2205
POL	GVVREQAELH	915	10	44	69						2206
POL	GVVREQAELH	915	10	13	20						2207
POL	DOAEHLKTAV	919	10	46	72						2208
POL	DOAEHLKTAV	919	10	13	20						2209
POL	ILKTAVQMAV	923	10	57	89						2210
POL	KTAVQMAVFI	925	10	56	88	0.0005					2211
POL	SAGERIIDIH	947	10	41	64	0.0002					2212
POL	SAGERIIDIH	947	10	14	22						2213
POL	RIDDIASDI	951	10	12	19						2214
POL	RIDDIATDI	951	10	29	45						2215
POL	RIVDIATDI	951	10	12	19						2216
POL	IASDIQTKEL	956	10	14	22						2217
POL	IATDIQTKEL	956	10	35	55						2218
POL	IQTKELQKQI	960	10	44	69						2219
POL	QTKELQKQII	961	10	10	16						2220
POL	QTKELQKQIT	961	10	32	50						2221
POL	QIKIQNFRV	968	10	12	19						2222
POL	QITKIQNFRV	968	10	35	55	0.0002					2223
POL	PIWKGPAKLL	985	10	35	55						2224
POL	PLWKGPAKLL	985	10	18	28						2225
POL	KLLWKGEQAV	992	10	60	94	0.0006					2226
POL	LLWKGEQAVV	993	10	61	95	0.0360					2227
POL	AVVICDNSDI	1000	10	37	58						2228

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SIQ ID NO
POL	AVVIQNSEII	1000	10	12	19						2229
POL	VIQDNSEIKV	1003	10	37	58	0.0013					2230
POL	VIQDNSEIKV	1003	10	12	19						2231
POL	IQDNSEIKVV	1004	10	38	59						2232
POL	IQDNSEIKVV	1004	10	12	19						2233
POL	DIKVVPRRKA	1009	10	39	61						2234
POL	EIKVVTRRKA	1009	10	13	20						2235
POL	KVVPFRKAKI	1011	10	51	80						2236
POL	KVVPFRKAKI	1011	10	11	17						2237
POL	VVPFRKAKII	1012	10	50	78						2238
POL	VVPFRKVKII	1012	10	11	17						2239
POL	KIKDYGRQM	1019	10	11	17						2240
POL	KIKDYGRQM	1019	10	50	78						2241
POL	IKDYGRQMA	1020	10	11	17						2242
POL	IKDYGRQMA	1020	10	49	77						2243
POL	KOMAGUDCVA	1026	10	44	69						2244
POL	GAISLSLPQIT	79	11	01	17						2245
POL	AISLSLPQITL	80	11	01	33						2246
POL	QITLWQRPLV	88	11	47	73						2247
POL	QITLWQRPLVT	89	11	37	58						2248
POL	ITLWQRPLVTI	90	11	19	30						2249
POL	ITLWQRPLVTI	90	11	18	28						2250
POL	PLVTIKIGGQL	96	11	13	20						2251
POL	TKIGGQLKEA	99	11	17	27						2252
POL	KIGGQLKEALL	101	11	23	36						2253
POL	QLIEALLDTGA	105	11	10	16						2254
POL	QLKEALLDTGA	105	11	34	53						2255
POL	EALLDTGADIT	108	11	60	94						2256
POL	ALLDTGADITV	109	11	61	95						2257
POL	LLDTGADITVL	110	11	61	95						2258
POL	NLIPGRWPKMI	124	11	35	55						2259
POL	MIGGIGGFIK	133	11	62	97						2260
POL	FIKVRQYDQIL	140	11	21	33						2261
POL	QILIEGCKKA	148	11	13	20						2262
POL	ILIEGCKKAI	149	11	13	20						2263
POL	EICGIRKAIGTV	152	11	19	30						2264
POL	EICGKKAIGTV	152	11	23	36						2265
POL	KAIGTVLVGPT	157	11	48	75						2266
POL	TVLVGPTPVNI	161	11	53	83						2267
POL	VLVGPTPVNII	162	11	51	80						2268
POL	PTPVNIIGRNL	166	11	26	41						2269
POL	PTPVNIIGRNM	166	11	24	38						2270
POL	PVNIIGRNLIT	168	11	26	41						2271
POL	PVNIIGRNLIT	168	11	23	36						2272
POL	NIIGRNLITQI	170	11	21	28						2273
POL	NIIGRNLITQI	170	11	18	23						2274
POL	NIIGRNLITQI	170	11	11	17						2275
POL	TOIGCTLNFP	178	11	41	64						2276
POL	TOIGCTLNFP	178	11	15	23						2277
POL	TLNFPISPIET	183	11	34	86						2278

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IIIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	ETVPVKLKPGM	192	11	51	80						2279
POL	KLKTGMDGPKV	197	11	47	73						2280
POL	PLTEEKIKALT	212	11	35	55						2281
POL	PLTEEKIKALT	212	11	15	23						2282
POL	EMEKEGKISKI	229	11	32	50						2283
POL	PIFAIKKKDST	248	11	22	34						2284
POL	IVFAIKKKDST	248	11	37	58						2285
POL	LVDFEELNKRT	263	11	60	94						2286
POL	TQDFWEVQLGI	273	11	55	86						2287
POL	VQLGHIHPAGL	279	11	54	84						2288
POL	PAGLKKRKSST	286	11	47	73						2289
POL	GLKKKKSSTVL	288	11	49	77						2290
POL	VLDDVGDYFVS	297	11	53	83						2291
POL	DVGDYFVSFPL	299	11	54	84						2292
POL	FLDKDFRKYTA	308	11	19	30						2293
POL	ETPGIRYQYNV	327	11	51	80						2294
POL	VLPGGAKGSPA	337	11	58	92						2295
POL	PAIFQSSMTKI	346	11	36	56						2296
POL	AIHQSSMTKIL	347	11	16	28						2297
POL	DIYIYQYMDIDL	366	11	36	56						2298
POL	FIYIYQYMDIDL	366	11	24	38						2299
POL	VIYQYMDIDL	368	11	51	80						2300
POL	YMDILYVGSIDL	372	11	61	95						2301
POL	DLEIGQIRAKI	381	11	26	41						2302
POL	RAKIEELREHL	388	11	20	31						2303
POL	RTKIEELRQHL	388	11	13	20						2304
POL	RQIILLRWGFTT	395	11	14	22						2305
POL	PQLPEKDSWT	432	11	12	19						2306
POL	PVLPEKDSWT	432	11	13	20						2307
POL	IQLPEKDSWT	433	11	13	20						2308
POL	IVLPEKDSWT	433	11	13	20						2309
POL	IQKLVGKLNWA	446	11	13	20						2310
POL	LVGKLNWASQI	449	11	61	95						2311
POL	WASQIYAGIKV	455	11	60	94						2312
POL	WASQIYAGIKV	455	11	27	42						2313
POL	QIVAGIKVVKOL	458	11	18	29						2314
POL	QIVPGIKVVKOL	458	11	11	17						2315
POL	QIVPGIKVVKOL	458	11	14	22						2316
POL	GIKVKQLCKLL	462	11	27	42						2317
POL	GIKVKQLCKLL	462	11	18	28						2318
POL	QLCKLLRGAKA	467	11	24	38						2319
POL	QLCKLLRGAKA	467	11	21	33						2320
POL	LLRGAKALTDI	471	11	22	34						2321
POL	LLRGAKALTVE	471	11	18	28						2322
POL	GAKALTDIVPL	474	11	17	27						2323
POL	GKALTEVPL	474	11	11	17						2324
POL	LTDIVPLTEEA	478	11	13	20						2325
POL	LTDIVPLTEEA	478	11	11	17						2326
POL	DIVPLTEEAEL	480	11	13	20						2327
POL	DIVPLTEEAEL	480	11	13	20						2328

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*6802	SEQ ID NO
POL	EVPLTEEAEL	480	11	11	17						2329
POL	PLTEEAELFA	483	11	29	45						2330
POL	ELELAENREIL	489	11	53	83						2331
POL	GVYDPSKDLI	508	11	31	48						2332
POL	EIQKQGQDWT	520	11	12	19						2333
POL	EIQKQGQDWT	520	11	15	23						2334
POL	KQGQDQWTYQI	523	11	13	20						2335
POL	KQGQDQWTYQI	523	11	25	39						2336
POL	YQIQEPPKNL	531	11	40	63						2337
POL	KTGKYAKMRTA	542	11	10	16						2338
POL	KTGKYARMRGA	542	11	13	21						2339
POL	GAITNDVKQLT	551	11	18	28						2340
POL	SAITNDVKQLT	551	11	12	19						2341
POL	TAITNDVKQLT	551	11	10	16						2342
POL	ITNDVKQLTEA	553	11	32	50						2343
POL	QLTEAVQKIA	558	11	24	38						2344
POL	QLTEAVQKIAT	559	11	11	17						2345
POL	EAVQKIATESI	562	11	10	16						2346
POL	AVQKIATESIV	563	11	10	16						2347
POL	VQKIATESIVI	564	11	14	22						2348
POL	ATESIVWCKT	568	11	16	25						2349
POL	VIWGRITKPKL	573	11	17	27						2350
POL	VIWGRITKPKL	573	11	29	45						2351
POL	RLPIQKETWET	582	11	18	28						2352
POL	IQKETWEAWWT	585	11	11	17						2353
POL	IQKETWEAWWT	585	11	21	33						2354
POL	ETWWTDYWQAT	591	11	10	16						2355
POL	QATWITWETV	599	11	51	81						2356
POL	KLWYQLEKDIPI	616	11	14	22						2357
POL	KLWYQLEKEPI	616	11	31	48						2358
POL	KLWYQLETEPI	616	11	11	17						2359
POL	YQLEKEPIVGA	619	11	16	25						2360
POL	GAETFYVDGAA	628	11	44	69						2361
POL	AAARETKLGA	637	11	30	47						2362
POL	ETKLGAAGYVT	641	11	35	55						2363
POL	YVTDGRGQKVV	649	11	27	42						2364
POL	RQKVVSLETT	655	11	10	16						2365
POL	LTDTTNQKTEL	661	11	19	30						2366
POL	LTDTTNQKTEL	661	11	25	39						2367
POL	DTTNQKTELQA	663	11	25	39						2368
POL	ETTNQKTELIA	663	11	11	17						2369
POL	ETTNQKTELQA	663	11	17	27						2370
POL	ETTNQKTELIAI	664	11	12	19						2371
POL	TTNQKTELOAI	664	11	42	66						2372
POL	NQKTELQAIIL	666	11	15	23						2373
POL	NQKTELQAIYL	666	11	12	19						2374
POL	KTELQAIILAL	668	11	15	23						2375
POL	KTELQAIYLAL	668	11	12	19						2376
POL	AIILALQDSGL	673	11	15	23						2377
POL	ILALQDSGLEV	675	11	15	23						2378

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SI:Q ID NO
POL	ALQDSGLEVNI	677	11	27	42						2379
POL	ALQDSGSEVNI	677	11	25	39						2380
POL	LQNSGLEVNIV	678	11	27	42						2381
POL	LQNSGSEVNIV	678	11	25	39						2382
POL	EVNIVTDSQYA	684	11	59	92						2383
POL	IVTDSQYALGI	687	11	58	91						2384
POL	VTDQYALGHI	688	11	58	91						2385
POL	QAQPDKSESEL	699	11	36	56						2386
POL	AQPDKSESELV	700	11	36	56						2387
POL	ELVNQIEQLI	708	11	18	28						2388
POL	ELVSCIEQLI	708	11	19	30						2389
POL	HEQLIRKEKV	713	11	28	44						2390
POL	EQLIKKEKYYL	715	11	28	44						2391
POL	QLIKKEKYYLA	716	11	19	30						2392
POL	YLAWVPATIKGI	724	11	22	34						2393
POL	YLSWVPAIKGI	724	11	37	58						2394
POL	GIGGNIQVDKL	733	11	58	91						2395
POL	EQVDKLYSAGI	738	11	15	23						2396
POL	EQVDKLYSSGI	738	11	29	45						2397
POL	KLVSAGIRKVL	742	11	15	23						2398
POL	KLVSAGIRKVL	742	11	26	41						2399
POL	GRKKVFLDGI	747	11	49	77						2400
POL	KVLFLLDGDKA	750	11	48	75						2401
POL	AMASDFNLPII	773	11	18	28						2402
POL	AMASDFNLPIV	773	11	25	39						2403
POL	MASDFNLPIV	774	11	20	31						2404
POL	MASDFNLPIV	774	11	25	39						2405
POL	NLPPIVAKIV	779	11	26	41						2406
POL	NLPPIVAKIV	779	11	27	42						2407
POL	ELVASCDCQQL	787	11	43	67						2408
POL	QLKGEAMIGQV	796	11	53	83						2409
POL	QVDCSFGIWQL	805	11	56	88						2410
POL	QLDCTHILEGKI	814	11	33	52						2411
POL	QLDCTHILEGKV	814	11	26	41						2412
POL	CTHILEGKILV	817	11	31	48						2413
POL	CTHILEGKVILV	817	11	23	36						2414
POL	ILEGKVILVAV	819	11	31	48						2415
POL	ILEGKVILVAV	819	11	23	36						2416
POL	LVAHVIVASGYI	826	11	47	73						2417
POL	AVIIVASGYIEA	828	11	52	81						2418
POL	HVASGYIEAEV	830	11	52	81						2419
POL	VASGYIEAEVI	831	11	52	81						2420
POL	YIEAEVIPAET	835	11	53	83						2421
POL	EVIPAETGOET	839	11	58	91						2422
POL	VIPAETGOETA	840	11	58	91						2423
POL	ETGOETAYFIL	844	11	31	48						2424
POL	ETGOETAYFLL	844	11	26	41						2425
POL	GOETAYFILKL	846	11	31	48						2426
POL	GOETAYFLLKL	846	11	26	41						2427
POL	FILKLGRWIPV	852	11	32	50						2428

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	FLKLAGRWVPV	852	11	25	39						2429
POL	KLGRWPVKTI	855	11	13	20						2430
POL	KLGRWPVKVI	855	11	22	34						2431
POL	TIHTDGSNFT	864	11	13	20						2432
POL	VIHTDGSNFT	864	11	23	36						2433
POL	IITDGSNFTSA	866	11	33	52						2434
POL	IITDGSNFTST	866	11	11	17						2435
POL	SAAVKAAACWVA	875	11	28	44						2436
POL	STIVKAAACWVA	875	11	14	22						2437
POL	AVKAAACWVAGI	877	11	10	16						2438
POL	TVKAAACWVAGI	877	11	20	31						2439
POL	GIPYNPQSGV	892	11	63	98						2440
POL	QVRDQAEIILKT	916	11	43	67						2441
POL	QVREQAEIILKT	916	11	13	20						2442
POL	QAEIILKTAVQM	920	11	57	89						2443
POL	FIINFRKGGI	933	11	58	91						2444
POL	GIGGYSAGERI	942	11	57	89						2445
POL	SAGERIIDIIA	947	11	40	63						2446
POL	SAGERIVDIIA	947	11	14	22						2447
POL	IIDIASDIQT	952	11	12	19						2448
POL	IIDIIATDIQT	952	11	27	42						2449
POL	IIDIIATDIQT	952	11	12	19						2450
POL	IIASDIQTKEL	955	11	14	22						2451
POL	IATDIQTKEL	955	11	34	53						2452
POL	DIQTKELQKQI	959	11	44	69						2453
POL	IQTKELQKQI	960	11	10	16						2454
POL	IQTKELQKQIT	960	11	30	47						2455
POL	KQIKIQNFRV	967	11	12	19						2456
POL	KQITKIQNFRV	967	11	34	54						2457
POL	RYYVYRDSRDI	976	11	34	53						2458
POL	RYYVYRDSRDPL	976	11	14	22						2459
POL	PAKLLWKGEA	990	11	59	92						2460
POL	KLLWKGEAGV	992	11	59	92						2461
POL	LLWKGEAGVVI	993	11	59	92						2462
POL	GAVVIQDMSDI	999	11	37	58						2463
POL	GAVVIQDMSDI	999	11	12	19						2464
POL	VVIQDMSDIK	1002	11	37	58						2465
POL	VVIQDMSDIK	1002	11	12	19						2466
POL	VVIQDMSDIKVV	1003	11	37	58						2467
POL	VQDMSDIKVV	1003	11	12	19						2468
POL	KVVPKRAKII	1011	11	50	78						2469
POL	KVVPKRAKVII	1011	11	11	17						2470
POL	KIKDYGKQMA	1019	11	11	17						2471
POL	KIIRDYKQMA	1019	11	49	77						2472
REV	LLKTVRLI	12	8	11	17						2473
REV	AVRIKIL	17	8	13	20						2474
REV	RQRQIISI	52	8	11	17						2475
REV	QLPIERL	78	8	14	22						2476
REV	QLPIERL	78	8	37	58						2477
REV	GTSGTQGV	94	8	21	33						2478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*0802	SIQ ID No.
REV	GTQSQGT	97	8	10	16						2479
REV	PQGTETGV	101	8	05	18						2480
REV	SQGTETGV	101	8	05	18						2481
REV	LVESPAVL	114	8	11	17						2482
REV	SISERILST	58	9	10	16						2483
REV	CLGRFAEPV	67	9	10	16						2484
REV	PAEPVPLQL	71	9	21	33						2485
REV	SAEPVPLQL	71	9	12	19						2486
REV	PVPLQLPM	74	9	11	17						2487
REV	PVPLQLPPL	74	9	35	55						2488
REV	LQLPIERL	77	9	11	17						2489
REV	LQLPFLERL	77	9	36	56						2490
REV	QLPFLERLT	78	9	18	28						2491
REV	TQGVGSPQI	98	9	11	18						2492
REV	RARQRIHIS	50	10	10	16						2493
REV	PLOLPPIERL	76	10	11	17						2494
REV	PLOLPPIERL	76	10	34	53						2495
REV	LQLPPIERLT	77	10	17	27						2496
REV	QLPFLERLT	78	10	18	28						2497
REV	GTQGVGSPQI	97	10	11	18						2498
REV	PLQLPIERLT	76	11	15	23						2499
REV	LQLPPIERLT	77	11	17	27						2500
REV	GTSGTQSQGT	94	11	10	16						2501
TAT	SQPKTACT	19	8	13	20	0.0001					2502
TAT	FLNKGLGI	41	8	14	22						2503
TAT	SQMRDPT	80	8	13	20						2504
TAT	KVERETET	97	8	12	19						2505
TAT	PTGPKESKKV	88	11	12	19						2506
VIF	QVMIVWQV	6	8	43	67						2507
VIF	INWQVDRM	9	8	59	92						2508
VIF	WQVDRMKI	11	8	13	20						2509
VIF	WQVDRMIR	11	8	48	75						2510
VIF	KIRTWNSL	17	8	12	19						2511
VIF	RIRTWKSL	17	8	15	23						2512
VIF	RIRTWNSL	17	8	15	23						2513
VIF	LVKIHIMYI	24	8	19	30						2514
VIF	LVKIHIMYV	24	8	21	33						2515
VIF	IIMYVSKKA	28	8	13	20						2516
VIF	KISSEVII	50	8	15	23						2517
VIF	KVSSEVII	50	8	20	31						2518
VIF	RISSEVII	50	8	15	23						2519
VIF	PLGDARLV	58	8	11	17						2520
VIF	PLGEARLV	58	8	19	30						2521
VIF	VIKTYWGL	67	8	10	16						2522
VIF	VITYWGL	67	8	22	34						2523
VIF	VVRTYWGL	67	8	10	16						2524
VIF	VVTYWGL	67	8	11	17						2525
VIF	TTYWGLHT	69	8	24	38						2526
VIF	HLGHGVSI	83	8	25	39						2527
VIF	HLGQGVSI	83	8	26	41						2528

Table VIII
IIIY Δ92 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*0802	SEQ ID NO
VIF	GVSIIEWRL	87	8	18	28						2529
VIF	STQIDPDL	100	8	12	19						2530
VIF	STQVDPGL	100	8	11	17						2531
VIF	TQIDPDLA	101	8	12	19						2532
VIF	TQVDPDLA	101	8	11	17						2533
VIF	TQVDPGLA	101	8	16	25						2534
VIF	LADQLIHL	107	8	25	39						2535
VIF	LADQLIIM	107	8	17	27						2536
VIF	SAIRKAIL	123	8	35	55						2537
VIF	SAIRNAIL	123	8	12	19						2538
VIF	YQAGIINKV	140	8	38	59						2539
VIF	KVGSLOYL	146	8	52	81						2540
VIF	SLOYLALA	149	8	12	19						2541
VIF	SLOYLALT	149	8	31	48						2542
VIF	LQYLALAA	150	8	12	19						2543
VIF	LQYLALKA	150	8	11	17						2544
VIF	LQYLALTA	150	8	34	53						2545
VIF	YLAL-TALI	152	8	28	44						2546
VIF	ALIKPKKI	157	8	10	16						2547
VIF	PLTSVKKL	168	8	21	33						2548
VIF	PLTSVKKL	168	8	14	22						2549
VIF	WQVMIVWQV	5	9	43	67						2550
VIF	MIVWQVDRM	8	9	46	72						2551
VIF	QVDRMKIRT	12	9	12	19						2552
VIF	QVDRMRINT	12	9	10	16						2553
VIF	QVDRMRIRT	12	9	31	48						2554
VIF	KIRTWNSLV	17	9	12	19						2555
VIF	RIRTWKSLV	17	9	15	23						2556
VIF	RIRTWNSLV	17	9	15	23						2557
VIF	SLVKIIMMYI	23	9	19	30						2558
VIF	SLVKIIMMYV	23	9	21	33						2559
VIF	EVHIIPLGDA	54	9	24	38						2560
VIF	EVHIIPLGEA	54	9	25	39						2561
VIF	IIPLCDAHL	56	9	13	20						2562
VIF	IIPLCGEARL	56	9	20	31						2563
VIF	PLGEARLVI	58	9	10	16						2564
VIF	LVIKTYWGL	66	9	10	16						2565
VIF	LVITYWGL	66	9	22	34						2566
VIF	LVITYWGLIT	68	9	16	25						2567
VIF	ITGERDWIIL	75	9	21	33						2568
VIF	ITGERDWIIL	75	9	12	19						2569
VIF	STQIDPDLA	100	9	12	19						2570
VIF	STQIDPGLA	100	9	11	17						2571
VIF	DLADQLIHL	106	9	18	28						2572
VIF	GLADQLIIM	106	9	15	23						2573
VIF	KVGSLOYL	146	9	52	81						2574
VIF	SLOYLALAA	149	9	12	19						2575
VIF	SLOYLALKA	149	9	11	17						2576
VIF	SLOYLALTA	149	9	31	48						2577
VIF	LOYLALAA	150	9	12	19						2578

0.0031

Table VIII
 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6K02	SHQ ID NO
VIF	LOYLALKAL	150	9	11	17						2579
VIF	LOYLALTAL	150	9	33	52						2580
VIF	KIKPLPSV	164	9	19	30						2581
VIF	KTKPLPSV	164	9	12	19						2582
VIF	PLPSVKKL	168	9	13	20						2583
VIF	VMIVWQVDRM	7	10	44	69						2584
VIF	IVWQVDRMKI	9	10	12	19						2585
VIF	IVWQVDRMKI	9	10	47	73						2586
VIF	WQVDEMKT	11	10	12	19						2587
VIF	WQVDEMKT	11	10	10	16						2588
VIF	WQVDEMKT	11	10	31	48						2589
VIF	RMKIRTWNSL	15	10	12	19						2590
VIF	RMKIRTWNSL	15	10	15	23						2591
VIF	RMKIRTWNSL	15	10	15	23						2592
VIF	KISSEVIHPL	50	10	14	22						2593
VIF	KISSEVIHPL	50	10	19	30						2594
VIF	RISSEVIHPL	50	10	13	20						2595
VIF	HIPLGEARLV	56	10	10	16						2596
VIF	HIPLGEARLV	56	10	19	30						2597
VIF	LVITYWGLIT	65	10	12	19						2598
VIF	VITYWGLIT	67	10	16	25						2599
VIF	LOTGERDWIL	74	10	12	19						2600
VIF	QIDPDLADQL	102	10	10	16						2601
VIF	QIDPDLADQL	102	10	14	22						2602
VIF	IVSPRCEYQA	133	10	11	17						2603
VIF	QAGIINKVGS	141	10	38	59						2604
VIF	KVGSLOYLAL	146	10	51	80	0.0008					2605
VIF	SLQYLALAL	149	10	12	19						2606
VIF	SLQYLALAL	149	10	11	17						2607
VIF	SLQYLALAL	149	10	31	48						2608
VIF	SLQYLALAL	149	10	28	44						2609
VIF	SLQYLALAL	149	10	16	25						2610
VIF	QVMIWQVDRM	188	11	43	67						2611
VIF	QVMIWQVDRM	6	11	43	67						2612
VIF	RMKIRTWNSL	8	11	12	19						2613
VIF	RMKIRTWNSL	15	11	15	23						2614
VIF	RMKIRTWNSL	15	11	15	23						2615
VIF	RTWKSLSKIIIM	19	11	14	22						2616
VIF	RTWKSLSKIIIM	19	11	24	38						2617
VIF	EVHPLGDARL	54	11	13	20						2618
VIF	EVHPLGDARL	54	11	20	31						2619
VIF	EVHPLGDARL	54	11	10	16						2620
VIF	LVITYWGLIT	66	11	16	25						2621
VIF	GLITGERDWIIL	73	11	21	33						2622
VIF	GLITGERDWIIL	73	11	12	19						2623
VIF	TOIDPDLADQL	101	11	10	16						2624
VIF	TOIDPDLADQL	101	11	13	20						2625
VIF	QIDPDLADQL	102	11	10	16						2626
VIF	QIDPDLADQL	102	11	14	22						2627
VIF	YQAGINKVGS	140	11	38	59						2628

Table VIII
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*0802	SFQ ID NO
VIF	KVGSLOYLALA	146	11	12	19						2629
VIF	KVGSLOYLALT	146	11	28	44						2630
VIF	SLQYLALTAI	149	11	27	42						2631
VIF	LKPKKIKPPL	158	11	10	16						2632
VIF	KTKGIIRGSIITM	188	11	15	23						2633
VPR	ALELLEEL	19	8	10	16						2634
VPR	TLELLEEL	19	8	44	69						2635
VPR	AVRIIFRI	30	8	14	22						2636
VPR	ETYGDITWA	48	8	16	25						2637
VPR	ETYGDIWT	48	8	11	17						2638
VPR	DTWAGVEA	52	8	16	25						2639
VPR	DTWEGVEA	52	8	23	36						2640
VPR	WAGVEAII	54	8	16	25						2641
VPR	GVEAIIIRI	56	8	34	53						2642
VPR	IIRLQQL	60	8	42	66						2643
VPR	ILQCLLFI	63	8	37	58						2644
VPR	LLFIHIFRI	67	8	44	69						2645
VPR	LLFVIFRI	67	8	12	19						2646
VPR	CQHSRIGI	77	8	45	70						2647
VPR	WALELLEEL	18	9	9	15						2648
VPR	WTLLELEEL	18	9	42	69	0.0035					2649
VPR	LLEELKNEA	22	9	17	27						2650
VPR	LLEELKSEA	22	9	16	25						2651
VPR	EAVRIIFRI	29	9	14	22	0.0001					2652
VPR	WLIIGLQIHI	38	9	20	31						2653
VPR	IHYETYGDT	45	9	17	27						2654
VPR	IHYETYGDT	45	9	14	22						2655
VPR	YIYETYGDT	45	9	14	22						2656
VPR	DTWAGVEAI	52	9	16	25						2657
VPR	DTWEGVEAI	52	9	20	31						2658
VPR	GVEAIIHIL	56	9	34	53						2659
VPR	IIRLQQL	59	9	39	61	0.0150	0.1900	0.2400	0.0960	0.0730	2660
VPR	IIRLQQLL	60	9	42	66	0.0004					2661
VPR	RILQQLLFI	62	9	36	56	0.2000	0.0028	0.0000	0.1000	0.0220	2662
VPR	QLLFHIFRI	66	9	44	69	0.0530	0.0002	0.0004	0.0023	0.0840	2663
VPR	QLLFVIFRI	66	9	10	16						2664
VPR	RIGCQHSRI	74	9	47	73						2665
VPR	RIGCQHSRI	74	9	12	19						2666
VPR	CQHSRIGI	77	9	16	25						2667
VPR	CQHSRIGIT	77	9	14	22						2668
VPR	RORRABNGA	90	9	13	20						2669
VPR	POREPYNEWI	10	10	29	45						2670
VPR	ELLEELKNEA	21	10	16	25						2671
VPR	ELLEELKSEA	21	10	16	25						2672
VPR	LLEELKNEAV	22	10	17	27						2673
VPR	LLEELKSEAV	22	10	16	25						2674
VPR	AVRIIFRIWL	30	10	14	22	0.0002					2675
VPR	AVRIIFRIPWL	30	10	14	22						2676
VPR	ETYGDIWAGV	48	10	16	25	0.0009					2677
VPR	ETYGDIWTGV	48	10	11	17						2678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
VPR	NTYGDTEGV	48	10	16	25						2679
VPR	DTWAGVEAI	52	10	16	25						2680
VPR	DTWEGVEAI	52	10	19	30						2681
VPR	WAGVEAIHI	54	10	15	23						2682
VPR	EAIRILOQL	58	10	33	52						2683
VPR	AIRILOQLL	59	10	39	61						2684
VPR	QQLLFHIFRI	65	10	44	69	0.0014					2685
VPR	QQLLFHIFRI	65	10	10	16						2686
VPR	QQLLFHIFRI	65	10	29	45						2687
VPR	POREFYNEWTL	10	11	16	25						2688
VPR	ELLEELKNEAV	21	11	16	25						2689
VPR	ELLEELKSEAV	21	11	16	25						2690
VPR	EAVRIIFPRWL	39	11	14	22						2691
VPR	EAVRIIFPRWL	39	11	14	22						2692
VPR	QQLLFHIFRI	43	11	34	53						2693
VPR	QQLLFHIFRI	43	11	17	27						2694
VPR	QQLLFHIFRI	43	11	13	20						2695
VPR	QQLLFHIFRI	43	11	13	20						2696
VPR	QQLLFHIFRI	43	11	13	20						2697
VPR	QQLLFHIFRI	43	11	13	20						2698
VPR	QQLLFHIFRI	43	11	13	20						2699
VPR	QQLLFHIFRI	43	11	13	20						2700
VPR	QQLLFHIFRI	43	11	13	20						2701
VPR	QQLLFHIFRI	43	11	13	20						2702
VPR	QQLLFHIFRI	43	11	13	20						2703
VPR	QQLLFHIFRI	43	11	13	20						2704
VPR	QQLLFHIFRI	43	11	13	20						2705
VPR	QQLLFHIFRI	43	11	13	20						2706
VPR	QQLLFHIFRI	43	11	13	20						2707
VPR	QQLLFHIFRI	43	11	13	20						2708
VPR	QQLLFHIFRI	43	11	13	20						2709
VPR	QQLLFHIFRI	43	11	13	20						2710
VPR	QQLLFHIFRI	43	11	13	20						2711
VPR	QQLLFHIFRI	43	11	13	20						2712
VPR	QQLLFHIFRI	43	11	13	20						2713
VPR	QQLLFHIFRI	43	11	13	20						2714
VPR	QQLLFHIFRI	43	11	13	20						2715
VPR	QQLLFHIFRI	43	11	13	20						2716
VPR	QQLLFHIFRI	43	11	13	20						2717
VPR	QQLLFHIFRI	43	11	13	20						2718
VPR	QQLLFHIFRI	43	11	13	20						2719
VPR	QQLLFHIFRI	43	11	13	20						2720
VPR	QQLLFHIFRI	43	11	13	20						2721
VPR	QQLLFHIFRI	43	11	13	20						2722
VPR	QQLLFHIFRI	43	11	13	20						2723
VPR	QQLLFHIFRI	43	11	13	20						2724
VPR	QQLLFHIFRI	43	11	13	20						2725
VPR	QQLLFHIFRI	43	11	13	20						2726
VPR	QQLLFHIFRI	43	11	13	20						2727
VPR	QQLLFHIFRI	43	11	13	20						2728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VP1	LIDRIRERA	58	9	12	19						2729
VP1	DOEELSALV	79	9	11	18						2730
VP1	VTLLSSSKL	94	9	01	50						2731
VP1	LAKVDYRIVI	5	10	01	25						2732
VP1	LAKVDYRLGV	5	10	01	25						2733
VP1	KVDYRIVIVA	7	10	01	33						2734
VP1	KVDYRLGVGA	7	10	01	33						2735
VP1	RIDYRLGVGA	7	10	01	33						2736
VP1	IIIVVWTIV	27	10	20	31						2737
VP1	AIIVVWTFI	29	10	14	22						2738
VP1	ILRQKIDRL	46	10	15	23						2739
VP1	LVTLSSSKL	91	10	01	50						2740
VP1	LAKVDYRIVIV	5	11	01	25						2741
VP1	KVDYRLGVGAL	7	11	01	33						2742
VP1	RIDYRLGVGAL	7	11	01	33						2743
VP1	KILRQKIDRL	45	11	15	23						2744
VP1	ILRQKIDRLI	46	11	13	20						2745

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*6801	SEQ ID NO
ENV	SLWQSLK	123	8	47	75					2746
ENV	QSLKPCVK	127	8	48	75					2747
ENV	ATQACPK	244	8	14	22					2748
ENV	TITQACPK	244	8	11	17					2749
ENV	VITQACPK	244	8	17	27					2750
ENV	PAGFAIK	266	8	38	59					2751
ENV	PAGYAILK	266	8	15	23					2752
ENV	AILKCNDK	270	8	20	31					2753
ENV	ILKCNDDK	271	8	12	19					2754
ENV	SVEINCTR	340	8	13	20					2755
ENV	GTAGNSR	375	8	01	33					2756
ENV	TTISFNCR	432	8	12	19					2757
ENV	ITLPCRIK	483	8	26	41					2758
ENV	NMWQEVGK	494	8	15	23					2759
ENV	ITGLLLTK	520	8	37	58					2760
ENV	RSLEYKYK	558	8	54	84					2761
ENV	PLGVAPTK	571	8	26	41					2762
ENV	PLGVAPTR	571	8	10	16					2763
ENV	GVAPTKAK	573	8	19	30					2764
ENV	VAPTKAKR	574	8	19	30					2765
ENV	VISTRTIHK	584	8	01	50					2766
ENV	STRTHLEK	586	8	01	50					2767
ENV	RVVERIEKR	587	8	32	50	0.0003	0.0001			2768
ENV	RVVQNEKR	587	8	17	27					2769
ENV	ITLTQAKR	621	8	32	50					2770
ENV	EAQQHLLK	646	8	12	19					2771
ENV	KLTVMGK	653	8	13	20					2772
ENV	QLTVWGK	653	8	44	69					2773
ENV	GKLOQAK	658	8	49	77					2774
ENV	LAVERYTK	667	8	26	41					2775
ENV	LAVERYLR	667	8	11	17					2776
ENV	GIWGCCK	680	8	52	81					2777
ENV	MTWMEWER	721	8	12	19					2778
ENV	ESQNOQEK	743	8	27	42					2779
ENV	AVLSINVR	795	8	31	48					2780
ENV	LSIVHRVR	797	8	38	59					2781
ENV	ALAWDDLK	831	8	25	39					2782
ENV	RIVELLGR	878	8	22	34					2783
ENV	IVELLGR	879	8	22	34					2784
ENV	RLGWEGLK	894	8	10	32					2785
ENV	AVAFETDR	928	8	31	48					2786
ENV	RAIIHPR	945	8	13	20					2787
ENV	ALIIHPR	946	8	13	20					2788
ENV	RIRQGLR	953	8	44	69					2789
ENV	TLFCASDAK	64	9	52	81	0.0930	0.5300	0.0017	0.0020	2790
ENV	VTNFENMAWK	102	9	31	48					2791
ENV	ISLWQSLK	122	9	47	73	0.0048	0.0890	0.0017	0.0021	2792
ENV	SAITQACPK	243	9	14	22					2793
ENV	STITQACPK	243	9	10	16					2794
ENV	SVITQACPK	243	9	17	27					2795

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*101	A*3101	A*3101	A*6801	SEQ ID NO
ENV	FAIKCNDK	269	9	14	22	0.0002	0.0002	0.0004	0.0015	0.0027	2796
ENV	AIKCNDDK	270	9	12	19						2797
ENV	TVQCTHIGK	290	9	28	44	0.0021	0.0460	0.0042	0.0017	0.0190	2798
ENV	TVQCTHIGIR	290	9	23	36	0.0018	0.0008	0.0080	0.0030	0.0120	2799
ENV	LAEEVVR	312	9	12	19	0.0002	0.0002	0.0004	0.0007	0.0002	2800
ENV	CTRPNNTR	345	9	28	44						2801
ENV	ITTHSFNCR	431	9	11	17						2802
ENV	NANITPCR	478	9	01	50						2803
ENV	NITLCRIK	482	9	11	17						2804
ENV	TITLCRIK	482	9	14	22						2805
ENV	NITGLLTR	519	9	35	55	0.0004	0.0001				2806
ENV	STNGTETFR	537	9	01	17						2807
ENV	ELYKYKVK	560	9	32	51						2808
ENV	GVAPTKAKR	573	9	19	30						2809
ENV	VAPTKAKRR	574	9	17	27	0.0002	0.0002	0.0004	0.0006	0.0002	2810
ENV	KAKRRVQIR	579	9	13	20	0.0002	0.0002	0.0000	0.0005	0.0002	2811
ENV	LIHITPIR	584	9	01	50						2812
ENV	ISRTIUREK	585	9	01	50						2813
ENV	NIITPIREK	586	9	01	50						2814
ENV	STRTHREKR	586	9	01	50						2815
ENV	SITLTVQAR	620	9	32	50						2816
ENV	QARVLAVLR	663	9	33	52						2817
ENV	VLAVERYLK	666	9	18	28						2818
ENV	VLAVERYLR	666	9	17	17						2819
ENV	NMTWMEWER	720	9	12	19	0.0009	0.0003	0.0320	0.0320	0.0007	2820
ENV	ISNWLWYIK	770	9	11	17						2821
ENV	ITKWLWYIK	770	9	16	25						2822
ENV	ITNWLWYIK	770	9	15	23						2823
ENV	IVGGJGLR	783	9	42	66						2824
ENV	FVGLIVNR	794	9	31	48						2825
ENV	VLSIVNKR	796	9	38	59						2826
ENV	GIEEGGER	829	9	12	19						2827
ENV	LALAWDDLK	850	9	25	39						2828
ENV	NLCLSYIIR	859	9	11	17						2829
ENV	SCLFSYIIR	859	9	31	48						2830
ENV	CLFSYIIR	861	9	42	66						2831
ENV	RIVELLGR	878	9	22	34	0.0550	0.0100	0.1300	0.0021	0.0180	2832
ENV	IAVAEGTDR	927	9	31	48	0.0004	0.0003	0.0003	0.0004	0.0030	2833
ENV	RAIHIPRR	945	9	13	20						2834
ENV	ILIHPRIR	947	9	13	20						2835
ENV	TVYGVVYWK	48	10	41	64						2836
ENV	TTLFCASDAK	61	10	50	78	3.0000	7.0000	0.0019	0.0020	0.0570	2837
ENV	NVTENFMWK	101	10	31	48	0.0920	0.2200				2838
ENV	ISLWIDQSLK	121	10	38	59						2839
ENV	TSAITQACPK	242	10	14	22						2840
ENV	TSVITQACPK	242	10	14	22						2841
ENV	CAPAGFAIK	264	10	29	45	0.0410	0.0540	0.0017	0.0020	0.0029	2842
ENV	FAIKCNDKK	269	10	10	16						2843
ENV	STVQCTHIGK	289	10	28	44						2844
ENV	STVQCTHIGIR	289	10	23	36						2845

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
ENV	SLAEIEVIR	311	10	12	19						2846
ENV	CTRPNNTRK	345	10	22	34						2847
ENV	ATGDIIGDIR	369	10	12	19						2848
ENV	EITTHISFNCR	430	10	11	17						2849
ENV	INIMWQEVGK	492	10	12	19						2850
ENV	GSENGTETFR	538	10	02	18						2851
ENV	PLGVAPTKAK	571	10	19	30						2852
ENV	GVAPTKAKRR	573	10	17	27						2853
ENV	VSTRTHREK	584	10	01	50						2854
ENV	ISTRTHREK	585	10	01	50						2855
ENV	NHTTHIREK	586	10	01	50						2856
ENV	ASITLTVOAR	619	10	28	44						2857
ENV	IVQQQNLLR	634	10	25	39	0.0024	0.0190	0.0130	0.0072	0.0035	2858
ENV	IVQQQNLLR	634	10	26	41						2859
ENV	AIEAQHLLK	644	10	12	19						2860
ENV	LLKLTWGIK	651	10	13	20						2861
ENV	LLQLTWGIK	651	10	34	53						2862
ENV	MLQLTWGIK	651	10	10	16	0.0055	0.0110				2863
ENV	RVLAVERYLK	665	10	18	28						2864
ENV	RVLAVERYLR	665	10	10	16						2865
ENV	LLGIWGCCK	678	10	50	78						2866
ENV	MIYGLIGLR	782	10	36	56						2867
ENV	AVLSIVNRVR	795	10	31	48						2868
ENV	FLALAWDDL	849	10	25	39						2869
ENV	RSCLFSYIIR	858	10	31	48						2870
ENV	GLRLGWGLK	892	10	10	32						2871
ENV	LLQVWSQELK	906	10	12	19						2872
ENV	AIIVAEGTDR	926	10	31	48						2873
ENV	AIILIPRRIR	946	10	12	19						2874
ENV	ITRIKQLER	951	10	12	19						2875
ENV	VTVYGVVPAK	47	11	41	64	0.8600	4.1000				2876
ENV	KTTLFCASDAK	60	11	12	19						2877
ENV	TTTLFCASDAK	60	11	22	34						2878
ENV	DISLWQSLK	120	11	38	59						2879
ENV	NTSALTQACTK	241	11	14	22						2880
ENV	NTSVITQACTK	241	11	13	20						2881
ENV	VSTVQCTHIGK	288	11	28	44						2882
ENV	VSTVQCTHIGR	288	11	23	36						2883
ENV	GSLAEIEVIR	310	11	12	19						2884
ENV	YATGDIIGDIR	368	11	11	17						2885
ENV	KLREIQFENK	405	11	01	25						2886
ENV	ITEGNITLQCR	478	11	01	50						2887
ENV	NANITPCRIK	478	11	01	50						2888
ENV	QINMWQEVGK	491	11	12	19						2889
ENV	SSNITGLLTR	516	11	19	30						2890
ENV	NTENKTETFR	537	11	01	17						2891
ENV	NTGNITETFR	537	11	01	17						2892
ENV	EIFRPGGDMR	544	11	15	23						2893
ENV	ETFRPGGDMR	544	11	20	31						2894
ENV	RSELYKYKVVK	558	11	29	45						2895

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
ENV	KIEPLGVPTK	568	11	15	24						2896
ENV	PLGVAPTAKR	571	11	19	30						2897
ENV	PTKAKRRVVOR	576	11	13	20						2898
ENV	KAKRRVVOREK	579	11	13	20						2899
ENV	INIITTHIREK	584	11	01	50						2900
ENV	VISTRTHIREK	584	11	01	50						2901
ENV	ASITLTVQAR	618	11	28	44						2902
ENV	GIVQQQNNLLR	633	11	25	39						2903
ENV	GIVQQQSNLLR	633	11	26	41						2904
ENV	ILLKLTWVGIR	650	11	13	20						2905
ENV	ILLQLTVWGIK	650	11	34	53						2906
ENV	TYWGIKQLQAR	655	11	48	75						2907
ENV	QLQARVLAVLR	661	11	33	52						2908
ENV	QLLGWGCSCGK	677	11	50	78						2909
ENV	NVPWSSWSNKK	693	11	10	16						2910
ENV	LIEESQQQIEK	740	11	20	31						2911
ENV	IMVGGILIGLR	781	11	34	54						2912
ENV	IIFAVLSIVNR	792	11	14	22						2913
ENV	IVFVLSIVNR	792	11	17	27						2914
ENV	FAVLSIVNRVR	794	11	31	48						2915
ENV	GHEEGGIEDR	829	11	12	19						2916
ENV	NLCFSYIIRLR	859	11	11	17						2917
ENV	SLCLFSYIIRLR	859	11	31	48						2918
ENV	LLGRRCWEALK	882	11	09	15						2919
ENV	NLLQYVWSQELK	905	11	12	19						2920
ENV	IAIAVAEGTDR	925	11	10	16						2921
ENV	IAIAVAEGTDR	925	11	21	33						2922
ENV	RAIITIPRIR	945	11	12	19						2923
GAG	GARA/SILR	2	8	10	16						2924
GAG	ASVLSGGK	5	8	29	45						2925
GAG	RLRNGGKK	20	8	49	77						2926
GAG	WASRELER	37	8	48	75						2927
GAG	QTGSEELR	71	8	12	19						2928
GAG	TLYCVIIQK	86	8	12	19						2929
GAG	TLYCVIIQK	86	8	15	23						2930
GAG	RIEVKDTK	93	8	13	20						2931
GAG	DTKEALDK	98	8	36	56						2932
GAG	DTKEALEK	98	8	12	19						2933
GAG	KIEEQNK	105	8	23	36						2934
GAG	PAADAEK	123	8	01	50						2935
GAG	RTLNAWVK	171	8	63	98						2936
GAG	WVKVVEEK	176	8	29	45						2937
GAG	WVKVVEEK	176	8	31	48						2938
GAG	QAAMQMLK	216	8	61	95						2939
GAG	PIPTQMR	243	8	19	27						2940
GAG	PIPTQMR	243	8	17	27						2941
GAG	PVAPQMR	281	8	10	16						2942
GAG	PVGEIYKR	281	8	18	28						2943
GAG	WILGLNK	289	8	40	63						2944
GAG	WILGLNK	289	8	57	89						2945

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.301$	$\Delta^*1.101$	$\Delta^*3.101$	$\Delta^*1.301$	Δ^*6801	SEQ ID NO
GAG	PTSILDIR	303	8	12	19						2946
GAG	PVSILDIR	303	8	16	25						2947
GAG	PVSILDIR	303	8	25	39						2948
GAG	GVGCPGIHK	376	8	37	58						2949
GAG	GVGCPGIHK	376	8	23	36	0.0012	0.0018				2950
GAG	ASAOQDLK	392	8	01	50						2951
GAG	ATAQQDLK	392	8	01	50						2952
GAG	AAAIMMQK	400	8	04	19						2953
GAG	AAAIMMQK	405	8	01	25						2954
GAG	SATIMMQK	405	8	01	25						2955
GAG	YTAVFMQR	405	8	02	50						2956
GAG	MMQKSNFK	409	8	10	16						2957
GAG	MMQKSNFK	409	8	10	16						2958
GAG	MMQKSNFK	409	8	23	36						2959
GAG	MMQKSNFK	409	8	49	77						2960
GAG	QMKDCTER	455	9	29	45						2961
GAG	RASVLSGGK	4	9	16	25						2962
GAG	KLDAWEKIR	12	9	10	16						2963
GAG	KLDAWEKIR	12	9	17	27						2964
GAG	DAWEKIRLR	14	9	44	69						2965
GAG	KIRLFGGK	18	9	34	53						2966
GAG	RLRFGGKK	20	9	17	27						2967
GAG	LLETSEGR	52	9	12	19						2968
GAG	ATLYCVIIQK	85	9	15	23	0.0150	0.7100				2969
GAG	MVHQASIPR	163	9	27	42	0.1800	0.0670	1.0000	2.1000	0.8400	2970
GAG	PIPVGEIYK	279	9	35	55	0.0002	0.0012	0.0006	0.0003	0.0003	2971
GAG	ILGLNKIVR	291	9	38	91	0.0008	0.0001	0.0012	0.0100	0.0004	2972
GAG	ILDIRQGPK	306	9	19	30						2973
GAG	NSATIMMQK	404	9	42	66	0.0420	0.0048	0.0006	0.0006	0.0002	2974
GAG	IMMQKSNFK	408	9	01	33						2975
GAG	IMMQKSNFK	408	9	10	16						2976
GAG	IVKCTNCGK	422	9	20	31						2977
GAG	IVKCTNCGK	422	9	13	20						2978
GAG	TVKCTNCGK	422	9	11	17						2979
GAG	IARNCRAPR	434	9	18	29						2980
GAG	IARNCRAPR	434	9	13	21	0.0049	0.0003	0.0330	0.0500	0.0039	2981
GAG	IARNCRAPR	434	9	20	32						2982
GAG	KIWPSSKGR	472	9	22	35						2983
GAG	KIWPSSKGR	472	9	13	21	0.0770	0.0005	0.4400	0.0087	0.0001	2984
GAG	KIWPSSKGR	472	9	10	16						2985
GAG	TAPPIESFR	496	9	15	23						2986
GAG	TAPPIESFR	508	9	02	67						2987
GAG	TAPPIESFR	508	9	01	33						2988
GAG	KIRLPGGKK	18	10	44	69	1.9000	0.0010	0.0008	0.0005	0.0001	2989
GAG	KLKIIIVWASR	31	10	13	20						2990
GAG	KLKIIIVWASR	31	10	17	27						2991
GAG	IVWASRELER	35	10	20	31						2992
GAG	IVWASRELER	35	10	26	41	0.0099	0.0066				2993
GAG	GLLETSEGR	51	10	16	25						2994
GAG	GLLETSEGR	51	10	16	25						2995

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*4801	SEQ ID NO
GAG	VATLYCVIQQ	84	10	12	19						2996
GAG	VATLYCVIQR	84	10	15	23						2997
GAG	KIHEQNKSK	105	10	15	23						2998
GAG	QMYHQNSIR	162	10	27	42						2999
GAG	NAWVKVIEEK	174	10	29	45			0.0740	0.1000	0.0430	3000
GAG	NAWVKVVEEK	174	10	30	47						3001
GAG	IAPGQMRPR	244	10	19	30						3002
GAG	PIPVGEIYKR	279	10	34	53						3003
GAG	IILGLNKIVR	290	10	57	89	0.0003	0.0001	0.0009	0.0010	0.0005	3004
GAG	YSPTSILDIR	301	10	12	19	0.0003	0.0006	0.0110	0.0260	0.0073	3005
GAG	YSPVSILDIR	301	10	16	25						3006
GAG	YSPVSILDIR	301	10	24	38						3007
GAG	SILDIRQGP	305	10	18	28						3008
GAG	SILDIRQGP	305	10	18	28						3009
GAG	YVDIRFKTLR	320	10	40	63	0.3100	0.7100	0.0017	0.0020	0.0060	3010
GAG	YVDIRFKTLR	320	10	27	42	0.0003	0.0006				3011
GAG	RAIQATQEVK	329	10	28	44						3012
GAG	RAIQATQEVK	329	10	12	19						3013
GAG	RAIQATQEVK	329	10	15	23						3014
GAG	RAIQATQEVK	329	10	27	42						3015
GAG	LYQANPDCR	346	10	59	92						3016
GAG	GVGGPSIIKAR	376	10	37	58	0.0002	0.0110				3017
GAG	GVGGPSIIKAR	376	10	37	58	0.0003	0.0001				3018
GAG	TIMMQRGNFR	407	10	22	34						3019
GAG	KTVMKFCNGK	421	10	12	21						3020
GAG	IIAKNCRAPR	433	10	08	16						3021
GAG	IIAKNCRAPR	433	10	18	28						3022
GAG	IIAKNCRAPR	433	10	13	20						3023
GAG	IIAKNCRAPR	433	10	20	31						3024
GAG	IIAKNCRAPR	434	10	16	25						3025
GAG	IIAKNCRAPR	434	10	13	21						3026
GAG	IIAKNCRAPR	434	10	13	21						3027
GAG	IIAKNCRAPR	434	10	20	32						3028
GAG	RAPRKIGCWK	439	10	51	80						3029
GAG	FLGKIWPSTK	469	10	23	36						3030
GAG	FLGKIWPSTK	469	10	23	36						3031
GAG	FLOKIWPSSK	469	10	13	20						3032
GAG	GTRPGNYVQK	480	10	10	16						3033
GAG	GTRPGNYVQK	480	10	01	50						3034
GAG	GTRPGNYVQK	480	10	01	50						3035
GAG	PTAPPEESR	495	10	15	23						3036
GAG	PTAPPEESR	507	10	02	67						3037
GAG	PTAPPEESR	507	10	01	33						3038
GAG	ITSLPKQEQK	526	10	01	50						3039
GAG	PSOKQEPIDK	528	10	11	18						3040
GAG	GARASVLSGK	2	11	29	46						3041
GAG	LSGOKLDAWEK	8	11	15	23						3042
GAG	KLDAWEKIRL	12	11	16	25						3043
GAG	KLDAWEKIRL	12	11	16	25						3044
GAG	KLRPGGKKK	18	11	30	47						3045
GAG	RLRPGGKKK	20	11	12	19						3046
GAG	RLRPGGKKK	20	11	19	30						3047
GAG	RLRPGGKKK	20	11	19	30						3048
GAG	HIVWASRELER	34	11	20	31						3049
GAG	HLVWASRELER	34	11	26	41						3050

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	TVATLYCVIIQK	83	11	12	19						3046
GAG	TVATLYCVIIQR	83	11	14	22						3047
GAG	EVKDTKEALDK	95	11	13	20						3048
GAG	ALDKIEEONK	102	11	17	27						3049
GAG	KIEEQNKSKK	105	11	15	23						3050
GAG	PAAADKEDSK	123	11	01	50						3051
GAG	ISPRTLNAWVK	168	11	36	56						3052
GAG	LSRPTLNWVK	168	11	17	27						3053
GAG	TINEFAAEWDR	225	11	53	83						3054
GAG	IIAGPIATGOMR	240	11	18	28						3055
GAG	IIAGPIPPQOMR	240	11	17	27						3056
GAG	PIAPQOMREPR	243	11	19	30						3057
GAG	PIPPQOMREPR	243	11	17	27						3058
GAG	WIILGLNKIVR	289	11	57	89						3059
GAG	TSILDIRQGPV	304	11	12	19						3060
GAG	VSILDIRQGPV	304	11	16	25						3061
GAG	VSILDIRQGPV	304	11	25	39						3062
GAG	DIKQGPKEPR	308	11	19	30						3063
GAG	DIKQGPKEPR	308	11	41	64						3064
GAG	LLVQNAIPDCV	345	11	58	91						3065
GAG	NANPDKTKILK	349	11	27	42						3066
GAG	NANPDKTKILK	349	11	18	28						3067
GAG	NANPDKTKILK	349	11	18	28						3068
GAG	ALIMIQKSNFK	406	11	06	15						3069
GAG	ATIMMQHGNFR	406	11	11	28						3070
GAG	MMQRGNFINQR	409	11	15	23						3071
GAG	IIIAKNCRAPRK	433	11	16	25						3072
GAG	IIIAKNCRAPRK	433	11	13	20						3073
GAG	IIIAKNCRAPRK	433	11	20	31						3074
GAG	IIIAKNCRAPRK	433	11	14	22						3075
GAG	IIIAKNCRAPRK	434	11	13	21						3076
GAG	IIIAKNCRAPRK	434	11	19	30						3077
GAG	IIIAKNCRAPRK	434	11	52	83						3078
GAG	CTERQANFLGK	459	11	01	50						3079
GAG	EITSLPKQEQK	525	11	10	16						3080
NEF	AVSQDLQK	48	8	11	17						3081
NEF	AVSRDLQK	48	8	11	17						3082
NEF	PLRPNTYK	102	8	10	16						3083
NEF	PLRPNTYK	102	8	49	77		0.0003				3084
NEF	LSFFLKEK	114	8	22	34						3085
NEF	LSHFLKEK	114	8	27	42						3086
NEF	GLIYSKKR	173	8	23	36						3087
NEF	YTPGPGIR	207	8	20	31						3088
NEF	YTPGPGIR	207	8	21	33						3089
NEF	YTPGPGIR	207	8	12	19						3090
NEF	YTPGPGIR	207	8	39	61						3091
NEF	LTFGWCFK	221	8	11	17						3092
NEF	KLVPYDPR	228	8	11	22						3093
NEF	ELIPEFYK	324	8	14	34						3094
NEF	ELIPEFYK	324	8	22	34						3095
NEF	ELIPEFYK	324	8	10	16						3096
NEF	GAVSQDLQK	47	9	11	17						3097
NEF	GAVSRDLQK	47	9	11	17						3098
NEF	PVAPQVPLR	95	9	48	75						3099

Table IX
HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
NEF	AVDLSIFLK	111	9	14	22	0.0740	1.1000	0.0009	0.0008	0.0025	3096
NEF	DLSPFLKEK	113	9	22	34						3097
NEF	GLSHFLKEK	113	9	27	42						3098
NEF	GLDGLIYSK	125	9	16	25						3099
NEF	GLEGLIYSK	125	9	10	16						3100
NEF	PLTFGWCFK	219	9	39	61						3101
NEF	AADGVGAVSR	42	10	09	15						3102
NEF	QVPLRMTYK	100	10	10	16						3103
NEF	QVPLRMTYK	100	10	46	72						3104
NEF	GAFDLSFLK	110	10	10	16						3105
NEF	GLDGLIYSK	125	10	14	22	0.6100	0.6300	0.0098	0.0130	0.0600	3106
NEF	GVGAVSDLDK	45	11	10	16						3107
NEF	GVGAVSDLEK	45	11	11	17						3108
NEF	AVDLSIFLK	111	11	13	20						3109
NEF	GLDGLIYSKR	125	11	14	22						3110
NEF	MAKELIPEYK	321	11	10	16						3111
POL	RANSPTR	26	8	16	25						3112
POL	RANSPTR	26	8	17	27						3113
POL	STNSPTSR	32	8	01	33						3114
POL	RANSPSSR	35	8	01	33						3115
POL	RANSPTR	37	8	01	50						3116
POL	ILIHICOK	149	8	14	22						3117
POL	LIEICGHIK	150	8	10	16						3118
POL	LIEICGCK	150	8	14	22						3119
POL	PIETVPVK	190	8	53	83						3120
POL	ETVPYKLIK	192	8	53	83	0.0049	0.0001				3121
POL	GMDGPKVK	201	8	51	80	0.0007	0.0004				3122
POL	PLTEEKIK	212	8	55	86						3123
POL	EICTEMEK	223	8	27	42						3124
POL	NTPIFAIK	246	8	24	38						3125
POL	NTPIFAIK	246	8	37	58	0.0003	0.0003				3126
POL	PFAIKKK	248	8	25	39						3127
POL	PFAIKKK	248	8	37	58	0.0003	0.0001				3128
POL	PAGLKKKK	286	8	52	81						3129
POL	PLDKDFRK	308	8	19	30						3130
POL	NVLRQGWK	336	8	63	100	0.0003	0.0012				3131
POL	KLEIFRK	355	8	23	36						3132
POL	DLGQIIR	381	8	52	81						3133
POL	ELGQIRAK	383	8	27	42						3134
POL	ELGQIRTK	383	8	22	34						3135
POL	RAKIEELR	388	8	26	41						3136
POL	RTKIEELR	388	8	22	34						3137
POL	ELRQHLLK	393	8	17	27						3138
POL	ELRQHLLK	393	8	15	23						3139
POL	WTVNDIQK	441	8	62	97		0.0001				3140
POL	DIQKLVGK	445	8	62	97	0.0003					3141
POL	ELELAENR	489	8	53	83						3142
POL	GVYYDPFK	508	8	43	67						3143
POL	DLIAEQK	516	8	28	44						3144
POL	QIYQEPFK	532	8	41	64	0.0010	0.0013				3145

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GAITNDVK	551	8	19	30						3146
POL	SAITNDVK	551	8	16	25						3147
POL	TAITNDVK	551	8	11	17						3148
POL	QLTEAVQK	559	8	37	58						3149
POL	QLTEVVQK	559	8	11	17						3150
POL	ESIVWQK	570	8	50	79						3151
POL	VIWQKTPK	573	8	48	75						3152
POL	KLWYQLEK	616	8	46	72						3153
POL	VVDGAANK	633	8	50	78	0.0003	0.0001				3154
POL	GAANRETK	636	8	45	70						3155
POL	KAGYVTRD	646	8	42	66						3156
POL	VTDRGRQK	650	8	40	63	0.0090	0.0065				3157
POL	LTDTTNRK	661	8	19	30						3158
POL	LTETTNQK	661	8	30	47						3159
POL	IIQAQPDK	697	8	40	63						3160
POL	IIQAQPDK	697	8	16	25						3161
POL	QHEQLIK	712	8	37	58						3162
POL	IIQELIK	713	8	37	58						3163
POL	LAWVPAIK	725	8	22	34						3164
POL	LSWVPAIK	725	8	37	58						3165
POL	KLVSAGIR	742	8	16	25						3166
POL	KLVSAGIR	742	8	29	45						3167
POL	LVSAGIRK	743	8	16	25						3168
POL	LVSAGIRK	743	8	27	42	0.0091	0.0054				3169
POL	KAQEIEIK	759	8	27	43						3170
POL	KAQEIEIK	759	8	16	25						3171
POL	NLPPVAVK	779	8	26	41						3172
POL	NLPPVAVK	779	8	27	42						3173
POL	EIVASCDK	787	8	45	70						3174
POL	ETAYFILK	848	8	31	48						3175
POL	ETAYFLK	848	8	27	42	0.0037	0.0430				3176
POL	FLKLAGR	852	8	32	50						3177
POL	FLKLAGR	852	8	25	39						3178
POL	LAGRWPK	856	8	50	78						3179
POL	GVVFSMNK	901	8	49	77						3180
POL	ESMNKELK	904	8	53	83						3181
POL	SMNKLKK	905	8	53	83						3182
POL	AVFIHNFK	931	8	62	97	0.0280	0.0380				3183
POL	FIHNFKKK	931	8	58	91						3184
POL	IASDQTK	956	8	14	22						3185
POL	IATDIQTK	956	8	36	56						3186
POL	ELQKQIK	964	8	13	21						3187
POL	ELQKQIK	964	8	35	56						3188
POL	ITKQNF	969	8	12	19						3189
POL	ITKQNF	969	8	36	57						3190
POL	RVVYRDSR	976	8	58	91						3191
POL	DSRDPIWK	981	8	35	55						3192
POL	DSRDPLWK	981	8	14	22						3193
POL	PIWKGPWK	985	8	36	56						3194
POL	PLWKGPWK	985	8	19	30						3195

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HIV Δ03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*3301	Δ*6801	SEQ ID NO
POL	DIKVVPRR	1009	8	48	75						3196
POL	EIKVVPRR	1009	8	16	25						3197
POL	VVPRKAK	1012	8	52	81	0.0027	0.0001				3198
POL	VVPRKVK	1012	8	11	17						3199
POL	KIKDYGK	1019	8	11	17						3200
POL	KIKDYGK	1019	8	50	78						3201
POL	LAFQGEAR	6	9	12	19						3202
POL	LAFQGEAR	6	9	16	25						3203
POL	QTRANSPT	21	9	15	24						3204
POL	NTNSPTSR	31	9	01	33						3205
POL	PTSRELQVR	36	9	01	33						3206
POL	PTSRELQVR	39	9	01	50	0.2700	0.0330	0.0010	0.0008	0.1100	3207
POL	TIKIGGOLK	99	9	17	27						3208
POL	DINLFGWK	122	9	13	20						3209
POL	ENLFGWK	122	9	12	19						3210
POL	NLFGWK	124	9	36	56						3211
POL	GIGGFIKVK	136	9	11	17						3212
POL	QIGGFIKVK	136	9	53	83	0.0008	0.0005	0.0062	0.0120	0.0001	3213
POL	QIGGFIKVK	148	9	14	22						3214
POL	ILHICGK	149	9	14	22						3215
POL	PTVNIIGR	166	9	54	84						3216
POL	QTEMIEGK	225	9	28	44	0.0008	0.0001	0.0007	0.0120	0.0002	3217
POL	NTPIFAIKK	246	9	24	38	0.0002	0.0001	0.0006	0.0006	0.0002	3218
POL	NTPIFAIKK	246	9	37	58	0.0330	0.0600	0.0006	0.0006	1.7000	3219
POL	AIKKDSTK	251	9	57	89	0.0017	0.0086	0.0018	0.0005	0.0001	3220
POL	LVDFRELNK	263	9	62	97	0.0110	0.0300	0.0006	0.0006	0.0002	3221
POL	GIPIPAGLK	282	9	56	89	0.2300	0.0650	0.0007	0.0005	0.0110	3222
POL	SVPLDKDFR	306	9	18	28						3223
POL	AFQSMTK	347	9	36	56	1.1000	0.9600	0.0076	0.0005	0.0230	3224
POL	MTKILEPFR	353	9	43	67	0.0008	0.0160	0.0008	0.4200	0.3100	3225
POL	TPDKKIIQK	404	9	57	89	0.0002	0.0042	0.0021	0.0029	0.0053	3226
POL	ASQIYAGIK	456	9	27	43	0.0013	0.3400	0.0005	0.0018	0.0001	3227
POL	ASQIYAGIK	456	9	28	44						3228
POL	QIYAGIKVK	458	9	20	32						3229
POL	QIYAGIKVK	458	9	12	19						3230
POL	QIYAGIKVK	458	9	14	22						3231
POL	GKVEQLCK	462	9	28	44						3232
POL	GKVEQLCK	462	9	19	30						3233
POL	LAENREIK	492	9	54	84						3234
POL	NLKTGKYAK	540	9	28	44	0.0002	0.0003	0.0004	0.0006	0.0001	3235
POL	NLKTGKYAR	540	9	29	46	0.0008	0.0001	0.0130	0.4400	0.0033	3236
POL	KTGKYAKMR	540	9	29	46						3237
POL	KTGKYAKMR	542	9	19	30						3238
POL	RSAITNDVK	542	9	13	21						3239
POL	IVWGTDPK	550	9	10	16						3240
POL	FVNTPLVK	572	9	48	75	0.0050	0.3700	0.9900	0.3000	0.0330	3241
POL	YVTDIGRQK	608	9	54	86	0.0120	0.0660	0.0009	0.0099	0.0380	3242
POL	SLTDITNQK	649	9	39	61	0.0011	0.0010	0.0006	0.0006	0.0039	3243
POL	SLTETTNQK	660	9	11	17						3244
POL	SLTETTNQK	660	9	21	33						3245
POL	GIHQAPDK	696	9	40	63	0.0009	0.0400	0.0006	0.0005	0.0003	3246

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
POL	GHQAPDR	696	9	16	25						3246
POL	QIEQLIKK	712	9	37	58	0.0091	0.1600	0.0006	0.0015	0.0120	3247
POL	YLAWVPATIK	724	9	22	34	0.0770	0.0570	0.0550	0.0800	4.0000	3248
POL	YLSWVPATIK	724	9	37	58						3249
POL	KLSAGIRK	742	9	16	25	0.1300	0.0770	0.0017	0.0020	0.0001	3250
POL	KLVSAGIRK	742	9	27	42						3251
POL	VLELXIDK	751	9	51	80	0.0380	0.0320	0.0006	0.0006	0.0004	3252
POL	ASCDKCLK	790	9	43	67	0.0027	0.0140	0.0020	0.0009	0.0001	3253
POL	KLGRWVPK	855	9	50	78	2.7000	0.0690	0.2100	0.0006	0.0002	3254
POL	AACWVAGIK	880	9	21	33	0.0130	0.0470	0.0023	0.0041	0.0014	3255
POL	ESMVKELK	904	9	53	83						3256
POL	MAVILNFK	930	9	60	94	0.0120	0.3000	0.0480	0.0560	3.2000	3257
POL	AVFIUNFKR	931	9	62	97	0.1700	1.8000	3.5000	0.2700	1.9000	3258
POL	IIASIIQTK	955	9	14	22						3259
POL	IIATIDIQTK	955	9	35	55	0.0250	0.0980	0.0007	0.0005	0.0002	3260
POL	DIQIKELQK	959	9	46	72	0.0009	0.0006	0.0006	0.0018	0.0001	3261
POL	QIKIQNER	968	9	12	19						3262
POL	QIKIQNER	968	9	35	55	0.0021	0.0035	0.2400	0.0060	0.2600	3263
POL	VIQDNDIK	1003	9	37	58	0.0009	0.0068	0.0006	0.0005	0.0001	3264
POL	VIQDNDSEIK	1003	9	12	19						3265
POL	NSDIKVVPR	1007	9	40	63						3266
POL	NSDIKVVPR	1007	9	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3267
POL	DIKVVPRK	1009	9	48	75						3268
POL	EIKVVPRK	1009	9	15	23						3269
POL	KVVPKAK	1011	9	52	81	0.0290	0.0039	0.3100	0.0008	0.0002	3270
POL	KVVPKRVK	1011	9	11	17						3271
POL	NLAFFQGEAR	5	10	10	16						3272
POL	NLAFFQGEAR	5	10	16	25						3273
POL	QTRANSPTTR	21	10	11	18						3274
POL	QTRANSPTSR	21	10	12	19						3275
POL	PSRANSPTSR	24	10	01	50						3276
POL	QTRANSPTSR	33	10	01	33						3277
POL	QTRANSPTTR	35	10	01	33						3278
POL	VTIKIGQLK	98	10	17	27	0.0370	0.2100	0.0017	0.0025	0.0640	3279
POL	VLEDINLPK	119	10	13	20						3280
POL	VLEDINLPK	119	10	12	19						3281
POL	MIGGIGGFK	133	10	62	97	0.0099	0.0550	0.0052	0.0012	0.3100	3282
POL	QILHICGKK	148	10	14	22						3283
POL	ISMETVPVK	188	10	53	83	0.0003	0.0310	0.0017	0.0025	0.0001	3284
POL	PIETVPVKLK	190	10	53	83	0.0002	0.0001	0.0009	0.0009	0.0003	3285
POL	KLKPGMDGPK	197	10	49	77	0.3900	0.0760	0.0009	0.0009	0.0003	3286
POL	LVETCTEMEK	221	10	15	24	0.0002	0.0120	0.0010	0.0013	0.0024	3287
POL	EMEKEGKISK	229	10	33	52	0.0004	0.0001	0.0009	0.0009	0.0003	3288
POL	NTPIFAIKK	246	10	24	38						3289
POL	NTPIFAIKK	246	10	37	58	0.0006	0.0046				3290
POL	FAIKKDDSTK	250	10	57	89	0.0004	0.0002				3291
POL	KLVDRELNK	262	10	62	97	0.5100	0.0900				3292
POL	LVDFRELNR	263	10	60	94						3293
POL	GIMPAAGLKK	282	10	54	86	0.0110	0.1700	0.0009	0.0009	0.0007	3294
POL	DAYESVPLDK	302	10	21	33						3295

Table IX
HIV Δ02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	Δ*1101	Δ*3101	Δ*3301	Δ*6801	SEQ ID NO
POL	FSVPLDKDFR	305	10	18	28						3296
POL	SVPLDKDFR	306	10	18	28						3297
POL	SINNETGIR	323	10	32	50						3298
POL	STNETGIR	323	10	11	17						3299
POL	PAIFQSSMTK	346	10	36	56		0.0830	0.0017	0.0025	0.0046	3300
POL	SMTKILEPFR	352	10	42	66	0.0760	0.0004				3301
POL	MTKILEPFR	353	10	22	34	0.0004	0.0004				3302
POL	GSDLEIGQIR	379	10	52	81	0.0150	0.0380	0.0150	0.0060	0.1100	3303
POL	DLEIGQIRAK	381	10	27	42						3304
POL	DLEIGQIRTK	381	10	21	33						3305
POL	FTPDKKIIQK	403	10	51	80	0.0002	0.0150	0.0010	0.0013	0.0273	3306
POL	WMGYELIIPDK	418	10	60	94	0.0005	0.0004	0.0009	0.0016	0.0003	3307
POL	TVQPIVLPEK	429	10	17	27						3308
POL	TVQPIVLPEK	429	10	13	20	0.1600	5.6000				3309
POL	DSWTVNDIQK	439	10	43	67	0.0007	0.0002				3310
POL	ESWTVNDIQK	439	10	11	17						3311
POL	WASQIYAGIK	455	10	27	42						3312
POL	WASQIYAGIK	455	10	28	44						3313
POL	KVKQLCKLLR	464	10	27	42						3314
POL	KVRQLCKLLR	464	10	19	30						3315
POL	QLCKLLRGAK	467	10	25	39						3316
POL	QLCKLLRGTK	467	10	21	33						3317
POL	EAELELAENR	487	10	53	83						3318
POL	EAELELAENR	491	10	54	84	0.0002	0.0003				3319
POL	ATESIVWCK	568	10	19	30						3320
POL	SVIWKTKPK	571	10	42	66						3321
POL	VIWGRTPKPK	573	10	17	27						3322
POL	VIWGRTPKPK	573	10	29	45						3323
POL	LVKLWYQLEK	614	10	46	72						3324
POL	AANRETKLKG	637	10	30	47			0.0075	0.0081	0.0097	3325
POL	KAGYVTDGR	646	10	39	61	0.0560	0.0016				3326
POL	VSLTDTNQK	659	10	10	16	0.0007					3327
POL	VSLTDTNQK	659	10	20	31						3328
POL	VSQIIEQLIK	710	10	19	30	0.0007	0.0370	0.0017	0.0025	0.0007	3329
POL	IEQLIKKIEK	713	10	30	47	0.0004	0.0003	0.0009	0.0008	0.0003	3330
POL	GIGNEQVDK	733	10	58	91	0.0005	0.0001	0.0009	0.0009		3331
POL	KVLELDGDK	750	10	48	75	0.3600	0.7800				3332
POL	VASCDKQLK	789	10	43	67	0.0004	0.0004				3333
POL	QLDCTIIEGK	814	10	60	95	0.0010	0.0003				3334
POL	GSNFTSAVK	870	10	26	41						3335
POL	GSNFTSTVK	870	10	11	17						3336
POL	KAACWAGIK	879	10	20	32	0.0300	0.0740	0.0017	0.0025	0.0002	3337
POL	VVESMANKEL	902	10	48	75						3338
POL	ELKKIGQVR	909	10	56	88	0.0009	0.0093				3339
POL	QVRDQAEILK	916	10	44	69						3340
POL	QVREQAEILK	916	10	13	20						3341
POL	QMAVEIINFK	929	10	60	94	0.6100	0.6400	0.0240	0.0083	0.0610	3342
POL	MAVEIINFKR	930	10	60	94	0.0068	0.0083				3343
POL	AVFIINFKR	931	10	58	91	0.6600	0.8500				3344
POL	GIGGYSAGER	942	10	58	91	0.0003	0.0001	0.0010	0.0029	0.0003	3345

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
POL	DIASDIQTK	954	10	14	22						3346
POL	DILATDIQTK	954	10	34	53						3347
POL	KIONERLYYYR	971	10	52	81				0.0170	0.0170	3348
POL	VVIQDINSDIK	1002	10	37	58				0.0850	0.0380	3349
POL	VVIQDINSSEIK	1002	10	12	19				0.0013	0.0018	3350
POL	NSDIKVVPRR	1007	10	40	63						3351
POL	NSEIKVVPRR	1007	10	12	19		0.0001				3352
POL	KAKIIRDYGR	1017	10	41	64						3353
POL	MAGDDCVAGR	1028	10	24	38		0.0018				3354
POL	MAGDDCVASR	1028	10	19	30						3355
POL	NSPTSRELQVR	34	11	01	33						3356
POL	NSPTSRELQVR	37	11	01	50						3357
POL	NSPTSRELQVR	39	11	01	50						3358
POL	FSFOITLWQR	85	11	14	22						3359
POL	TLWORPLVTIK	91	11	17	27						3360
POL	TLWORPLVTIK	91	11	13	20						3361
POL	LVTKIGGQGLK	97	11	13	20						3362
POL	TVLEIDNLPCK	118	11	13	20						3363
POL	TVLEIDNLPCK	118	11	12	19						3364
POL	DINLPCKWKPK	122	11	13	20						3365
POL	EINLPCKWKPK	122	11	12	19						3366
POL	KMIGGIGGFK	132	11	62	97						3367
POL	PSIPIETVPVK	187	11	53	83	2.3000	0.7000				3368
POL	KVKQWPLTEEK	207	11	46	72						3369
POL	ALVEICTEMEK	220	11	15	23	0.0750	0.0330				3370
POL	EICTEMEKEGK	223	11	27	42						3371
POL	AIKKKDKSTKWR	231	11	57	89						3372
POL	STKWRKLVDFR	257	11	58	91						3373
POL	KLVDREFLNKR	262	11	60	94						3374
POL	QLGPIPIAGLK	280	11	36	89						3375
POL	GIPIIAPAGLKKK	282	11	53	84						3376
POL	FSVPLDKDFRK	305	11	18	28						3377
POL	PSNNLTPIGR	322	11	31	48						3378
POL	PSNNEITPIGR	322	11	32	17						3379
POL	SSMTKILEPFR	351	11	32	50						3380
POL	SMTKILEPFRK	352	11	22	34						3381
POL	KIEELREILLK	390	11	13	20						3382
POL	KIEELRQILLR	390	11	15	23						3383
POL	LLKRGFTTDDK	398	11	23	36						3384
POL	LLRWGFTTDDK	398	11	23	36						3385
POL	WTVQPIQLPEK	428	11	17	27						3386
POL	WTVQPIVLPEK	428	11	13	20	0.0011	0.0510				3387
POL	TVNDIQKLVGK	442	11	61	95	0.0400	0.1700				3388
POL	ASQIYAGIKVK	456	11	20	32						3389
POL	ASQYFGIKVK	456	11	12	19						3390
POL	ASQIYFGIKVK	456	11	14	22						3391
POL	YAGIKVKQLCK	460	11	18	28						3392
POL	PVIIGVYDFSK	505	11	39	61						3393

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.301$	$\Delta^*1.101$	$\Delta^*3.101$	$\Delta^*6.801$	SEQ ID NO
POL	QIYQEPFKNLK	532	11	40	63	0.2800	0.2900			3396
POL	NLKTGKYAKMR	540	11	18	29					3397
POL	NLKTGKYARMR	540	11	13	21					3398
POL	RMGAIITNDVK	548	11	12	19					3399
POL	DVKQLTEAVQK	556	11	33	52	0.0048	0.0240			3400
POL	IATESIVIWGK	567	11	14	22					3401
POL	ESIVIWGKTPK	570	11	41	65					3402
POL	IWIWGKTPFK	572	11	17	27					3403
POL	IWIWGKTPKFR	572	11	29	45					3404
POL	KTPKFLPIQK	577	11	14	22					3405
POL	KTPKFLPIQK	577	11	22	34					3406
POL	PLVKLWYQLEK	613	11	45	70					3407
POL	ETFYVDGAANR	630	11	43	67					3408
POL	YVDGAANRETK	633	11	44	69					3409
POL	GAANRETKLQK	636	11	30	47					3410
POL	KLCKAGYVTDK	643	11	24	38					3411
POL	VVSLTUTINQK	658	11	10	16					3412
POL	VVSLTUTINQK	658	11	11	17					3413
POL	ALGHQAPDK	694	11	39	61					3414
POL	ALGHQAPDKR	694	11	15	23					3415
POL	LVNQIEQLIK	709	11	15	23					3416
POL	LVNQIEQLIK	709	11	18	28					3417
POL	VSQIEQLIK	710	11	19	30					3418
POL	QIEQLIKKEK	712	11	30	47					3419
POL	KVYLAWVPALIK	722	11	20	32	R.6000	2.3000			3420
POL	KVYLSWVPALIK	722	11	23	37					3421
POL	QVDKLVSSGIR	739	11	15	23					3422
POL	QVDKLVSSGIR	739	11	29	45					3423
POL	GIDKAQEIEIK	756	11	25	39					3424
POL	GIDKAQEIEIK	756	11	14	22					3425
POL	VAKETVASCDC	784	11	45	71					3426
POL	IVASCDCQLK	788	11	43	67	0.0970	0.1000			3427
POL	TAYFLLKLAGR	849	11	31	48					3428
POL	TAYFLLKLAGR	849	11	24	38					3429
POL	ILKLACRWPK	853	11	30	47					3430
POL	LLKLACRWPK	853	11	20	31					3431
POL	QSQGVVSMNK	898	11	49	77					3432
POL	GVVSMNKELK	901	11	48	75					3433
POL	VVSMNKELK	902	11	48	75					3434
POL	QMAVFIINFKR	939	11	60	94					3435
POL	MAYFIINFKR	930	11	57	89					3436
POL	ASDIQTKELQK	957	11	11	17	0.0051	0.1800			3437
POL	ATDIQTKELQK	957	11	35	55					3438
POL	QTKELQKQIK	961	11	10	16					3439
POL	QTKELQKQIK	961	11	32	50	0.0050	0.0100			3440
POL	AVVQDNSEIK	1000	11	37	58	0.0004	0.0150			3441
POL	AVVQDNSEIK	1000	11	12	19					3442
POL	NSDIKVVPRRK	1007	11	40	63					3443
POL	NSDIKVVPRRK	1007	11	11	17					3444
POL	DIKVVFRKAK	1009	11	39	61					3445

Table IX
 IIIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	EIKVPRKAK	1009	11	13	20						3446
POL	VVPRKAKIR	1012	11	42	66						3447
POL	OMAGDDCVAGR	1027	11	24	38						3448
POL	OMAGDDCVAGR	1027	11	19	30						3449
REV	DSDEELK	7	8	12	19						3450
REV	QARKNRR	40	8	17	27						3451
REV	QARKNRR	40	8	38	59						3452
REV	RARQRI	50	8	12	19						3453
REV	ILSTCLGR	63	8	12	19						3454
REV	GTETGVGR	103	8	06	19						3455
REV	LLKTVRLIK	12	9	10	16						3456
REV	GTRQARKNR	36	9	15	23						3457
REV	GTRQARKNR	36	9	34	53						3458
REV	GTRQARKNR	37	9	01	50						3459
REV	TTRQARKNR	37	9	01	50						3460
REV	QARKNRRR	40	9	16	25						3461
REV	QARKNRRR	40	9	38	59						3462
REV	RILSTCLGR	62	9	12	19						3463
REV	PLQLPIER	76	9	11	17						3464
REV	PLQLPIER	76	9	35	55						3465
REV	PSPEGTQARK	31	10	13	20						3466
REV	GTRQARKNR	36	10	15	23						3467
REV	GTRQARKNR	36	10	34	53						3468
REV	GTRQARKNR	37	10	01	50						3469
REV	TTRQARKNR	37	10	01	50						3470
REV	RSGDSEELK	4	11	11	17						3471
REV	PSPEGTQARK	31	11	13	20						3472
REV	GTRQARKNR	36	11	14	22						3473
REV	GTRQARKNR	36	11	34	53						3474
REV	GTRQARKNR	37	11	01	50						3475
REV	TTRQARKNR	37	11	01	50						3476
REV	QARKNRRRWR	40	11	16	25						3477
REV	QARKNRRRWR	40	11	37	58						3478
REV	PVPLQLPIER	74	11	11	17						3479
REV	PVPLQLPIER	74	11	34	53						3480
TAT	GLGISYGR	45	8	55	87						3481
TAT	GLISYGRKK	47	8	58	91						3482
TAT	ISYGRKKR	48	8	58	91						3483
TAT	PTGPKESK	88	8	20	31						3484
TAT	TACNNCYCK	23	9	17	27						3485
TAT	TACTNCCYCK	23	9	10	16						3486
TAT	GLGISYGRK	45	9	55	87						3487
TAT	GLISYGRKKR	47	9	57	89						3488
TAT	ISYGRKKR	48	9	57	89						3489
TAT	PTGPKESK	88	9	46	72						3490
TAT	ESKKVESK	93	9	18	28						3491
TAT	PVDPRLFPWK	3	10	12	19						3492
TAT	TACNNCYCKK	23	10	11	17						3493
TAT	GLGISYGRKK	45	10	55	87						3494
TAT	GLISYGRKKR	47	10	45	70						3495

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*1301	Δ^*6801	SEQ ID NO
TAT	PTGPKESKKK	88	10	12	19						3496
TAT	KAGPGYPRR	101	10	01	50						3497
TAT	GLGISYGRKKR	45	11	54	86						3498
TAT	ISYGRKKRRQR	48	11	39	61						3499
TAT	KAGPGYPRRK	101	11	01	50						3500
VIF	LIVWQVDR	8	8	10	16						3501
VIF	MIWQVDR	8	8	46	72						3502
VIF	QVDRMKIR	12	8	13	20						3503
VIF	QVDRMKIR	12	8	34	53						3504
VIF	RMINTWK	15	8	10	16						3505
VIF	RMINTWK	15	8	15	23						3506
VIF	RTWKSIVK	19	8	15	23						3507
VIF	RTWNSIVK	19	8	15	23						3508
VIF	HIPLGDAR	56	8	27	42						3509
VIF	HIPLGEAR	56	8	13	20						3510
VIF	GVSEWRK	87	8	16	25						3511
VIF	GVSEWRK	87	8	15	23						3512
VIF	GVSEWRK	87	8	15	23						3513
VIF	GVSEWRK	87	8	15	23						3514
VIF	GVSEWRK	87	8	15	23						3515
VIF	GVSEWRK	87	8	15	23						3516
VIF	GVSEWRK	87	8	15	23						3517
VIF	GVSEWRK	87	8	15	23						3518
VIF	GVSEWRK	87	8	15	23						3519
VIF	GVSEWRK	87	8	15	23						3520
VIF	GVSEWRK	87	8	15	23						3521
VIF	GVSEWRK	87	8	15	23						3522
VIF	GVSEWRK	87	8	15	23						3523
VIF	GVSEWRK	87	8	15	23						3524
VIF	GVSEWRK	87	8	15	23						3525
VIF	GVSEWRK	87	8	15	23						3526
VIF	GVSEWRK	87	8	15	23						3527
VIF	GVSEWRK	87	8	15	23						3528
VIF	GVSEWRK	87	8	15	23						3529
VIF	GVSEWRK	87	8	15	23						3530
VIF	GVSEWRK	87	8	15	23						3531
VIF	GVSEWRK	87	8	15	23						3532
VIF	GVSEWRK	87	8	15	23						3533
VIF	GVSEWRK	87	8	15	23						3534
VIF	GVSEWRK	87	8	15	23						3535
VIF	GVSEWRK	87	8	15	23						3536
VIF	GVSEWRK	87	8	15	23						3537
VIF	GVSEWRK	87	8	15	23						3538
VIF	GVSEWRK	87	8	15	23						3539
VIF	GVSEWRK	87	8	15	23						3540
VIF	GVSEWRK	87	8	15	23						3541
VIF	GVSEWRK	87	8	15	23						3542
VIF	GVSEWRK	87	8	15	23						3543
VIF	GVSEWRK	87	8	15	23						3544
VIF	GVSEWRK	87	8	15	23						3545

Table IX
 HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.301$	$\Delta^*1.101$	$\Delta^*3.101$	$\Delta^*6.801$	SEQ ID NO
VIF	ALTALIKPKK	154	10	11	17					3546
VIF	PSVKLTEDR	173	10	13	20					3547
VIF	VMIVWQVDRMR	7	11	41	64					3548
VIF	IVWQVDRMKIR	9	11	12	19					3549
VIF	IVWQVDRMRIR	9	11	33	52					3550
VIF	QVDRMKINTWK	12	11	10	16					3551
VIF	QVDRMKINTWK	12	11	14	22					3552
VIF	SLVKHHIMYVSK	23	11	12	19					3553
VIF	LVKHHIMYVSKK	24	11	12	19					3554
VIF	ITYWGLITIGER	69	11	22	34					3555
VIF	ILGIGVSEWR	83	11	22	34					3556
VIF	ILGQGVSEWR	83	11	25	39					3557
VIF	YLALTALIKPK	152	11	13	20					3558
VIF	LALTALIKPKK	153	11	11	17					3559
VIF	LTEDRWNKPKQ	178	11	21	33					3560
VIF	LVEDRWNKPKQ	178	11	10	16	0.0390	0.0130			3561
VPR	ELKNEAVR	25	8	17	27					3562
VPR	ELKSEAVR	25	8	16	25					3563
VPR	EAVRIIFPR	29	8	59	92					3564
VPR	QLLFVIFR	66	8	44	69					3565
VPR	QLLFVIFR	66	8	10	16					3566
VPR	RIGGQHSR	74	8	47	73					3567
VPR	RIGGQHSR	74	8	10	16					3568
VPR	ISRIQIR	79	8	10	16					3569
VPR	ISRIQIR	79	8	11	17					3570
VPR	ISRIQIR	81	8	10	16					3571
VPR	ISRIQIR	85	8	01	50					3572
VPR	ISRIQIR	85	8	01	50					3573
VPR	ISRIQIR	93	8	19	30					3574
VPR	ISRIQIR	93	8	10	16					3575
VPR	ISRIQIR	19	9	44	69					3576
VPR	ISRIQIR	19	9	16	25					3577
VPR	ISRIQIR	54	9	11	17					3578
VPR	ISRIQIR	69	9	11	17					3579
VPR	ISRIQIR	81	9	10	16					3580
VPR	ISRIQIR	81	9	39	62					3581
VPR	ISRIQIR	3	10	09	15					3582
VPR	ISRIQIR	18	10	42	69					3583
VPR	ISRIQIR	18	10	14	22					3584
VPR	ISRIQIR	27	10	10	16					3585
VPR	ISRIQIR	79	10	10	16					3586
VPR	ISRIQIR	22	11	17	27					3587
VPR	ISRIQIR	22	11	16	25					3588
VPR	ISRIQIR	52	11	18	28					3589
VPR	ISRIQIR	52	11	35	55					3590
VPR	ISRIQIR	63	11	11	17					3591
VPR	ISRIQIR	67	11	10	16					3592
VPR	ISRIQIR	79	11	10	16					3593
VPR	ISRIQIR	35	8	12	19					3594
VPR	ISRIQIR	36	8	01	50					3595
VPR	ISRIQIR	43	8	15	23					3596
VPR	ISRIQIR	52	8							3597

Table IX
 HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*6801	SEQ ID NO
VPU	LIDRIR	58	8	14	22					3596
VPU	VTLLSSK	94	8	01	50					3597
VPU	WTIVFIEYR	34	9	10	16					3598
VPU	LYQRKQDR	43	9	01	50					3599
VPU	ILRQEKIDR	46	9	15	23					3600
VPU	KLIDRIR	56	9	10	16					3601
VPU	LVTLSSSK	91	9	01	50					3602
VPU	KILRQKIDR	45	10	15	23	0.0039	0.0001			3603
VPU	KIDRLIDRIR	52	10	10	16					3604
VPU	VVWTTV/FIEYR	31	11	10	16					3605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LILGLVII	21	8	09	15		3606
ENV	KLWTVYY	44	8	11	17		3607
ENV	NLWTVYY	44	8	35	56		3608
ENV	VYGVVW	49	8	55	86		3609
ENV	DTEVINW	75	8	19	30		3610
ENV	NVTENFM	101	8	34	53		3611
ENV	VTFENFMW	101	8	34	53		3612
ENV	SLKPCVKL	102	8	34	53		3613
ENV	LTPLCVTL	128	8	55	86		3614
ENV	HYCAPAGF	135	8	54	84		3615
ENV	IYCTPAGF	262	8	27	42		3616
ENV	CTPAGFAI	264	8	11	17		3617
ENV	TVQCTHGI	290	8	10	16		3618
ENV	PVSTQLL	300	8	51	80		3619
ENV	VVSTQLLL	301	8	60	94		3620
ENV	QLLLNGSL	305	8	60	94		3621
ENV	NTKRSIRI	351	8	57	89		3622
ENV	RIGPGQTF	357	8	10	16		3623
ENV	GIGPGQTF	360	8	11	17		3624
ENV	SYSGQAF	360	8	01	33		3625
ENV	FYATGDII	367	8	01	19		3626
ENV	KLREIQF	405	8	12	25		3627
ENV	SPNCUGHF	437	8	01	56		3628
ENV	SPNCRGEF	437	8	36	25		3629
ENV	FYCNISGL	445	8	16	33		3630
ENV	ITEGNITL	478	8	21	50		3631
ENV	NITLPCRI	482	8	01	17		3632
ENV	TITLPCRI	482	8	14	22		3633
ENV	RIKOINNM	488	8	30	47		3634
ENV	RIKOINNM	488	8	12	19		3635
ENV	QIRCSNI	512	8	11	17		3636
ENV	STNGTETF	537	8	01	17		3637
ENV	KVKIEPL	565	8	25	39		3638
ENV	AVGIGAVF	595	8	11	17		3639
ENV	STMGAASI	614	8	39	61		3640
ENV	LTVOARQL	623	8	38	59		3641
ENV	TVQARQLL	624	8	36	56		3642
ENV	IVQQNNL	634	8	26	41		3643
ENV	IVQQSNL	634	8	32	50		3644
ENV	AIQAQQL	644	8	49	77		3645
ENV	HILLKLTW	650	8	13	20		3646
ENV	HILLKLTW	650	8	34	53		3647
ENV	HMLQLTW	650	8	10	16		3648
ENV	TVWGIKQL	655	8	59	92		3649
ENV	RVLAVERY	665	8	33	52		3650
ENV	VLAVERYL	666	8	34	53		3651
ENV	RYLKDOQL	671	8	30	47		3652
ENV	RYLRDQQL	671	8	18	28		3653
ENV	YLRDQQL	672	8	31	48		3654
ENV	YLRDQQL	672	8	18	28	0.0001	3655

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ2401	SEQ ID NO
ENV	IWGCSCKL	681	8	48	75		3656
ENV	NVPWNSW	693	8	13	20		3657
ENV	EWDMNTW	716	8	13	20		3658
ENV	IWDMNTWM	717	8	11	17		3659
ENV	IWNMTWM	717	8	17	27		3660
ENV	WMEWEREI	723	8	12	19		3661
ENV	DLALDKW	754	8	21	33		3662
ENV	ELLELDKW	754	8	20	31		3663
ENV	ALDKWASL	757	8	11	17		3664
ENV	ELDKWASL	757	8	18	28		3665
ENV	KWASLWNW	760	8	26	41		3666
ENV	SLWNWFDI	763	8	17	27		3667
ENV	WFDITNWL	767	8	10	16		3668
ENV	DITNWLWY	769	8	10	16		3669
ENV	ITKWLWYI	770	8	16	25		3670
ENV	ITNWLWYI	770	8	19	30		3671
ENV	KWLWYIKI	772	8	19	30		3672
ENV	NWLWYIKI	772	8	25	39		3673
ENV	WLWYIKIF	773	8	50	77		3674
ENV	LWYIKIFI	774	8	49	77		3675
ENV	WYIKIFIM	775	8	43	67		3676
ENV	YIKIFIMI	776	8	43	67		3677
ENV	FIMVGGI	780	8	44	69		3678
ENV	IMVGGI	781	8	35	56		3679
ENV	IVGGLGL	783	8	42	66		3680
ENV	IVGGLVGL	783	8	10	16		3681
ENV	GLIGLRII	786	8	15	23		3682
ENV	LIGLRIIF	787	8	16	25		3683
ENV	LIGLRIVF	787	8	29	45		3684
ENV	IFAVLSI	792	8	15	23		3685
ENV	IVFAVLSI	792	8	20	31		3686
ENV	PLSFQTL	809	8	10	16		3687
ENV	SIRLVNGF	842	8	13	20		3688
ENV	SIRLVSGF	842	8	13	20		3689
ENV	LVNGFLAL	845	8	14	22		3690
ENV	LVSGFLAL	845	8	14	22		3691
ENV	AWDDLKSL	853	8	20	31		3692
ENV	DLRNLCLF	856	8	17	27		3693
ENV	DLRSLCLF	856	8	38	59		3694
ENV	CLFSYHRL	861	8	42	66		3695
ENV	SYIIRLRF	864	8	18	28		3696
ENV	SYHRLRDL	864	8	23	36		3697
ENV	RURDLCLI	867	8	13	20		3698
ENV	ELLGRHSL	881	8	09	15		3699
ENV	ELLGRRGW	881	8	23	37		3700
ENV	GWEALKYL	896	8	12	19		3701
ENV	GWEGLKYL	896	8	12	19		3702
ENV	YWNLLQY	902	8	15	23		3703
ENV	WNNLLQYW	903	8	15	23		3704
ENV	SLLNATAI	920	8	14	22		3705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	ILIHPRRI	947	8	13	20		3706
ENV	PTIRQQL	951	8	12	19		3707
ENV	TVYGVVW	48	9	55	86		3708
ENV	VWKEATTL	55	9	22	34	0.0300	3709
ENV	PTDFNPOEI	89	9	25	39		3710
ENV	NVTENFNW	101	9	34	53		3711
ENV	NFNWKNNDM	105	9	12	19		3712
ENV	NFNWKNNDM	105	9	18	28		3713
ENV	MVEQNIHEDI	113	9	23	36		3714
ENV	QMHIEDISL	116	9	29	45		3715
ENV	IISLWDQSL	121	9	38	59		3716
ENV	VISLWDQSL	121	9	10	16		3717
ENV	KLTLCVTL	134	9	52	81		3718
ENV	EIKNCSFNI	181	9	20	13		3719
ENV	LINCNTSAI	237	9	15	23		3720
ENV	KVSFEPIH	252	9	30	47		3721
ENV	SFEMPHY	254	9	31	48		3722
ENV	ILKCNPKKF	271	9	12	19		3723
ENV	STVQCTHGI	289	9	51	80		3724
ENV	PVYSTQLL	300	9	60	94		3725
ENV	SLAEIEVVI	311	9	13	20		3726
ENV	RIGPGQTFY	357	9	11	17		3727
ENV	GIGPGQTFY	360	9	01	33		3728
ENV	SIGSQAFY	360	9	01	33		3729
ENV	ATGDHIGDI	369	9	12	19		3730
ENV	DIRQAIICNI	380	9	15	23		3731
ENV	DLEITTHSF	428	9	21	33		3732
ENV	SFNCRGIEFF	437	9	35	55		3733
ENV	FLYCNISGL	437	9	16	25		3734
ENV	FLYCNISGLF	444	9	21	33		3735
ENV	TLPCRIRKQI	445	9	26	41		3736
ENV	RIKQINMW	484	9	30	47		3737
ENV	RIKQINMW	488	9	12	19		3738
ENV	MWQEVGKAM	495	9	15	23		3739
ENV	MWQEVGQAM	495	9	10	16		3740
ENV	IFRPGGGDM	545	9	17	27		3741
ENV	TRPGGGDM	545	9	25	39		3742
ENV	NWRSELYKY	556	9	54	84		3743
ENV	LYKYKVVVI	561	9	13	20	0.0200	3744
ENV	LYKYKVVVI	561	9	29	45		3745
ENV	AVGIGAVFL	595	9	11	17		3746
ENV	GIGAVFLGF	598	9	11	17		3747
ENV	MLGAMFLGF	599	9	04	18		3748
ENV	TIGAMFLGF	599	9	03	16		3749
ENV	FLGAAGSTM	608	9	55	86		3750
ENV	TMGAAITL	615	9	39	61		3751
ENV	TLTVQARQL	622	9	37	58		3752
ENV	LTVQARQL	623	9	36	56		3753
ENV	GIVQQNNL	633	9	26	41		3754
ENV							3755

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta\epsilon_{2401}$	SEQ ID NO
ENV	GIVQQSNL	633	9	32	50		3756
ENV	IVQQQNNL	634	9	26	41		3757
ENV	IVQQSNLL	634	9	32	50		3758
ENV	AVEAQHLL	644	9	48	75		3759
ENV	LLKLTWGI	651	9	13	20		3760
ENV	MLQLTVWGI	651	9	34	53		3761
ENV	MLQLTVWGI	651	9	10	16		3762
ENV	LTWVGKQL	654	9	59	92		3763
ENV	RVLAVERYL	665	9	33	52		3764
ENV	RYLKDQQL	671	9	29	45	0.7600	3765
ENV	RYLRDQQL	671	9	17	27	0.2300	3766
ENV	GIWGCCKL	680	9	48	75		3767
ENV	IWGCCKLI	681	9	48	75		3768
ENV	LICTTAVPW	688	9	19	30	0.0270	3769
ENV	LICTTAVPW	688	9	17	27		3770
ENV	LICTTAVPW	688	9	12	19		3771
ENV	TWMEWEREI	722	9	12	19		3772
ENV	EWERIEDNY	725	9	11	17		3773
ENV	ALDKWASLW	757	9	11	17		3774
ENV	ELDKWASLW	757	9	18	28		3775
ENV	KWASLWNWF	760	9	26	41		3776
ENV	WFDITNWLW	767	9	10	16		3777
ENV	DITNWLWYI	769	9	10	16		3778
ENV	KWLWYKIF	772	9	16	25		3779
ENV	NWLWYKIF	772	9	25	39		3780
ENV	WLWYKIFI	773	9	49	77		3781
ENV	LWYKIFIM	774	9	43	67		3782
ENV	WYKIFIMI	775	9	43	67		3783
ENV	IFIMVGGI	779	9	41	64		3784
ENV	IFIMVGGI	780	9	35	55		3785
ENV	MIVGGLIGL	782	9	36	56		3786
ENV	GLIGLRIF	786	9	15	23		3787
ENV	GLIGLRIF	786	9	29	45		3788
ENV	GLRIFAVL	789	9	17	27		3789
ENV	GLRIFAVL	789	9	28	44		3790
ENV	RIIFAVLSI	791	9	14	22		3791
ENV	IVNRVQGY	791	9	19	30		3792
ENV	IVNRVQGY	799	9	38	59		3793
ENV	RVQRGYSP	802	9	55	86		3794
ENV	SIRLVNGFL	842	9	11	17		3795
ENV	SIRLVNGFL	842	9	13	20		3796
ENV	RLVNGFLAL	844	9	12	19		3797
ENV	RLVSGFLAL	844	9	19	30		3798
ENV	FLALAWDDL	849	9	25	39		3799
ENV	SYHRLRDFI	864	9	13	20		3800
ENV	SYHRLRDL	864	9	22	34		3801
ENV	LIAARTVEL	873	9	12	19		3802
ENV	SLKGLRLGW	889	9	11	17		3803
ENV	SIRGLQGW	889	9	05	08		3804
ENV	QLRLGWEC	892	9	10	32		3805

Table X
 HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RLGWGLKY	894	9	09	29		3806
ENV	KYWANLLQY	901	9	14	22		3807
ENV	YVWNLQY	902	9	15	23		3808
ENV	LLQYWSQEL	906	9	16	25		3809
ENV	ELKNSAINL	913	9	10	16		3810
ENV	ELKNSAISL	913	9	10	16		3811
ENV	ELKNSAVSL	913	9	12	19		3812
ENV	AVAEGLDRI	928	9	16	25		3813
ENV	ALILPRRI	946	9	12	19		3814
ENV	VTVYGVVFW	47	10	55	86		3815
ENV	PVWKEATTL	54	10	22	34		3816
ENV	VWKEATTLF	55	10	22	34		3817
ENV	LFASDAKAY	65	10	42	66	0.2700	3818
ENV	AYDTEVINW	73	10	18	28		3819
ENV	MWKNMVEQ	108	10	35	55		3820
ENV	NMVEQMIEDI	112	10	20	31	0.0004	3821
ENV	QMHEDIHDI	113	10	23	36		3822
ENV	QMHEDIHDI	116	10	29	45		3823
ENV	DIISLWQSL	120	10	38	59		3824
ENV	DVLSLWQSL	120	10	10	16		3825
ENV	RLNCNTSAT	236	10	15	24		3826
ENV	ITQACPKVSF	245	10	29	45		3827
ENV	PIIYCAGAGF	260	10	27	42		3828
ENV	PIIYCTPAGF	260	10	27	42		3829
ENV	IICAPAGFAI	262	10	10	16		3830
ENV	IYCTPAGFAI	262	10	10	16		3831
ENV	ILKCNDRKF	270	10	12	19		3832
ENV	GIRPVVSTQL	297	10	33	52		3833
ENV	GIRPVVSTQL	297	10	26	41		3834
ENV	STQLLNGSL	301	10	57	89		3835
ENV	NTSPRSVAY	376	10	01	33		3836
ENV	SNCGGEFF	437	10	35	55		3837
ENV	SNCGGEFF	437	10	16	25		3838
ENV	FFYCNSTSL	443	10	21	33		3839
ENV	FFYCNSTSL	444	10	21	33		3840
ENV	ITLPCRIKQI	483	10	25	39		3841
ENV	TLPCRIKQI	484	10	15	23		3842
ENV	NMWQEVCKA	494	10	15	23	0.0001	3843
ENV	NMWQEVCKAM	495	10	15	23		3844
ENV	MWQVGGQAM	495	10	10	16		3845
ENV	NTETNKTET	537	10	01	17		3846
ENV	NTETNKTET	537	10	01	17		3847
ENV	EIRPGGDM	544	10	17	27		3848
ENV	EIRPGGDM	544	10	21	33		3849
ENV	DMRDNWASEL	552	10	37	58		3850
ENV	ELYKYKVVET	560	10	13	21		3851
ENV	ELYKYKVVET	560	10	29	46		3852
ENV	KYKVVVIEPL	563	10	25	39		3853
ENV	GIGAVFLGFL	598	10	11	18		3854
ENV	MLGAMFLGFL	599	10	04	36		3855

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	TIGAMFLGFL	599	10	03	27		3856
ENV	GFLGAAGSTM	606	10	55	86		3857
ENV	STMGAASFIL	614	10	39	61		3858
ENV	ITLTVQARQL	621	10	27	42		3859
ENV	TLTVQARQL	622	10	35	55		3860
ENV	GIVQQQNNLL	633	10	26	41		3861
ENV	GIVQQQNNLL	633	10	32	50		3862
ENV	ILLKLTVMGI	650	10	13	20		3863
ENV	ILLKLTVMGI	650	10	34	53		3864
ENV	KLTVWGIKQL	653	10	13	20		3865
ENV	KLTVWGIKQL	653	10	44	69		3866
ENV	GIKQLOARVL	658	10	40	63		3867
ENV	YLRDQQLLGI	672	10	27	42		3868
ENV	YLRDQQLLGI	672	10	18	28		3869
ENV	GIWGCCKLI	680	10	48	75		3870
ENV	KLCTTAVPW	687	10	19	30		3871
ENV	KLCTTAVPW	687	10	17	27		3872
ENV	KLCTTAVPW	687	10	12	19		3873
ENV	TINVPWNSS	691	10	11	17		3874
ENV	IWNMTWME	717	10	10	16		3875
ENV	MTWMEWERE	721	10	12	19		3876
ENV	LLALDKWASL	755	10	11	17		3877
ENV	LLALDKWASL	755	10	18	28		3878
ENV	WFDITNWLW	767	10	10	16		3879
ENV	ITKWLWYIKI	770	10	15	23		3880
ENV	ITNWLWYIKI	770	10	14	22		3881
ENV	KWLWYIKIFI	772	10	16	25		3882
ENV	NWLWYIKIFI	772	10	25	39		3883
ENV	WLWYIKIFIM	773	10	43	67		3884
ENV	WLWYIKIFIM	774	10	43	67		3885
ENV	KIFIMVGGI	778	10	38	59		3886
ENV	IFMIVGGI	779	10	33	54		3887
ENV	IVGGIIGLI	781	10	34	54		3888
ENV	IVGGIIGLI	783	10	42	66		3889
ENV	SIVNLRVQGY	798	10	36	56		3890
ENV	GYSPLSFQIL	806	10	29	45		3891
ENV	LVSGLALAW	845	10	16	25		3892
ENV	GFLALAWDDL	848	10	25	39		3893
ENV	ALAWDDLRLSL	851	10	19	30		3894
ENV	AWDDLRLSL	853	10	20	31		3895
ENV	DLRLCLFSY	856	10	16	25		3896
ENV	DLRLCLFSY	856	10	11	17		3897
ENV	NCLFSYIIRL	859	10	31	48		3898
ENV	SLCLFSYIIRL	859	10	18	28		3899
ENV	LFSYIIRLDF	862	10	22	34		3900
ENV	LFSYIIRLDF	862	10	13	20		3901
ENV	SYIIRLDFIL	864	10	12	19		3902
ENV	SYIIRLDFIL	864	10	11	17		3903
ENV	LIARTVELL	873	10	22	34		3904
ENV	IVELLGRGW	879	10	22	34		3905

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LLGRBWEAL	882	10	09	15		3906
ENV	RLGWGLKYL	894	10	09	29		3907
ENV	KYWNLLQY	901	10	14	22		3908
ENV	NLLQYWSQEL	905	10	16	25		3909
ENV	ELKNSAVSL	913	10	10	16		3910
ENV	AVSLNATAI	918	10	11	17		3911
ENV	AVAEGTDRII	928	10	15	23		3912
ENV	AVAEGTDRVI	928	10	14	22		3913
ENV	IIIPKRIQGL	949	10	13	21		3914
ENV	NIPKRIQGL	949	10	11	17		3915
ENV	RIRQGLRAL	953	10	34	53		3916
ENV	WVTVYGVVPV	46	11	55	86		3917
ENV	PWKKEATITL	54	11	22	34		3918
ENV	TLFCASDARA	64	11	40	63		3919
ENV	CVPTDIPNQEI	87	11	25	39		3920
ENV	PTDIPNQEVL	89	11	12	19		3921
ENV	NMWKNMVE	107	11	30	47		3922
ENV	NMVEQMIEDII	112	11	20	31		3923
ENV	SLKIPCYKLTP	128	11	54	84		3924
ENV	CVKLTPLCVT	132	11	52	81		3925
ENV	VITQACPKVSF	244	11	14	22		3926
ENV	KVSFEPIPIHY	252	11	28	44		3927
ENV	IYCAPAGFAIL	262	11	27	42		3928
ENV	NVSTVQCTIGI	287	11	51	80		3929
ENV	GIRPVVSTQLL	297	11	26	41		3930
ENV	GIRPVVSTQLL	367	11	11	17		3931
ENV	GTAGNSSRAA	375	11	01	17		3932
ENV	TTIISFNCGE	432	11	16	33		3933
ENV	TTIISFNCGE	432	11	12	25		3934
ENV	VMIISFNCGE	432	11	13	19		3935
ENV	EFFYCNTSGLF	443	11	21	33		3936
ENV	NITLPCRIKQI	482	11	11	17		3937
ENV	ITLPCRIKQI	482	11	13	20		3938
ENV	ITLPCRIKQI	483	11	15	20		3939
ENV	NMWQEVGKA	494	11	15	23		3940
ENV	EVGKAMYAPPI	498	11	18	28		3941
ENV	RVGQAMYAPP	498	11	10	16		3942
ENV	QIRCSSNITGL	512	11	11	17		3943
ENV	DMRDNRVSEL	552	11	37	58		3944
ENV	VVEREKAVGI	588	11	11	17		3945
ENV	AVGIGAVFLGF	595	11	11	17		3946
ENV	SITLTVQARQL	620	11	27	42		3947
ENV	ITLTVQARQL	621	11	27	42		3948
ENV	TVQARQLLSGI	624	11	36	56		3949
ENV	LLRAIEAQHIL	641	11	45	70		3950
ENV	AIEAQHILKL	644	11	12	19		3951
ENV	AIEAQHILQL	644	11	35	55		3952
ENV	AVERYLKDOQ	668	11	23	36		3953
ENV	AVERYLRDQQ	668	11	11	17		3954
ENV							3955

Table X
 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RYLKDQQLGI	671	11	25	39		3956
ENV	RYLRDQQLGI	671	11	17	27		3957
ENV	YLRDQQLGI	672	11	27	42		3958
ENV	YLRDQQLGI	672	11	18	28		3959
ENV	LLGHVGCCKL	678	11	46	72		3960
ENV	CTTNVTVNS	690	11	11	17		3961
ENV	NMTWMEWER	720	11	12	19		3962
ENV	WMWEIERIDN	723	11	10	16		3963
ENV	ELLKDKWAS	754	11	15	23		3964
ENV	LLALDKWASL	755	11	11	17		3965
ENV	LELDK WASL	755	11	18	28		3966
ENV	ALDK WASLW	757	11	10	16		3967
ENV	ELDK WASLW	757	11	16	25		3968
ENV	KWASLWNWF	760	11	15	23		3969
ENV	WFDITNWLW	767	11	10	16		3970
ENV	IKWLWYKIF	770	11	12	19		3971
ENV	ITNWLWYKIF	770	11	14	22		3972
ENV	KWLWYKIFIM	772	11	15	23		3973
ENV	NWLWYKIFIM	772	11	15	23		3974
ENV	WLYWYKIFIM	773	11	43	67		3975
ENV	KIFIMVIGLI	778	11	48	72		3976
ENV	FINVIGLIGL	780	11	34	53		3977
ENV	MINVIGLIGL	782	11	36	56		3978
ENV	IVGGLIGLRI	783	11	19	19		3979
ENV	LIGLRIFAVL	787	11	15	23		3980
ENV	LIGLRIFAVL	787	11	15	23		3981
ENV	GLRIFA VLSI	789	11	14	22		3982
ENV	GLRIFA VLSI	789	11	19	30		3983
ENV	RVRQGYSPFS	802	11	47	73		3984
ENV	SIRLVSGFLAL	842	11	11	17		3985
ENV	RLVSGFLALA	844	11	16	25		3986
ENV	AWDDLRSICL	853	11	20	31		3987
ENV	CLFSYIIRLRF	861	11	18	28		3988
ENV	CLFSYIIRLRF	861	11	20	31		3989
ENV	LFSYIIRLRF	862	11	13	20		3990
ENV	SYIIRLRLDL	864	11	13	20		3991
ENV	SYIIRLRLDL	864	11	10	16		3992
ENV	RIVELLGRKG	878	11	22	34		3993
ENV	ELGRRGWEA	881	11	09	15		3994
ENV	GLRGWEGELK	892	11	09	29		3995
ENV	RLGWEGELKYL	894	11	07	23		3996
ENV	YWGQELKNSA	909	11	12	19		3997
ENV	AIAVAEGTDRI	926	11	16	25		3998
ENV	RIRQGLERALL	953	11	33	52		3999
GAG	SVLSGGEL	6	8	11	17		4000
GAG	SVLSGGEL	6	8	28	44		4001
GAG	KLDWWEKI	12	8	18	28		4002
GAG	KLDKWEKI	12	8	10	16		4003
GAG	IVWASREL	35	8	21	33		4004
GAG	LVWASREL	35	8	36	56		4005

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SI:Q ID NO
GAG	RFALNPGL	45	8	20	31		4006
GAG	RFVNPGL	45	8	16	25		4007
GAG	GTELRSL	73	8	12	19		4008
GAG	LENTVATL	80	8	16	25		4009
GAG	LYNTVATL	80	8	22	34		4010
GAG	LYCVIIQRI	87	8	13	20		4011
GAG	LYCVIIQRI	87	8	18	28		4012
GAG	KVSNQYPI	148	8	15	27		4013
GAG	KVSNQYPI	148	8	27	48		4014
GAG	NYHYONL	152	8	31	48		4015
GAG	KVIEKAF	178	8	24	38		4016
GAG	KVIEKAF	178	8	28	44		4017
GAG	VIPMFAL	189	8	46	72		4018
GAG	VIPMFAL	189	8	14	22		4019
GAG	ATIQDLNM	200	8	12	19		4020
GAG	DLNMMLNI	204	8	12	19		4021
GAG	TLQEQIAW	263	8	12	19		4022
GAG	TLQEQIGW	263	8	27	42		4023
GAG	WMTNNPPI	270	8	20	31		4024
GAG	WMTNNPPI	270	8	20	25		4025
GAG	PIPVGDIY	279	8	16	17		4026
GAG	PIPVGDIY	279	8	35	55		4027
GAG	DIYKRWH	284	8	17	27		4028
GAG	IYKRWH	284	8	39	61		4029
GAG	IYKRWH	285	8	54	84		4030
GAG	IILGLNKI	290	8	57	89		4031
GAG	GLNKIVRM	293	8	60	94		4032
GAG	RMYSPVSI	299	8	14	22		4033
GAG	RMYSPVSI	299	8	14	22		4034
GAG	MYSPTSIL	300	8	40	63		4035
GAG	MYSPTSIL	300	8	14	22		4036
GAG	ATQEVKNW	333	8	42	66		4037
GAG	ATQEVKNW	333	8	15	23		4038
GAG	NWMTDTLL	339	8	18	28		4039
GAG	NWMTDTLL	339	8	36	56		4040
GAG	ALGPAATL	360	8	16	25		4041
GAG	ALGPAATL	360	8	18	28		4042
GAG	IMMQKSNF	408	8	11	17		4043
GAG	IMMQKSNF	408	8	27	42		4044
GAG	CTERQANF	459	8	55	87		4045
GAG	ETIDKDLV	537	8	01	25		4046
GAG	ELYPLASL	543	8	14	22		4047
GAG	ELYPLTSL	543	8	11	17		4048
GAG	PLSLKSL	548	8	15	23		4049
GAG	PLSLKSL	548	8	12	19		4050
GAG	PLSLKSL	548	8	12	19		4051
GAG	LTSLSL	549	8	13	20		4052
GAG	LTSLSL	549	8	12	19		4053
GAG	SLFGNDPL	554	8	12	19		4054
GAG	SLFGSDPL	554	8	11	17		4055

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	Nh. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	KYRLKIIIVW	29	9	10	16		4056
GAG	KYRLKIIIVW	29	9	16	25		4057
GAG	IIIVWASREL	34	9	21	33		4058
GAG	IIIVWASREL	34	9	36	36		4059
GAG	RFALNPGLL	45	9	20	31		4060
GAG	RFVNPGLL	45	9	16	16	0.0100	4061
GAG	ETSEGRQI	54	9	25	25		4062
GAG	ILQLOPISL	62	9	16	17		4063
GAG	SLQIGSEL	69	9	14	22		4064
GAG	SLNTVATL	79	9	16	25		4065
GAG	SLNTVATL	79	9	22	34		4066
GAG	LFNTVATLY	80	9	15	23		4067
GAG	LYNTVATLY	80	9	22	34		4068
GAG	TYCVIIQKI	86	9	12	19		4069
GAG	TYCVIIQKI	86	9	15	23		4070
GAG	IVKDTKEAL	95	9	11	17		4071
GAG	EVKDTKEAL	95	9	20	31		4072
GAG	DTKEALEKI	98	9	32	50		4073
GAG	DTKEALEKI	98	9	10	16		4074
GAG	IVQNAQGM	155	9	21	33		4075
GAG	IVQNLQQM	155	9	29	45		4076
GAG	TLNAWVKVI	172	9	30	47		4077
GAG	AFSPFVIHM	184	9	50	78		4078
GAG	EVIPMFAL	188	9	46	72		4079
GAG	EVIPMFAL	188	9	14	22		4080
GAG	ATPQDLNMM	200	9	12	19		4081
GAG	ATPQDLNMM	200	9	42	66		4082
GAG	IVGGIIQAAM	211	9	12	19		4083
GAG	TVGGIIQAAM	211	9	47	73		4084
GAG	AMQMLKFTI	218	9	33	52		4085
GAG	AMQMLKFTI	218	9	26	41		4086
GAG	TINEEAEEW	225	9	53	83		4087
GAG	DIAGTISTL	236	9	48	75		4088
GAG	TISTLQEQI	260	9	45	71		4089
GAG	STLQEQIAW	262	9	12	19		4090
GAG	STLQEQIGW	262	9	27	42		4091
GAG	TLQEQIAWM	263	9	12	19		4092
GAG	TLQEQIGWM	263	9	27	42		4093
GAG	GWMTNTPFI	269	9	18	28	0.0140	4094
GAG	GWMTNTPFI	269	9	10	16		4095
GAG	PVGDIYKRW	281	9	18	28		4096
GAG	PVGEIYKRW	281	9	40	63		4097
GAG	DIYKRWIL	284	9	17	27		4098
GAG	DIYKRWIL	284	9	37	58		4099
GAG	WILGLNKI	289	9	57	89		4100
GAG	GLNKIVRMY	293	9	60	94		4101
GAG	RMYSPTSIL	299	9	14	22		4102
GAG	RMYSPTSIL	299	9	40	63		4103
GAG	PFDDYVDRF	316	9	63	98		4104
GAG	YVDRFFKTL	320	9	27	42		4105

Table X
 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*2401	SEQ ID NO
GAG	YVDFYKTL	320	9	28	44		4106
GAG	ATQDVKNWM	333	9	15	23		4107
GAG	ATQEVKNWM	333	9	18	28		4108
GAG	NIMMQRGNF	407	9	10	17		4109
GAG	TIMMQRGNF	407	9	13	22		4110
GAG	CTERQANFL	459	9	55	87		4111
GAG	PTAPPESF	495	9	20	31		4112
GAG	PTAPPESF	495	9	15	23		4113
GAG	PTAPPESF	507	9	02	67		4114
GAG	PTAPPESF	507	9	01	33		4115
GAG	PIDKELYPL	534	9	12	19		4116
GAG	PIDKELYPL	538	9	01	25		4117
GAG	PLSLKSLF	548	9	15	23		4118
GAG	PLSLKSLF	548	9	12	19		4119
GAG	PLSLKSLF	548	9	12	19		4120
GAG	VLSGKLDAAW	7	10	15	23		4121
GAG	KLDAAWEKRL	12	10	16	25		4122
GAG	KLDAAWEKRL	12	10	10	16		4123
GAG	RLRGGKKKY	20	10	34	53		4124
GAG	VWASRELERF	36	10	45	70		4125
GAG	ETSEGCROIL	54	10	14	22		4126
GAG	QILGLOPQL	61	10	11	17		4127
GAG	QTSEELRSL	71	10	12	19		4128
GAG	SLFNTVATLY	79	10	15	23		4129
GAG	SLYNTVATLY	79	10	22	34		4130
GAG	ATLYCVIIQRI	85	10	15	19		4131
GAG	PIVQNAQGQM	154	10	21	33		4132
GAG	PIVQNLQGM	154	10	29	45		4133
GAG	ALSPRTLNAW	167	10	29	45		4134
GAG	ALSPRTLNAW	167	10	10	16		4135
GAG	RTLNAWVKVI	171	10	30	47		4136
GAG	WVKVVEEKAF	176	10	24	38		4137
GAG	WVKVVEEKAF	176	10	28	44		4138
GAG	AFSPEVPMF	184	10	50	78	0.0078	4139
GAG	ATQDLNML	200	10	12	19		4140
GAG	ATQDLNML	200	10	42	66		4141
GAG	NIVGGHQAAM	210	10	12	19		4142
GAG	NTYGGHQAAM	210	10	47	73		4143
GAG	DTINEEAAEW	224	10	31	48		4144
GAG	ETINEEAAEW	224	10	22	34		4145
GAG	RLIPIVIAAGPI	235	10	22	34		4146
GAG	RVIPIVIAAGPI	235	10	14	22		4147
GAG	QMRPRGSDI	248	10	44	69		4148
GAG	GTTLTLEQI	259	10	45	70		4149
GAG	STLQEQI/AWM	262	10	12	19		4150
GAG	STLQEQI/AWM	262	10	27	42		4151
GAG	PVGDIYKRWI	281	10	17	27		4152
GAG	PVGDIYKRWI	281	10	40	63		4153
GAG	PVGDIYKRWI	281	10	40	63		4154
GAG	PVGDIYKRWI	281	10	40	63		4155

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IYRWILGL	285	10	54	84	0.0140	4156
GAG	RWILGLNKI	288	10	56	88		4157
GAG	ILGLNKIVRM	291	10	57	89		4158
GAG	IVRMYSPTSI	297	10	14	22		4159
GAG	IVRMYSVSI	297	10	40	63		4160
GAG	MYSPSILDI	300	10	13	20		4161
GAG	MYSPSILDI	300	10	10	63		4162
GAG	DIKQGPKEPF	308	10	19	30		4163
GAG	DIRQGPKEPF	308	10	41	64		4164
GAG	PERDYVDRFF	316	10	35	55		4165
GAG	PERDYVDRFY	316	10	28	44		4166
GAG	DYVDRFFKTL	319	10	27	42		4167
GAG	DYVDRFFKTL	319	10	28	44		4168
GAG	DVRNWMTDI	336	10	12	19	0.0010	4169
GAG	DVRNWMTDI	336	10	17	17		4170
GAG	EVRNWMTEFL	336	10	25	39		4171
GAG	ATIMMOGNGF	406	10	11	28		4172
GAG	CENCGRGIII	425	10	27	42		4173
GAG	CENCGRGIII	425	10	27	42		4174
GAG	TTFSOKQEM	522	10	09	45		4175
GAG	ETIDKDLPL	537	10	01	25		4176
GAG	RTIENSLYPL	538	10	01	25		4177
GAG	LYPLASLKL	544	10	09	17		4178
GAG	SVLSGCKLDA	6	11	15	23		4179
GAG	IYWSRELRF	35	11	19	30		4180
GAG	IYWSRELRF	35	11	25	39		4181
GAG	ELERFALNPL	42	11	14	22		4182
GAG	ELERFALNPL	42	11	15	23		4183
GAG	LLFETSGCRQI	91	11	16	25		4184
GAG	RIEVKDTKEAL	91	11	12	19		4185
GAG	NLQGMVLIQA	158	11	15	23		4186
GAG	MYTIQAIAPRTL	163	11	27	42		4187
GAG	AWKVVEEKA	175	11	24	38		4188
GAG	AWKVVEEKA	175	11	28	44		4189
GAG	ALSEGATPDL	195	11	58	91		4190
GAG	IVGGIIQAAMQ	211	11	11	17		4191
GAG	IVGGIIQAAMQ	211	11	11	17		4192
GAG	TTSTLQEQIA	260	11	47	73		4193
GAG	TTSTLQEQIG	260	11	27	43		4194
GAG	QIGWMTSNPPI	267	11	18	29		4195
GAG	QIGWMTSNPPI	267	11	10	16		4196
GAG	PIPYGEIYKRW	279	11	34	53		4197
GAG	PIPYGEIYKRW	279	11	17	27		4198
GAG	IVGDIYKRWII	281	11	39	61		4199
GAG	PVGEIYKRWII	281	11	17	27		4200
GAG	DIYKRWIILGL	284	11	37	58		4201
GAG	EYKRWIILGL	284	11	37	58		4202
GAG	ILGLNKIVRM	290	11	56	88		4203
GAG	ILGLNKIVRM	290	11	57	89		4204
GAG	KIVRMYSPTSI	291	11	14	22		4205
GAG	KIVRMYSPTSI	296	11	39	61		4206

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HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SIQ ID NO
GAG	IVRMYSITSIL	297	11	14	22		4206
GAG	IVRMYSFVSIL	297	11	40	63		4207
GAG	RMYSPTSILDI	299	11	13	20		4208
GAG	RMYSFVSILDI	299	11	38	59		4209
GAG	DVRNWMITDT	336	11	12	19		4210
GAG	DVRNWMITET	336	11	11	17		4211
GAG	EVKNWMTETL	336	11	25	39		4212
GAG	ILKALGPAATL	357	11	16	25		4213
GAG	ALGPAATLEE	360	11	16	25		4214
GAG	ALGPAATLEE	360	11	17	27		4215
GAG	ATAQDQLKGG	392	11	01	50		4216
GAG	CWKCKEGIIQ	446	11	46	72		4217
GAG	PTAPPAESFRF	495	11	10	16		4218
GAG	PTAPPAESFRF	495	11	14	22		4219
GAG	PTAPPAESFRF	507	11	02	67		4220
GAG	LYPLASLSKSLF	507	11	09	33		4221
GAG	SLKSLFGNDPL	544	11	12	19		4222
NEF	DLEKIGAI	571	8	14	22		4223
NEF	ATNADCAW	71	8	12	22		4224
NEF	PVRQVPL	95	8	48	75		4225
NEF	PMYKGAFL	105	8	12	19		4226
NEF	TYKGAFL	107	8	12	19		4227
NEF	AFDLSIFL	111	8	18	28		4228
NEF	ALDLSIFL	111	8	11	17		4229
NEF	AVDLSIFL	111	8	15	23		4230
NEF	FLKEKGGI	117	8	56	88		4231
NEF	DLDLWVY	185	8	20	31		4232
NEF	EILDWVY	185	8	33	52		4233
NEF	WVYIITQGY	191	8	13	20		4234
NEF	WVYIITQGY	191	8	21	33		4235
NEF	VYIITQGY	192	8	13	20		4236
NEF	VYIITQGY	192	8	21	33		4237
NEF	FFPDWQNY	199	8	17	27		4238
NEF	YHWDWQNY	199	8	36	56		4239
NEF	NYTPGFI	206	8	20	31		4240
NEF	GIRYPLTF	213	8	13	20		4241
NEF	GTRFPLTF	213	8	13	20		4242
NEF	RPLTFGW	216	8	20	32		4243
NEF	RYLTFGW	216	8	27	43		4244
NEF	PLTFGWCF	219	8	43	67		4245
NEF	TFGWCFKL	222	8	40	63		4246
NEF	GVGASQDL	45	9	11	17		4247
NEF	GVGASQDL	45	9	21	33		4248
NEF	GVGASQDL	45	9	17	27		4249
NEF	ATNADCAWL	45	9	12	22		4250
NEF	QVPLRPMTF	100	9	10	16		4251
NEF	QVPLRPMTF	100	9	46	72		4252
NEF	MTYKGAFL	106	9	12	19		4253
NEF	FFLKEKGGI	116	9	26	41		4254
NEF							4255

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SIQ ID NO
NEF	IIFLKEGGIL	116	9	29	45		4256
NEF	IYSKKROEI	175	9	18	29		4257
NEF	LWVYHTQGF	190	9	13	20		4258
NEF	WVYHTQGY	190	9	21	33		4259
NEF	WVYHTQGF	191	9	13	20		4260
NEF	WVYHTQGY	191	9	21	33		4261
NEF	IITQGFEDW	194	9	14	22		4262
NEF	IITQGYERDW	194	9	25	39		4263
NEF	NIQGYERDW	194	9	12	19		4264
NEF	GFFPDWQNY	198	9	17	27		4265
NEF	GYFPDWQNY	198	9	36	56		4266
NEF	YTPGGRIRY	207	9	17	27		4267
NEF	YTPGGRIRY	207	9	13	20		4268
NEF	LTFCWCFL	221	9	39	61		4269
NEF	KWSKSSVGVW	4	10	20	31		4270
NEF	GFVIRPQVPL	93	10	48	75		4271
NEF	PMYKGAIDL	105	10	12	19		4272
NEF	SFFLKEKGL	115	10	22	34		4273
NEF	LIYSKKRQEI	174	10	18	28		4274
NEF	IYSKKRQEI	175	10	18	29		4275
NEF	DLWVYHTQGF	188	10	13	20		4276
NEF	DLWVYHTQGY	188	10	21	33		4277
NEF	LWVYHTQGF	190	10	13	20		4278
NEF	LWVYHTQGY	190	10	21	33		4279
NEF	NYTPGGRIRY	206	10	17	27		4280
NEF	NYTPGGRIRY	206	10	13	20		4281
NEF	GIRYLTFGW	213	10	13	20		4282
NEF	GTRFPLTFGW	213	10	12	19		4283
NEF	RFPLTFGWCF	216	10	17	27		4284
NEF	RYPLTFGWCF	216	10	21	33		4285
NEF	PLTFGWCFKL	219	10	39	61		4286
NEF	LLIIPICQIIGM	257	10	10	16		4287
NEF	LLIIPMSQIIGM	257	10	12	19		4288
NEF	IMARELIPEY	320	10	10	16		4289
NEF	NTAATNADCA	68	11	12	19		4290
NEF	PVRQVPLRP	95	11	47	73		4291
NEF	PLRDMYKGA	102	11	12	19		4292
NEF	FLKEGGLEDGL	117	11	26	41		4293
NEF	FLKEGGLEDGL	117	11	29	45		4294
NEF	GLIYSKKRQEI	173	11	18	28		4295
NEF	LIYSKKRQEI	174	11	18	28		4296
NEF	DLWVYHTQGF	188	11	13	20		4297
NEF	DLWVYHTQGY	188	11	21	33		4298
NEF	VYHTQGFDPD	192	11	13	20		4299
NEF	VYHTQGYFPD	192	11	13	20		4300
NEF	DWQNYTTPGPG	203	11	21	33		4301
NEF	YTPGGRIRYPL	207	11	16	25		4302
NEF	YTPGGRIRYPL	207	11	13	20		4303
NEF	CLLIIPMSQIIG	256	11	10	16		4304
NEF	IMARELIPEY	320	11	10	16		4305

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FFREDLAF	1	8	15	23		4306
POL	FERENLAF	1	8	41	64		4307
POL	GTLCNCFQI	80	8	01	33		4308
POL	PTFNFPQI	80	8	01	33		4309
POL	NFQQTILW	86	8	22	34		4310
POL	SEFQITLW	86	8	23	36		4311
POL	ITLWQRP	90	8	47	73		4312
POL	TIKIGGQ	99	8	17	27		4313
POL	TVKIGGQ	99	8	11	17		4314
POL	TVLEINL	118	8	13	20		4315
POL	TVLEINL	118	8	15	23		4316
POL	DINLPKW	122	8	13	20		4317
POL	EINLPKW	122	8	12	19		4318
POL	MIGGIGF	133	8	62	97		4319
POL	GFIKVRQY	139	8	53	83		4320
POL	KVRQYDQI	142	8	41	64		4321
POL	ELGIIKAI	152	8	19	30		4322
POL	EICGKAI	152	8	24	38		4323
POL	NIGRNLL	170	8	26	41		4324
POL	NIGRNML	170	8	31	48		4325
POL	LTQIGCTL	177	8	42	66		4326
POL	LTQIGCTL	177	8	15	23		4327
POL	QIGCTLNF	179	8	41	64		4328
POL	QLGCTLNF	179	8	16	25		4329
POL	PVKLKPGM	195	8	56	88		4330
POL	KIKALTEI	217	8	28	44		4331
POL	KIKALVEI	217	8	15	23		4332
POL	LVEICTEM	221	8	15	24		4333
POL	EMEKEGKI	229	8	42	66		4334
POL	KIGPENPY	238	8	51	80		4335
POL	RIGPENPY	238	8	11	17		4336
POL	KWRKLVDF	259	8	59	92		4337
POL	KLVDFFEL	262	8	63	98		4338
POL	FWEVQLGI	276	8	57	89		4339
POL	GIPHPAGL	282	8	56	89		4340
POL	VLDVGDAY	297	8	60	94		4341
POL	SVPLDKDF	306	8	18	28		4342
POL	DFRKYTAF	312	8	42	66		4343
POL	GWKGSPTAI	341	8	59	92		4344
POL	MTKILEPF	353	8	44	69		4345
POL	DIVIQYQM	366	8	18	28		4346
POL	EIVIQYQM	366	8	24	38		4347
POL	IYQYMDL	369	8	61	95		4348
POL	DLVVGSDI	375	8	63	98		4349
POL	YVGSOLEI	377	8	58	91		4350
POL	FLWMGYEL	416	8	64	100		4351
POL	WTVPQIQL	428	8	28	44		4352
POL	WTVPQIVL	428	8	13	20		4353
POL	QLIEKDSW	434	8	13	20		4354
POL	VLPEKDSW	434	8	13	20		4355

Table X
IIIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*2401	SIQ ID NO
POL	TVNDIQKL	442	8	62	97		4356
POL	KLVGKLNW	448	8	62	97		4357
POL	KLNWASQI	452	8	61	95		4358
POL	KVKQLCKL	464	8	29	45		4359
POL	KVRQLCKL	464	8	19	30		4360
POL	LLRGAKAL	471	8	30	47		4361
POL	LLRGTKAL	471	8	24	38		4362
POL	ALTDIVPL	477	8	21	33		4363
POL	ALTEVIPL	477	8	16	25		4364
POL	PLTEAEL	483	8	30	47		4365
POL	ELAENREI	491	8	57	89		4366
POL	YYDPSKDL	510	8	43	67		4367
POL	KTGKYAKM	542	8	19	30		4368
POL	KTGKYARM	542	8	13	21		4369
POL	ITNDVVKQL	553	8	49	77		4370
POL	LTEAVOKI	560	8	34	53		4371
POL	ATESIVIV	568	8	19	30		4372
POL	IWGRTPKF	574	8	11	17		4373
POL	ETWWTIDYW	591	8	48	75		4374
POL	DYWQATWI	596	8	10	16		4375
POL	EYWQATWI	596	8	20	31		4376
POL	TWIPWEIF	601	8	37	58		4377
POL	EFVNTPL	607	8	52	81		4378
POL	NTPPLVKL	610	8	54	84		4379
POL	LVKLWYQL	614	8	57	89		4380
POL	PVGAETFY	625	8	58	91		4381
POL	IVGAETFY	626	8	28	44		4382
POL	TINOKTEL	664	8	28	44		4383
POL	KTELQAIY	664	8	55	86		4384
POL	NIVTDSQY	686	8	12	19		4385
POL	VTDSQYAL	688	8	62	97		4386
POL	LIKKEKYY	717	8	59	92		4387
POL	WVPAIKGI	727	8	35	55		4388
POL	GIRKVLFL	747	8	63	98		4389
POL	KVLFLDGI	750	8	51	80		4390
POL	AMASDFNL	773	8	50	78		4391
POL	QVDCSPGI	805	8	45	70		4392
POL	CTILEGKI	817	8	57	89		4393
POL	ILEGKIIL	819	8	35	55		4394
POL	ILEGKVL	819	8	31	48		4395
POL	AVIIVASGY	828	8	36	23		4396
POL	GYIEAEVI	834	8	59	92		4397
POL	ETQGETAY	844	8	54	84		4398
POL	ILKLAGRW	853	8	59	92		4399
POL	LLKLAGRW	853	8	34	53		4400
POL	ITDNGSNF	866	8	25	39		4401
POL	ITVKAACW	876	8	51	80		4402
POL	AVKAACWW	877	8	15	23		4403
POL	TVKAACWW	877	8	32	50		4404
POL	TVKAACWW	877	8	24	38		4405

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	GKQEFGL	886	8	22	34		4406
POL	GIQEFGL	886	8	11	17		4407
POL	IILKTAVQM	923	8	57	89		4408
POL	AVQMAVFI	927	8	60	94		4409
POL	NFKRKGGI	936	8	60	94		4410
POL	GYSAGERI	945	8	57	89		4411
POL	QIKIQNF	968	8	12	19		4412
POL	QIKIQNF	968	8	35	55		4413
POL	KIQNFRVY	971	8	52	81		4414
POL	IWKGFAPL	986	8	36	56		4415
POL	LWKGPAKL	986	8	19	30		4416
POL	VIQDSDI	1003	8	37	58		4417
POL	VIQDSEI	1003	8	12	19		4418
POL	PTRELQVW	30	9	13	20		4419
POL	GTILNFIQI	79	9	01	17		4420
POL	ASLSLIQI	80	9	01	33		4421
POL	SFSIPQITL	84	9	14	22		4422
POL	QITLWQIRL	89	9	47	73		4423
POL	LWQRILVTI	92	9	21	33	0.0190	4424
POL	VTIKGGQL	98	9	17	27		4425
POL	VTIKGGQL	98	9	11	17		4426
POL	DTGADDTVL	112	9	61	95		4427
POL	DTVLEDIML	117	9	13	20		4428
POL	DTVLEENL	117	9	14	22		4429
POL	KMGGGGGF	132	9	62	97	0.0011	4430
POL	MIGGGGFI	133	9	62	97		4431
POL	KVRQYDQIL	142	9	21	33		4432
POL	QYDQILIEI	145	9	27	42		4433
POL	LVGFTPVNI	145	9	12	19		4434
POL	PVNIIGRNL	163	9	54	84		4435
POL	PVNIIGRNL	168	9	26	41		4436
POL	LVNIIGRNL	176	9	24	38		4437
POL	LLTQIGCTL	176	9	21	33		4438
POL	MLTQIGCTL	176	9	18	28		4439
POL	MLTQIGCTL	176	9	10	16		4440
POL	TLNFRISII	183	9	61	97		4441
POL	PIETVIVKL	190	9	53	83		4442
POL	QWPLTEERI	210	9	56	88		4443
POL	LTEFKIKAL	213	9	56	88		4444
POL	ALVEICTEM	220	9	15	23		4445
POL	PYNTIPFAL	244	9	24	38	0.0310	4446
POL	PYNTIPFAL	244	9	37	58		4447
POL	ELNKRQDF	268	9	57	89		4448
POL	DFWEVQLGI	275	9	56	88		4449
POL	TVLDVGDAY	296	9	57	89		4450
POL	VLDVGDAYF	297	9	60	94		4451
POL	PLDKDERKY	308	9	19	30		4452
POL	YTATPISI	316	9	37	58		4453
POL	SINNETPGI	323	9	32	50		4454
POL	STNNETPGI	323	9	11	17		4455

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ETPGIRYQY	327	9	52	81		4456
POL	GIRYQYNVL	330	9	52	81		4457
POL	QYNVLQGW	334	9	63	98	0.0036	4458
POL	GWKGSPIF	341	9	59	92		4459
POL	IFQSSMTKI	348	9	38	59	0.0029	4460
POL	SMTKILEPF	352	9	43	67	0.0110	4461
POL	PFRRKONPDI	359	9	16	25		4462
POL	VYQYMDL	368	9	51	80		4463
POL	IYQYMDL	369	9	61	95	0.0130	4464
POL	LYVGSIDLEI	376	9	58	91		4465
POL	EIGQIRAKI	383	9	26	41		4466
POL	EIGQIRTKI	383	9	21	33		4467
POL	KIEELREIL	390	9	19	30		4468
POL	KIEELRQIL	390	9	17	27		4469
POL	ELREILLKW	393	9	15	23		4470
POL	ELRQILLRW	393	9	15	23		4471
POL	PLWNGVEL	415	9	64	100		4472
POL	GVELIPDKW	420	9	60	94	0.0001	4473
POL	KWTVOHQL	427	9	28	44		4474
POL	KWTVOHVL	427	9	12	19		4475
POL	IVLPEKDSW	433	9	13	20		4476
POL	WTVNDIQKL	441	9	62	97		4477
POL	DIQKLVGKL	445	9	62	97		4478
POL	KLWASQIV	452	9	60	94		4479
POL	KVKQLCKLL	464	9	28	44		4480
POL	KVRQLCKLL	464	9	19	30		4481
POL	KLRGAKAL	470	9	25	40		4482
POL	KLRGTAKAL	470	9	24	38		4483
POL	GTKALTEVI	474	9	11	17		4484
POL	LTEAELEL	484	9	37	58		4485
POL	ELAEIREIL	491	9	57	89		4486
POL	VYDPSKDL	509	9	39	61	0.0004	4487
POL	VYDPSKDLI	510	9	35	55		4488
POL	TYQIQEIPF	530	9	42	66	0.3000	4489
POL	IYQIEPKNL	533	9	40	63	0.0520	4490
POL	QLTEAVQKI	559	9	34	53		4491
POL	KIATESIVI	566	9	14	22		4492
POL	VIWGTIPKF	573	9	47	73		4493
POL	KTPKFKLP	577	9	17	27		4494
POL	KTPKFKRLPI	577	9	29	45		4495
POL	KLPIKETW	582	9	20	31		4496
POL	RLPIKETW	582	9	26	41		4497
POL	TWETWWTIDY	589	9	10	16		4498
POL	TWETWWTIEY	589	9	10	16		4499
POL	WTDYWQATW	594	9	14	22		4500
POL	WTDYWQATW	594	9	24	38		4501
POL	ATWIPWEEF	600	9	52	81		4502
POL	NTPLVLKLV	610	9	57	89		4503
POL	PLVLKLVYQL	613	9	54	84		4504
POL	WYQLEKDP	618	9	14	22		4505

Table X
IIIY A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	WYQLEKEM	618	9	31	48	0.0001	4506
POL	WYQLETEPI	618	9	11	17		4507
POL	PIVGAETFY	625	9	28	44		4508
POL	ETKLGKAGY	641	9	35	55		4509
POL	DTTNQKTEL	663	9	26	41		4510
POL	ETTNQKTEL	663	9	29	45		4511
POL	KTELQAIHL	668	9	15	23		4512
POL	KTELQAIYL	668	9	12	19		4513
POL	ELQAIHLAL	670	9	16	25		4514
POL	ELQAIYLAL	670	9	12	19		4515
POL	ILALQDSQL	675	9	15	23		4516
POL	IVTDSQYAL	687	9	59	92		4517
POL	LVNQIEQL	709	9	19	30		4518
POL	LVSQIEQL	709	9	19	30		4519
POL	OLIKKEKVV	716	9	28	44		4520
POL	LIKKEKVV	717	9	35	55		4521
POL	AWVPAIKGI	726	9	22	34		4522
POL	SWVPAIKGI	726	9	37	58		4523
POL	KYIISNWRAM	766	9	28	44		4524
POL	RYIISNWRAM	766	9	11	17		4525
POL	NWRAMASDF	770	9	43	67	0.0016	4526
POL	QVDCSPGIW	805	9	57	89	0.0095	4527
POL	IWQLDCTHL	812	9	59	92		4528
POL	CTHLEOKII	817	9	35	55		4529
POL	CTHLEQKVI	817	9	26	41		4530
POL	AVIIVASGYI	828	9	53	83		4531
POL	ETGQETAYF	844	9	57	89		4532
POL	ETAYFLKL	848	9	31	48		4533
POL	FLKLAGRW	852	9	27	42		4534
POL	FLKLAGRW	852	9	32	50		4535
POL	STTVKAACW	875	9	25	39		4536
POL	TTVKAACW	876	9	15	23		4537
POL	WWAGIKQEF	883	9	15	23	0.0120	4538
POL	WWAGIQQEF	883	9	21	33		4539
POL	VVESMNKEL	902	9	11	17		4540
POL	SMNKELKI	905	9	48	75		4541
POL	QVRDQAEHL	916	9	53	83		4542
POL	QVREQAEHL	916	9	48	75		4543
POL	KTAVQMAVF	925	9	13	20		4544
POL	QMAVFIINF	929	9	57	89		4545
POL	GYSAGERII	945	9	60	94	0.0190	4546
POL	IIDIHSDI	952	9	41	64		4547
POL	IIDIHATDI	952	9	12	19		4548
POL	IVDIHATDI	952	9	29	45		4549
POL	ATDIOTKEL	957	9	12	19		4550
POL	QTKELQKQI	961	9	35	55		4551
POL	ELQKQIKI	964	9	46	72		4552
POL	ELQKQITKI	964	9	13	21		4553
POL	KIQNFRVYY	971	9	34	54		4554
POL				52	81		4555

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SIQ ID NO
POL	YYRDSRDI	978	9	34	53		4556
POL	YYRDSRDI	978	9	14	22		4557
POL	PLWKGPAKL	985	9	36	56		4558
POL	PLWKGPAKL	985	9	19	30		4559
POL	PLWKGPAKL	986	9	35	55		4560
POL	PLWKGPAKL	986	9	18	28		4561
POL	VVIQDNSDI	1002	9	37	58		4562
POL	VVIQDNSDI	1002	9	12	19		4563
POL	VVPRKAKI	1012	9	51	80		4564
POL	VVPRKAKI	1012	9	11	17		4565
POL	IKDYCKQM	1020	9	11	17		4566
POL	IIRDYCKQM	1020	9	50	78		4567
POL	AFQGEAREF	7	10	16	16		4568
POL	STNSPTSREL	32	10	01	33		4569
POL	GTLCNPQITL	80	10	01	33		4570
POL	PTFNFIQITL	80	10	01	33		4571
POL	SSFIQITLW	84	10	13	20		4572
POL	TLWQRIIVTI	91	10	21	33		4573
POL	LVTKIGGQL	97	10	13	20		4574
POL	KIGGQLKEAL	101	10	23	36		4575
POL	NLFKWKPKM	124	10	35	55		4576
POL	KWKPKMIGGI	128	10	42	66		4577
POL	RWKPKMIGGI	128	10	17	27		4578
POL	KMIGGIGGI	132	10	62	97	0.0001	4579
POL	FKVRQYDQI	140	10	41	64		4580
POL	KVRQYDQIL	142	10	20	31		4581
POL	KVRQYDQIP	142	10	13	20		4582
POL	LIEICGHIKAI	150	10	10	16		4583
POL	LIEICGHIKAI	150	10	13	20		4584
POL	VLVGIPIVNI	162	10	53	83		4585
POL	LVGIPIVNI	163	10	52	81		4586
POL	PVNIIGRNLL	168	10	26	41		4587
POL	PVNIIGRNML	168	10	24	38		4588
POL	IIGRNLLTQI	171	10	21	33		4589
POL	IIGRNMLTQI	171	10	18	28		4590
POL	IGRNMLTQL	171	10	11	17		4591
POL	NLLTQIGCTL	175	10	21	33		4592
POL	NMLTQIGCTL	175	10	18	28		4593
POL	NMLTQIGCTL	175	10	10	16		4594
POL	LTOIGCTLNF	177	10	41	64		4595
POL	LTOIGCTLNF	177	10	15	23		4596
POL	QLGCTLNFI	179	10	41	64		4597
POL	QLGCTLNFI	179	10	16	25		4598
POL	CTLNFIPI	182	10	60	94		4599
POL	TVPVKLRKFGM	193	10	54	84		4600
POL	GMDGPKVKQ	201	10	51	80		4601
POL	PLTEKIKAL	212	10	54	84		4602
POL	CTEMEKECKI	225	10	27	42		4603
POL	AIKKKDKTKW	251	10	57	89		4604
POL	STKWRKLVDF	257	10	58	91		4605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	ELNKRQTDFW	268	10	57	89		4606
POL	RTQDFWEVQL	272	10	53	83		4607
POL	QLGIPHFAGL	280	10	56	89		4608
POL	VTVLVDVGDAY	295	10	56	88		4609
POL	TVLDVGDAYF	296	10	57	89		4610
POL	YFSVPLDKDF	304	10	18	29		4611
POL	DFRKYTAFTI	312	10	42	66		4612
POL	KYTAFTIPSI	315	10	37	58		4613
POL	AIFQSSMTKI	347	10	36	56		4614
POL	IFQSSMTKIL	348	10	38	59	0.0002	4615
POL	IVYQYMDDL	367	10	42	66		4616
POL	VIVYQYMDIDL	368	10	51	80		4617
POL	DLVYVGSDEL	375	10	58	91		4618
POL	KIELREHILL	390	10	19	30		4619
POL	KIFELRQHILL	390	10	17	27		4620
POL	PIQLPEKDSW	432	10	13	20		4621
POL	PIVLPKDSW	432	10	13	20		4622
POL	SWTVNDIQKL	440	10	54	84		4623
POL	NWASQIYAGI	454	10	27	42		4624
POL	NWASQIYPGI	454	10	29	45		4625
POL	IYAGIKVKOL	459	10	18	28		4626
POL	IYPGIKVKOL	459	10	11	17		4627
POL	IYPGIKVROL	459	10	15	23		4628
POL	GIKVKQLCKL	462	10	28	44		4629
POL	GIKVRQLCKL	462	10	18	28		4630
POL	IVPLTEEAEL	481	10	13	20		4631
POL	VIPLTEEAEL	481	10	11	17		4632
POL	PLTEEAEL	483	10	30	47		4633
POL	ELFLAENREI	489	10	53	83		4634
POL	ILKEPVIIGVY	498	10	40	63		4635
POL	GVYYDPSKDL	508	10	38	59		4636
POL	VYYDPSKDL	509	10	31	48		4637
POL	EIQKQGQDQW	520	10	13	20		4638
POL	EIQKQGQDQW	520	10	15	23		4639
POL	WTYQIYQERF	529	10	42	66		4640
POL	QYQEPFKNL	532	10	40	63		4641
POL	PFKNLKTGKY	537	10	45	70		4642
POL	NLKTGKYAKM	540	10	18	29		4643
POL	NLKTGKYARM	540	10	13	21		4644
POL	AVQKIATESI	563	10	10	16		4645
POL	KIATESIVW	566	10	14	22		4646
POL	IWIWGTPEF	572	10	47	73		4647
POL	IWGTPEFRL	574	10	17	27		4648
POL	IWGTPEFRL	574	10	30	47		4649
POL	PIQKETWEAW	584	10	15	23		4650
POL	PIQKETWETW	584	10	27	42		4651
POL	ETWETWWTW	588	10	10	16		4652
POL	ETWETWWTW	588	10	10	16		4653
POL	ETWETWWTW	588	10	10	16		4654
POL	WWTDYWQAT	593	10	14	22		4655

Table X
IIIY A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	WTEYWOAT	593	10	23	36		4656
POL	WTDYWOATW	594	10	14	22		4657
POL	WTEYWOATW	594	10	24	38		4658
POL	YWOATWIFE	597	10	52	81		4659
POL	EWFEVNTIPL	605	10	50	78	0.0660	4660
POL	FVNTPLVKL	608	10	54	86		4661
POL	NTIPLVKLWY	610	10	57	89		4662
POL	LWYQLEKIP	617	10	14	22		4663
POL	LWYQLEKIP	617	10	31	48		4664
POL	LWYQLETER	617	10	11	17		4665
POL	EVNIVTDSQY	684	10	59	92		4666
POL	NIVTDSQYAL	686	10	59	92		4667
POL	VTDISOYALGI	688	10	58	91		4668
POL	ELVNOHIEQL	708	10	18	28		4669
POL	ELVNOHIEQL	708	10	19	30		4670
POL	LVNOHIEQL	709	10	19	30		4671
POL	LVNOHIEQL	709	10	19	30		4672
POL	QIKKEKVVYL	716	10	28	44		4673
POL	QVIXLVSSGI	739	10	15	23		4674
POL	LVSSGIRKVL	743	10	15	23		4675
POL	LVSSGIRKVL	743	10	26	41		4676
POL	NLPPIVVAKEI	779	10	26	41		4677
POL	IVASCDKCOL	779	10	27	42		4678
POL	GIWQDCTHIL	788	10	43	67		4679
POL	CTIIEGKIL	811	10	59	92		4680
POL	CTIIEGKVL	817	10	31	48		4681
POL	LVAVIIVASGY	826	10	23	36		4682
POL	ETGQETAYEL	844	10	53	83		4683
POL	ETGQETAYEL	844	10	31	48		4684
POL	YFLKLAGRW	851	10	26	41		4685
POL	YFLKLAGRW	851	10	31	48		4686
POL	TIITDNGSNF	864	10	25	39		4687
POL	TIITDNGSNF	864	10	14	22		4688
POL	STTVKAACW	875	10	24	38		4689
POL	CWVAGIKQEF	882	10	15	23		4690
POL	CWVAGIKQEF	882	10	21	33		4691
POL	GIKQEFIPY	886	10	11	17		4692
POL	GIKQEFIPY	886	10	22	34		4693
POL	GVVESHMKEL	901	10	11	17		4694
POL	SMNKLKII	905	10	48	75		4695
POL	KTAVQMAVFI	925	10	53	83		4696
POL	RIDIASDI	931	10	56	88		4697
POL	RIVDIATDI	931	10	12	19		4698
POL	QTKELQKQII	951	10	29	45		4699
POL	IKIQNFRVY	961	10	12	19		4700
POL	IKIQNFRVY	969	10	10	16		4701
POL	IKIQNFRVY	969	10	12	19		4702
POL	VYVRSRDPPI	977	10	36	57		4703
POL				34	53		4704
POL							4705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SI:Q ID NO
POL	VYRDSRDPL	977	10	14	22		4706
POL	YYRDSRDPIW	978	10	34	53		4707
POL	YYRDSRDPLW	978	10	14	22		4708
POL	PIWKGPAKLL	985	10	35	55		4709
POL	PLWKGPAKLL	985	10	18	28		4710
POL	IWKGPAPKLLW	986	10	35	55		4711
POL	LWKGPAPKLLW	986	10	18	28		4712
POL	LWKGEFAYVI	994	10	59	92		4713
POL	AVVQIUNSDI	1000	10	37	58		4714
POL	AVVQIUNSEI	1000	10	12	19		4715
POL	KVPRRKAKI	1011	10	51	80		4716
POL	KVPRRKVKI	1011	10	11	17		4717
POL	VVPRRKAKII	1012	10	50	78		4718
POL	VVPRRKVKII	1012	10	11	17		4719
POL	KIKDYGKQM	1019	10	11	17		4720
POL	KIKDYGKQM	1019	10	50	78		4721
POL	GTILNFQITF	79	11	01	17		4722
POL	ASLSLQITL	80	11	01	33		4723
POL	GTILNCIQITL	80	11	01	33		4724
POL	PIFNFPQITLW	80	11	01	33		4725
POL	ITLWQRPVITI	90	11	19	30		4726
POL	LWQRPVITIKI	92	11	14	22		4727
POL	LWQRPVITVK	92	11	12	19		4728
POL	PLVTRIGGQL	96	11	13	20		4729
POL	KIGGQKKEALL	101	11	23	36		4730
POL	LLDTGADDTV	110	11	61	95		4731
POL	VLEINLPKWW	119	11	13	20		4732
POL	VLEINLPKWW	119	11	12	19		4733
POL	NLPKWKPKM	124	11	35	55		4734
POL	GIGGFIKVRQY	136	11	53	83		4735
POL	GFIKVRQYDQI	139	11	41	64		4736
POL	FIKVRQYDQIL	140	11	21	33		4737
POL	ILIEICGKKAI	149	11	13	20		4738
POL	TVLVGIPVNI	161	11	53	83		4739
POL	VLVGPVNI	162	11	51	80		4740
POL	PIPVNIIGRNL	166	11	26	41		4741
POL	PIPVNIIGRNM	166	11	38	41		4742
POL	NIIGRNLLTQI	170	11	21	33		4743
POL	NIIGRNMLTQI	170	11	18	28		4744
POL	NIIGRNMLTQL	170	11	11	17		4745
POL	LLTIQIGCTLNF	176	11	21	33		4746
POL	MLTQIGCTLNF	176	11	17	27		4747
POL	MLTQIGCTLNF	176	11	10	16		4748
POL	ETVPVKLPG	192	11	51	80		4749
POL	EMEKEGKISKI	229	11	32	50		4750
POL	KISKIGPENPY	235	11	11	64		4751
POL	KISKIGPENPY	235	11	11	17		4752
POL	KWRKLVDFRE	259	11	59	92		4753
POL	GLKKKKSIVT	288	11	49	77		4754
POL	SVTVLDVGD	294	11	56	88		4755

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VTVDVGDY	295	11	56	88		4756
POL	DVGDAYESVP	299	11	54	84		4757
POL	AYFSVPLDKDF	303	11	18	28		4758
POL	SVPLDKDFRK	306	11	18	28		4759
POL	SINNETTGIRY	323	11	32	50		4760
POL	STNNETTGIRY	323	11	11	17		4761
POL	RYQYNVLQKG	332	11	63	98		4762
POL	AFQSSMTKIL	347	11	36	56		4763
POL	PRKQNPDI	359	11	14	22		4764
POL	DIVIQYMDL	366	11	18	28		4765
POL	EIVIQYMDL	366	11	24	38		4766
POL	IIVIQYMDLY	367	11	42	66		4767
POL	YMDDL YVCSO	372	11	61	95		4768
POL	DLIGQIRAKI	381	11	26	41		4769
POL	DLIGQIRTKI	381	11	20	31		4770
POL	RTKHELRQHIL	388	11	14	22		4771
POL	ELREHLKRWG	393	11	14	22		4772
POL	ELROHLRWG	393	11	12	19		4773
POL	WMGYELLHDK	418	11	60	94		4774
POL	DIQLVGKLN	445	11	62	97		4775
POL	LVGKLNWASQ	449	11	60	94		4776
POL	QIYAGIKVKQL	458	11	18	29		4777
POL	QIYGIKVKQL	458	11	11	17		4778
POL	QIYGIKVRQL	458	11	14	22		4779
POL	GKVRQLCKLL	462	11	27	42		4780
POL	GKVRQLCKLL	462	11	18	28		4781
POL	LLRGAKALTDI	471	11	22	34		4782
POL	GFKALTEVIPL	474	11	11	17		4783
POL	DIVPLTEAEAL	480	11	13	20		4784
POL	EVPLTEAEAL	480	11	11	17		4785
POL	ELELAENREIL	489	11	53	83		4786
POL	EIKEPVIGVY	497	11	40	63		4787
POL	ILKEPVIQVY	498	11	38	59		4788
POL	GVYDFSKDLI	508	11	31	48		4789
POL	QWTYQIYQEP	528	11	42	66		4790
POL	SIVIWGKTPKF	571	11	41	64		4791
POL	VIVGKTPKF	573	11	17	27		4792
POL	VIVGKTPFR	573	11	29	45		4793
POL	KFKLPQKETW	580	11	20	31		4794
POL	KFKLPQKETW	580	11	26	41		4795
POL	PIKETWIAW	584	11	15	23		4796
POL	PIKETWETW	584	11	27	42		4797
POL	ETWETWTD	588	11	10	16		4798
POL	TWTDYWQA	592	11	10	16		4799
POL	TWTDYWQA	592	11	12	19		4800
POL	WWTDYWQAT	593	11	14	22		4801
POL	WWTDYWQAT	593	11	23	36		4802
POL	DYWQATWIPE	596	11	19	30		4803
POL	EYWQATWIPE	596	11	33	52		4804
POL	EFVNTPLVLKL	607	11	54	84		4805

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FVNTPLVKL	608	11	54	86		4806
POL	KLWYQLEKDPH	616	11	14	22		4807
POL	KLWYQLEKEPH	616	11	31	48		4808
POL	KLWYQLETEM	616	11	11	17		4809
POL	LTDITNQKTE	661	11	19	30		4810
POL	LTEITNQKTE	661	11	25	39		4811
POL	TTNOKTELIAI	664	11	12	19		4812
POL	TTNOKTELOAI	664	11	42	66		4813
POL	KTELQAIILAL	668	11	15	23		4814
POL	KTELQAIYLAL	668	11	12	19		4815
POL	AIILALQDSGL	673	11	15	23		4816
POL	ALQDSGLFVNI	677	11	27	42		4817
POL	ALQDSGSEVNI	677	11	25	39		4818
POL	IVTDSQYALGI	687	11	58	91		4819
POL	VITDSQYALGII	688	11	58	91		4820
POL	ELVNSQIIEQLI	708	11	18	28		4821
POL	ELVNSQIIEQLI	708	11	19	30		4822
POL	LIKKEKVYLA	717	11	20	31		4823
POL	LIKKEKVYLSW	717	11	13	20		4824
POL	YLAWVPAIKG	724	11	22	34		4825
POL	YLSWVPAIKG	724	11	37	58		4826
POL	GIGGNEQVDKL	733	11	58	91		4827
POL	KLVSAGIRKVL	742	11	15	23		4828
POL	KLVSAGIRKVL	742	11	26	41		4829
POL	LVSAGIRKVL	743	11	15	23		4830
POL	LVSSGIRKVL	743	11	26	41		4831
POL	GIRKVLFLDGI	747	11	49	77		4832
POL	NWRAMASDF	770	11	41	64		4833
POL	EIVASCDKCOL	787	11	18	28		4834
POL	QVDCSPGIWQ	805	11	43	67		4835
POL	QLDCTHLEGR	814	11	56	88		4836
POL	ILVAVIIVASGY	825	11	33	52		4837
POL	LVAVIIVASGYI	826	11	53	83		4838
POL	ETGQETAYFIL	844	11	47	73		4839
POL	ETGQETAYFLL	844	11	31	48		4840
POL	AYELKLAGR	850	11	26	41		4841
POL	AYELKLAGR	850	11	31	48		4842
POL	KLAGRWPVKI	855	11	25	39		4843
POL	KLAGRWPVKV	855	11	13	20		4844
POL	KVIITDNGSNF	863	11	22	34		4845
POL	FTSAAVKAAC	873	11	21	33		4846
POL	FTSTTVKAAC	873	11	27	42		4847
POL	AVKAACWVA	877	11	14	22		4848
POL	TVKAACWVA	877	11	10	16		4849
POL	WWAGIKQFEG	883	11	20	31		4850
POL	WWAGIQFEG	883	11	21	33		4851
POL	IILKTAVQMAV	923	11	11	17		4852
POL	AVQMAVFIIN	927	11	57	89		4853
POL	FIINFRKKGGI	933	11	60	94		4854
POL			11	58	91		4855

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 HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	NFKRGGGGY	936	11	59	92		4856
POL	GIGGYSAGERI	942	11	57	89		4857
POL	GYSGAGRIIDI	945	11	40	63		4858
POL	GYSGAGRIVDI	945	11	14	22		4859
POL	IASDIQTKEL	955	11	14	22		4860
POL	IATDIQTKEL	955	11	34	53		4861
POL	DIQTKELQKI	959	11	44	69		4862
POL	QIKIQNFRVY	968	11	12	19		4863
POL	QIKIQNFRVY	968	11	35	55		4864
POL	IKIQNFRVY	969	11	12	19		4865
POL	IKIQNFRVY	969	11	36	57		4866
POL	RYYRDSRDI	976	11	34	53		4867
POL	RYYRDSRDI	976	11	14	22		4868
POL	YYRDSRDI	977	11	34	53		4869
POL	YYRDSRDI	977	11	14	22		4870
POL	PIWKGIPAKLL	985	11	35	55		4871
POL	PLWKGIPAKLL	985	11	18	28		4872
POL	LLWKGIGAVV	993	11	59	92		4873
POL	KVPRIRKAKII	1011	11	50	78		4874
POL	KVPRIRKAKII	1011	11	11	17		4875
REV	LLKTIVLL	12	8	11	17		4876
REV	AVRIKIL	17	8	13	20		4877
REV	ILYQSNPY	23	8	27	42		4878
REV	QLPIERL	78	8	14	22		4879
REV	QLPIERL	78	8	37	58		4880
REV	LVSPAVL	114	8	11	17		4881
REV	AVRIKILY	17	9	13	20		4882
REV	KILYQSNPY	22	9	26	41		4883
REV	RVIARQKQI	48	9	35	55		4884
REV	RWRERQKQI	48	9	11	17		4885
REV	PVPLQLPI	74	9	11	17		4886
REV	PVPLQLPI	74	9	35	55		4887
REV	PLQLPIERL	76	10	11	17		4888
REV	PLQLPIERL	76	10	34	53		4889
REV	QLPIERLTL	78	10	18	28		4890
REV	QLQGVGSQI	97	10	11	18		4891
REV	IKILYQSNPY	20	11	18	28		4892
TAT	CYCKKCCF	28	8	11	17		4893
TAT	CYCKKCCY	28	8	11	17		4894
TAT	CHICQVCF	34	8	11	17		4895
TAT	FLNKGGLI	41	8	14	22		4896
TAT	PVDNLEPW	3	9	20	31		4897
TAT	PVDNLEPW	3	9	14	22		4898
TAT	CFLNKGGLI	40	9	14	22		4899
TAT	FLNKGGLISY	41	10	14	22		4900
TAT	CFLNKGGLISY	40	11	14	22		4901
VIF	RWQVLIW	4	8	10	16		4902
VIF	RWQVMIVW	4	8	43	67		4903
VIF	IWWQVDRM	9	8	59	92		4904
VIF	KIRTWNSL	17	8	12	19		4905

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	RIRTWKSL	17	8	15	23		4906
VIF	RIRTWNSL	17	8	15	23		4907
VIF	SLVKIIMY	23	8	44	69		4908
VIF	LVKIIIMYI	24	8	19	30		4909
VIF	GWFYRIIHY	37	8	20	31		4910
VIF	KISSEVHH	50	8	15	23		4911
VIF	KISSEVHH	50	8	20	31		4912
VIF	RISSEVHH	50	8	15	23		4913
VIF	RLVITYW	65	8	12	19		4914
VIF	RLVITYW	65	8	10	16		4915
VIF	VKITYWGL	67	8	22	34		4916
VIF	VKITYWGL	67	8	10	16		4917
VIF	VKITYWGL	67	8	11	17		4918
VIF	VKITYWGL	67	8	25	39		4919
VIF	HLGKIVSI	83	8	26	41		4920
VIF	HLGKIVSI	83	8	18	28		4921
VIF	GVSEWRLL	87	8	12	19		4922
VIF	STQIDPDL	100	8	11	17		4923
VIF	STQIDPDL	100	8	14	22		4924
VIF	QLIHLVYF	110	8	14	22		4925
VIF	QLIHLVYF	110	8	16	25		4926
VIF	ILYIFKCF	113	8	15	23		4927
VIF	IMITYFDCF	113	8	14	22		4928
VIF	IVSRCEY	133	8	52	81		4929
VIF	KVGSLOYL	146	8	12	19		4930
VIF	QYLALAAAL	151	8	11	17		4931
VIF	QYLALAAAL	151	8	33	52		4932
VIF	QYLALAAAL	151	8	28	44		4933
VIF	YLALATAL	152	8	10	16		4934
VIF	ALIKPKKI	157	8	21	33		4935
VIF	PLPSVKKL	168	8	14	22		4936
VIF	PLPSVKKL	168	8	46	72		4937
VIF	MIVWQVDRM	8	9	13	20		4938
VIF	MIVWQVDRM	10	9	48	75		4939
VIF	VWQVDRMKI	10	9	19	30		4940
VIF	SLVKIIMYI	23	9	13	20		4941
VIF	HLPLGDARL	56	9	20	31		4942
VIF	HLPLGEARL	56	9	10	16		4943
VIF	PLGEARLVI	58	9	10	16		4944
VIF	LVKITWGL	66	9	22	34		4945
VIF	LVKITWGL	66	9	22	34		4946
VIF	GLITGERDW	73	9	12	19		4947
VIF	GLITGERDW	73	9	21	33		4948
VIF	HLTGERDWI	75	9	12	19		4949
VIF	QITGERDWI	75	9	11	17		4950
VIF	SEVRLRY	89	9	18	28		4951
VIF	DLADQLIHL	106	9	15	23		4952
VIF	GLADQLIHL	106	9	28	44		4953
VIF	QYLALATAL	151	9	44	69		4954
VIF	VMIWQVDR	7	10	12	19		4955
VIF	IVWQVDRMKI	9	10				

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	IVQVDRMRI	9	10	47	73		4956
VIF	QVDRMKIRTW	12	10	12	19		4957
VIF	QVDRMRINTW	12	10	10	16		4958
VIF	QVDRMRINTW	12	10	31	48		4959
VIF	RMKIRTWNSL	15	10	12	19		4960
VIF	RMKIRTWNSL	15	10	15	23		4961
VIF	RMKIRTWNSL	15	10	15	23		4962
VIF	TKWSLVKIII	20	10	16	25		4963
VIF	TWNSLVKIII	20	10	25	39		4964
VIF	KISSEVIHPL	50	10	14	22		4965
VIF	KVSEVIHPL	50	10	19	30		4966
VIF	RISSEVIHPL	50	10	13	20		4967
VIF	RLVITYWGL	65	10	12	19		4968
VIF	DWILGIGVSI	81	10	21	33		4969
VIF	DWILGQVSI	81	10	18	28		4970
VIF	ILGHIGVSIEW	83	10	25	39		4971
VIF	ILGQGVSIIEW	83	10	26	41		4972
VIF	RYSTQVDIPL	98	10	10	16		4973
VIF	QIHDLDADQL	102	10	10	16		4974
VIF	QVDRGLADQL	102	10	14	22		4975
VIF	LHILYFDFCF	111	10	16	25		4976
VIF	LHIMIFYDFCF	111	10	15	23		4977
VIF	YFDFCFESAI	116	10	28	44		4978
VIF	KVGSQYLAL	146	10	51	80		4979
VIF	SLOYLALAL	149	10	12	19		4980
VIF	SLOYLAKAL	149	10	11	17		4981
VIF	SLQYLALAL	149	10	31	48		4982
VIF	SVKLTEDRW	174	10	13	20		4983
VIF	QVMVWQVDR	6	11	43	67		4984
VIF	MIVWQVDRM	8	11	43	67		4985
VIF	RTWKSIVKIII	19	11	14	22		4986
VIF	RTWNSLVKIII	19	11	24	38		4987
VIF	TWNSLVKIII	20	11	16	25		4988
VIF	TWNSLVKIII	20	11	22	34		4989
VIF	EVHPLGDARL	54	11	13	20		4990
VIF	EVHPLGEARL	54	11	20	31		4991
VIF	IHPLGEARLVI	56	11	10	16		4992
VIF	YWGLTGERD	71	11	22	34		4993
VIF	YWGLTGERD	71	11	12	19		4994
VIF	GLITGTGERDWII	73	11	21	33		4995
VIF	GLTGTGERDWII	73	11	12	19		4996
VIF	GVSIEWRLRR	87	11	10	16		4997
VIF	QIHDLDADQL	102	11	10	16		4998
VIF	QVDRGLADQL	102	11	14	22		4999
VIF	GLADQLIIMII	106	11	11	17		5000
VIF	QLIHLYYDFCF	110	11	13	20		5001
VIF	QLIHMIYDFCF	110	11	14	22		5002
VIF	YFDFCFESAI	115	11	20	31		5003
VIF	CFSDSAIRKAI	119	11	10	16		5004
VIF	CFSESAIRKAI	119	11	12	19		5005

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	Nr. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	CFSIAIRNAI	119	11	12	19		5006
VIF	SLOYALTAII	149	11	27	42		5007
VIF	LIKPKIKIPPL	150	11	10	16		5008
VIF	KTKGIRGSIT	181	11	15	23		5009
VPR	ALELLEEL	15	8	10	16		5010
VPR	TELELEEL	19	8	44	69		5011
VPR	AVRIIPRI	30	8	14	22		5012
VPR	WLIIGLQY	38	8	11	17		5013
VPR	TWAGVEAI	53	8	16	25		5014
VPR	TWEGVEAI	53	8	20	31		5015
VPR	GVEAIIRI	56	8	34	53		5016
VPR	IIRIIQQL	60	8	42	66		5017
VPR	RILOQLLF	62	8	45	70		5018
VPR	ILQQLFI	63	8	37	58		5019
VPR	LLFIIFRI	67	8	44	69		5020
VPR	LYNEWTELE	14	9	12	19	0.1400	5021
VPR	WTLELEEL	18	9	30	47		5022
VPR	AVRIIPRIW	30	9	42	69		5023
VPR	AVRIIPRPW	30	9	14	22		5024
VPR	PWLHGLQY	37	9	34	53		5025
VPR	WLHGLQIII	38	9	11	17		5026
VPR	IYETYGDTW	46	9	20	31		5027
VPR	IYNTYGDTW	46	9	31	48		5028
VPR	DTWAGVEAI	52	9	18	28	0.0580	5029
VPR	DTWEGVEAI	52	9	16	25		5030
VPR	DTWEGVEAI	53	9	20	31		5031
VPR	TWAGVEAI	53	9	16	25		5032
VPR	TWEGVEAI	53	9	19	30		5033
VPR	GVEAIRIL	56	9	34	53		5034
VPR	AIRILQQL	59	9	39	61		5035
VPR	IIRILQQL	60	9	42	66		5036
VPR	RILOQLLF	62	9	36	56		5037
VPR	QLLFIIIFRI	66	9	44	69		5038
VPR	QLLFVIFRI	66	9	10	16		5039
VPR	RIGCQISR	74	9	47	73		5040
VPR	RIGCQISR	74	9	12	19		5041
VPR	LYNEWTELE	14	10	30	47		5042
VPR	EWTELELEEL	17	10	40	63		5043
VPR	ELKNEAVRIIF	25	10	17	27		5044
VPR	ELKSEAVRIIF	25	10	15	23		5045
VPR	AVRIIPRIWL	30	10	14	22		5046
VPR	AVRIIPRPWL	30	10	34	53		5047
VPR	HEPRIWLISL	33	10	10	16		5048
VPR	IIPRIWLHGL	33	10	24	38		5049
VPR	PWLHGLQIII	37	10	12	19		5050
VPR	WLHGLQIIIY	38	10	20	31		5051
VPR	IYETYGDTW	45	10	17	27		5052
VPR	IYIYTYGDTW	45	10	14	22		5053
VPR	IYIYTYGDTW	45	10	14	22		5054
VPR	DTWAGVEAI	52	10	16	25		5055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VPR	DTWEGVEAII	52	10	19	30		5056
VPR	AIRILQQLL	59	10	39	61		5057
VPR	IRILQQLLF	60	10	41	64		5058
VPR	ILQQLFHIF	63	10	35	55		5059
VPR	PWLHGLGQHII	37	11	12	19		5060
VPR	QYIYETGDT	44	11	14	22		5061
VPR	TWAGVEAIRI	53	11	15	23		5062
VPR	TWEGVEAIRI	53	11	14	22		5063
VPR	AIRILQQLLF	59	11	38	59		5064
VPR	IRILQQLLF	60	11	33	52		5065
VPR	RILQQLFHIF	62	11	34	53		5066
VPR	IFRIGCQHSRI	71	11	44	69		5067
VPR	IFRIGCQHSRI	71	11	11	17		5068
VPR	RIGCQHSRIGI	74	11	45	70		5069
VPR	RIGCQHSRIGI	74	11	11	17		5070
VPU	KVDYRIVI	7	8	01	33		5071
VPU	LIAIVVW	26	8	10	16		5072
VPU	IVVWTVF	30	8	15	23		5073
VPU	VVWTVFI	31	8	15	23		5074
VPU	WTVFHEY	34	8	12	19		5075
VPU	VHEIYRKI	37	8	12	19		5076
VPU	KILRQRKI	45	8	15	23		5077
VPU	EMGHIIAPW	89	8	11	17		5078
VPU	NYELAVGAL	5	9	01	25		5079
VPU	DYKLGVGAL	10	9	02	29		5080
VPU	DYRLGVGAL	10	9	03	43		5081
VPU	IIAIVVWII	27	9	23	36		5082
VPU	AIVVWTVF	29	9	14	22		5083
VPU	IVVWTVFI	30	9	14	23		5084
VPU	VWTVFHEY	33	9	15	23		5085
VPU	VHEIYRKI	36	9	12	19		5086
VPU	KIDKLIDRI	33	9	14	22		5087
VPU	VTLLSSKL	94	9	01	25		5088
VPU	NYELAVGALI	5	10	01	25		5089
VPU	DYKLGVGALI	10	10	02	29		5090
VPU	DYRLGVGALI	10	10	03	43		5091
VPU	AIVVWTVFI	29	10	14	22		5092
VPU	VWTVFHEY	31	10	12	19		5093
VPU	ILRQRKIDRL	46	10	15	23		5094
VPU	GVEMGHIIAP	91	10	01	50		5095
VPU	LVTLSSSKL	91	10	01	50		5096
VPU	KVDYRIVIVAF	7	11	01	33		5097
VPU	KVDYRLGVGA	7	11	01	33		5098
VPU	RIDYRLGVGAL	7	11	01	33		5099
VPU	IVVWTVFHEY	30	11	12	19		5100
VPU	EYRKILRQRKI	41	11	13	21		5101
VPU	KILRQRKIDRL	45	11	15	23		5102
VPU	ILRQRKIDRLI	46	11	13	20		5103
VPU	RIKEIRDDSDY	64	11	01	50		5104
VPU	RINEIRDDSDY	64	11	01	50		5105

Table XI
 HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	H ⁺ 0702	SEQ ID NO.
ENV	DINPQEVV	91	8	13	20		5106
ENV	APAGEAIL	265	8	29	45		5107
ENV	KIVVSTQL	299	8	34	53		5108
ENV	RIVVSTQL	299	8	26	41		5109
ENV	GGQTFYA	362	8	11	17		5110
ENV	LPCRKQI	485	8	31	48		5111
ENV	SPLSFQTL	808	8	30	47		5112
ENV	GHDRPEGH	822	8	15	23		5113
ENV	EPDRPERI	823	8	01	33		5114
ENV	PDNRDEGI	823	8	01	33		5115
ENV	DINPQEVVL	91	9	12	19	0.0002	5116
ENV	KPCVKLTPL	130	9	55	86	0.4100	5117
ENV	CPKVSFEPI	250	9	30	47	0.0550	5118
ENV	DPPIIYCA	256	9	12	19		5119
ENV	EPPIIYCA	256	9	26	41	0.0001	5120
ENV	IPPIIYCAPA	259	9	36	56	0.0130	5121
ENV	IPPIIYCTPA	259	9	18	28		5122
ENV	GPCKNVSTV	283	9	15	23		5123
ENV	GPCINVESTV	283	9	11	17	0.0019	5124
ENV	KIVVSTQLL	299	9	34	53	0.0012	5125
ENV	RPVVSQTL	299	9	26	41	0.0084	5126
ENV	DEIVMHSF	428	9	14	22	0.0001	5127
ENV	LPCRKQI	485	9	20	31	0.0011	5128
ENV	LPCRKQIV	485	9	10	16		5129
ENV	APTKAKRRV	575	9	22	34	0.0082	5130
ENV	SPLSFQTL	808	9	10	16		5131
ENV	IPRIKQGF	950	9	10	16		5132
ENV	IPRIKQGL	950	9	24	38		5133
ENV	IPRIKQGL	950	9	11	17		5134
ENV	VPTDIPNQEI	88	10	25	39		5135
ENV	VPTDIPNQEV	88	10	21	33	0.0008	5136
ENV	KPVVSTQLL	299	10	34	53		5137
ENV	RPVVSQTL	299	10	26	41	0.0038	5138
ENV	RPNNTKSI	347	10	17	27		5139
ENV	EPLGVAPTKA	570	10	21	33	0.0005	5140
ENV	APTKAKRRV	575	10	22	34	0.1200	5141
ENV	VPVWKEATT	53	11	22	34	0.0022	5142
ENV	VPTDIPNQEV	88	11	13	20		5143
ENV	KPCVKLTPLC	130	11	54	84	0.0004	5144
ENV	CPKVSFEPI	250	11	30	47		5145
ENV	DPPIIYCAPA	256	11	10	16		5146
ENV	EPPIIYCAPA	256	11	24	38		5147
ENV	IPPIIYCTPA	259	11	10	16		5148
ENV	IPPIIYCAPAG	259	11	26	41		5149
ENV	IPPIIYCTPAG	259	11	10	16		5150
ENV	48:	48:	11	18	28		5151
ENV	LPCRKQINNM	48:	11	38	59		5152
ENV	RPGGDMRDN	54:	11	35	55		5153
GAG	RPGGKKKY	22	8	15	23		5154
GAG	NPGLLETA	49	8	57	89	0.0036	5155
GAG	SPRTLNAW	169	8				

Table XI
IIIY.D07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	II*0702	SEQ ID NO.
GAG	SPVPIPMF	186	8	55	86	0.0012	5156
GAG	TPQDLNMM	201	8	12	19		5157
GAG	TPQDLNTM	201	8	42	66	0.0001	5158
GAG	IIPVIAQIM	237	8	38	59	0.0001	5159
GAG	GPAPQOM	242	8	19	30	0.0005	5160
GAG	GPPIPCOM	242	8	17	27		5161
GAG	GPVAPQOM	242	8	10	16		5162
GAG	EPKQSDIA	251	8	36	88	0.0001	5163
GAG	PMIPVGD	278	8	10	16		5164
GAG	PMIPVGEI	278	8	35	55	0.0001	5165
GAG	SPVSILDI	302	8	13	20		5166
GAG	NPDKSIL	351	8	11	63		5167
GAG	NPDKTIL	351	8	46	72	0.0003	5168
GAG	GPGLIKARV	379	8	36	56	0.0002	5169
GAG	GPSIKARV	379	8	19	30		5170
GAG	APKKGCV	440	8	55	86	0.0004	5171
GAG	PPAESFGF	498	8	10	16		5172
GAG	PPAESFRF	498	8	15	23		5173
GAG	PPAESFRF	510	8	67	02		5174
GAG	PPAESFRF	510	8	01	33		5175
GAG	EPDKELY	533	8	12	19		5176
GAG	EPDKELY	537	8	01	25		5177
GAG	SPKLNNAV	169	9	57	89	0.5500	5178
GAG	TPQDLNMM	201	9	12	19		5179
GAG	TPQDLNTM	201	9	42	66	0.0008	5180
GAG	IIPVIAQPIA	237	9	19	30	0.0590	5181
GAG	NIPVVDI	277	9	10	16		5182
GAG	NIPVGEI	277	9	34	54	0.0002	5183
GAG	PMIPVGD	278	9	10	16		5184
GAG	PMIPVGEI	278	9	35	55	0.0002	5185
GAG	GPKEPRDY	312	9	98	98	0.0002	5186
GAG	GPAAILEM	362	9	63	25	0.0002	5187
GAG	GPATILEM	362	9	16	28	0.0014	5188
GAG	GPGLIKARV	379	9	18	28		5189
GAG	GPSIKARV	379	9	35	55	0.0290	5190
GAG	RPEPTAPPA	490	9	19	30		5191
GAG	RPEPTAPPA	497	9	30	47	0.0014	5192
GAG	APPAESFGF	497	9	10	16		5193
GAG	APPAESFRF	497	9	15	23		5194
GAG	RPEPTAPPA	504	9	01	50	0.0046	5195
GAG	APPAESFRF	509	9	02	67	0.0014	5196
GAG	APPAESFRF	509	9	01	33		5197
GAG	TPSQKQEM	527	9	10	17		5198
GAG	YPLASLKS	545	9	08	17		5199
GAG	YPLASLKS	545	9	07	15		5200
GAG	PPLASLKS	546	9	04	24		5201
GAG	EPLTALRS	547	9	01	33		5202
GAG	PPLASLKS	547	9	01	33		5203
GAG	PPLASLKS	547	9	01	33		5204
GAG	RPGKKKKYKL	22	10	10	16	0.9900	5205

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	P < 0.002	SEQ ID NO.
GAG	RPGGKKYRL	22	10	16	25		5206
GAG	SPEVPMESA	186	10	41	64	0.0002	5207
GAG	SPEVPMFTA	186	10	13	20		5208
GAG	NPPIVGDIV	277	10	16	16		5209
GAG	NPPIVGEIV	277	10	34	54	0.0002	5210
GAG	IPVGDYKRW	280	10	11	17		5211
GAG	IPVGEYKRW	280	10	34	53	0.0002	5212
GAG	GPKPEHDYV	312	10	63	98	0.0002	5213
GAG	EPFRDYVDIF	315	10	63	98	0.0002	5214
GAG	NPDCITLKA	351	10	28	44	0.0002	5215
GAG	NPDCITLKA	351	10	18	28		5216
GAG	GPAATLEMM	362	10	16	25	0.0020	5217
GAG	GPATLEMM	362	10	18	28		5218
GAG	GPATKARVLA	379	10	35	55	0.0002	5219
GAG	GPATKARVLA	379	10	19	30		5220
GAG	PPAEPTAPPA	491	10	01	50		5221
GAG	EPTAIPAESE	494	10	20	31		5222
GAG	EPTAIPAESE	494	10	15	23	0.0002	5223
GAG	EPTAIPAESE	506	10	01	50		5224
GAG	EPAPPESE	506	10	01	50		5225
GAG	PPESFEEA	511	10	01	33		5226
GAG	EPDKELYPL	533	10	12	19	0.0019	5227
GAG	EPDKELYPL	537	10	01	25	0.0019	5228
GAG	YPLASLSLF	545	10	08	17		5229
GAG	YPLASLSLF	545	10	07	15	0.0140	5230
GAG	PPLASLSLF	546	10	04	24		5231
GAG	EPLALRSLF	547	10	01	33		5232
GAG	PPLASLSLF	547	10	01	33		5233
GAG	PPLSLKSLF	547	10	01	33		5234
GAG	QPSLOTGSEEL	67	11	13	20		5235
GAG	YPIVQNAQQ	133	11	20	31		5236
GAG	YPIVQNLQQ	133	11	29	45		5237
GAG	SPRTLNAAWK	159	11	55	86	0.0076	5238
GAG	SPEVPMESAL	186	11	41	64	0.0003	5239
GAG	SPEVPMETAL	186	11	13	20		5240
GAG	IPMFSALEGA	190	11	45	70	0.0004	5241
GAG	IPMFALSEGA	190	11	15	23		5242
GAG	TPQDLNMMMLN	201	11	11	17		5243
GAG	IPVGDYKRWI	280	11	10	16		5244
GAG	IPVGEYKRWI	280	11	34	53	0.0001	5245
GAG	EPFRDYVDIF	315	11	35	55		5246
GAG	EPFRDYVDIF	315	11	28	44	0.0001	5247
GAG	NPDCITLKA	351	11	28	44	0.0001	5248
GAG	NPDCITLKA	351	11	18	28		5249
GAG	WPSNKGKPGN	474	11	23	36		5250
GAG	WPSNKGKPGN	474	11	14	22		5251
GAG	PPESFEEA	510	11	11	17		5252
NEF	APTAAKGV	34	8	01	33		5253
NEF	VPLRPMTF	101	8	10	16		5254
							5255

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	U*0702	SIQ ID NO.
NEF	VPLRPMTY	101	8	46	73	0.0001	5256
NEF	RPMTYKAA	104	8	23	36		5257
NEF	RPMTYKGA	104	8	25	39		5258
NEF	TPGPGIRY	208	8	17	27		5259
NEF	TPGPGTIF	208	8	13	20		5260
NEF	GPGRYPL	210	8	17	27		5261
NEF	GPGRFPL	210	8	13	20		5262
NEF	VPVDPREV	210	8	11	17		5263
NEF	HPICQIGM	259	8	10	16		5264
NEF	HPMSQIGM	259	8	12	19		5265
NEF	EPAAAGVGA	40	9	05	19	0.0001	5266
NEF	FPAAAGVGA	40	9	04	15		5267
NEF	FPVRQVPL	94	9	48	75	0.7600	5268
NEF	RQVPLRPM	98	9	47	73	1.7000	5269
NEF	RPMTYKGF	104	9	12	19		5270
NEF	PLTIGWCF	217	9	17	27		5271
NEF	YPLTGWCF	217	9	24	38		5272
NEF	APAAAGVGA	34	10	01	33		5273
NEF	EPAAAGVGA	40	10	04	33		5274
NEF	VPLRPMTYKA	101	10	20	32	0.0001	5275
NEF	TPGPGIRYPL	208	10	16	25		5276
NEF	TPGPGTIFPL	208	10	13	20		5277
NEF	GPGRYPLTF	210	10	13	20		5278
NEF	GPGRYPLTF	210	10	13	20		5279
NEF	APAAAGVGA	34	11	01	33		5280
NEF	RQVPLRPMIT	98	11	10	16		5281
NEF	RQVPLRPMIT	98	11	36	56		5282
NEF	VPLRPMTYKA	101	11	19	30		5283
NEF	VPLRPMTYKA	101	11	23	37		5284
NEF	RPMTYKGF	104	11	12	19		5285
NEF	PLTIGWCFK	217	11	17	27		5286
NEF	YPLTGWCFK	217	11	20	31		5287
POL	EPGEDREL	69	8	01	17		5288
POL	GPRLALSV	70	8	01	20		5289
POL	RPLVTIKI	95	8	14	22		5290
POL	RPLVTIKI	95	8	12	19		5291
POL	KPKMIGGI	130	8	60	94	0.0023	5292
POL	GPTIVNII	165	8	54	84	0.0001	5293
POL	SPMETVPV	189	8	56	88	0.0021	5294
POL	WPLTEEKI	211	8	56	88	0.0001	5295
POL	NPYNTPIF	243	8	24	38		5296
POL	NPYNTPIF	243	8	38	59	0.0008	5297
POL	TPGIRYQY	328	8	52	81	0.0001	5298
POL	PPFLWMGY	414	8	64	100	0.0001	5299
POL	EPVIGVYV	504	8	41	64	0.0001	5300
POL	DPSKDLIA	512	8	34	53		5301
POL	TPKFKLPI	578	8	17	27		5302
POL	TPKFKLPI	578	8	30	47		5303
POL	LPIQKETW	583	8	47	73	0.0001	5304
POL	TPPLVKLW	611	8	57	89	0.0001	5305

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	IV*0702	SEQ ID NO.
POL	PPLVKLWY	612	8	57	89	0.0001	5306
POL	PPVAKKEI	781	8	27	42		5307
POL	PPVAKKEI	781	8	29	45	0.0001	5308
POL	NPQSQGVV	896	8	59	92	0.0001	5309
POL	DPIWKGFA	984	8	37	58		5310
POL	DPLWKGFA	984	8	15	23		5311
POL	VPRKKAKI	1013	8	51	80	0.0018	5312
POL	VPRKKAKI	1013	8	11	17		5313
POL	FPQGEAREF	29	9	10	16		5314
POL	SPTRELOV	35	9	14	22	0.0210	5315
POL	SPTSRELOV	35	9	01	33		5316
POL	SPSSRELOV	38	9	01	50		5317
POL	VPTNFPOI	79	9	01	17		5318
POL	LPQKWKPKM	125	9	01	61		5319
POL	LPGRWKPKM	125	9	39	25	0.0038	5320
POL	FMSPIETV	186	9	16	61	0.0016	5321
POL	VPVCLKPGM	191	9	56	88	0.0003	5322
POL	KFGMDGPKV	191	9	56	88	0.0002	5323
POL	GRKVKQWPL	205	9	51	80	0.0150	5324
POL	NPYNTMFA	241	9	31	80		5325
POL	NPYNTMFA	241	9	24	38	0.0002	5326
POL	SPAIFQSSM	345	9	37	58	0.4100	5327
POL	NPDIVIQY	364	9	42	66	0.0001	5328
POL	NPEIVIQY	364	9	17	27		5329
POL	EPFLWMGY	413	9	23	36	0.0001	5330
POL	LPEKDSWTV	435	9	63	98	0.0001	5331
POL	YFGIKVKQL	460	9	40	63	0.0001	5332
POL	YFGIKVKQL	460	9	11	17		5333
POL	IPLIEAEI	482	9	15	23		5334
POL	VPLTEAEI	482	9	11	17		5335
POL	TPPLVKLWY	611	9	19	30		5336
POL	EPVGAETP	624	9	57	89	0.0001	5337
POL	QPDKSESEL	701	9	21	33	0.0001	5338
POL	LPRIVAKKEI	780	9	37	58	0.0006	5339
POL	LPVVAKEI	780	9	27	42		5340
POL	PPVAKKEI	781	9	28	44	0.0006	5341
POL	PPVAKKEI	781	9	26	41		5342
POL	VPRKKAKI	1013	9	28	44	0.0001	5343
POL	VPRKKAKI	1013	9	50	78	0.4800	5344
POL	SPTRELOVW	29	10	11	17	0.0025	5345
POL	EPGEDRELSV	69	10	13	20		5346
POL	GPRLSVCL	70	10	01	17		5347
POL	LPQKWKPKMI	125	10	01	20		5348
POL	LPGRWKPKMI	125	10	39	61	0.0002	5349
POL	TPVNIQRNL	167	10	15	23	0.0003	5350
POL	TPVNIQRNL	167	10	26	41		5351
POL	SPIETPVKL	189	10	24	38		5352
POL	WPLTEEKIK	211	10	53	83	0.0028	5353
POL	GPENPYNTPI	240	10	54	84	0.0018	5354
POL	GPENPYNTPI	240	10	24	38		5355
POL	GPENPYNTPI	240	10	38	59	0.0002	5355

Table XI
HIV-107 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	D*0702	SEQ ID NO.
POL	NPYNTIRFAL	243	10	24	38		5356
POL	NPYNTPVFAL	243	10	37	58	0.0034	5357
POL	VPLDKDFRKY	307	10	18	28	0.0002	5358
POL	TPGIRYQYNV	328	10	51	80	0.0004	5359
POL	LPQGWKGSFA	338	10	58	92	0.0120	5360
POL	EPFRKQNPDI	338	10	16	25	0.0002	5361
POL	NPDIIVIQYM	364	10	17	27	0.0005	5362
POL	NPEIIVIQYM	364	10	23	36		5363
POL	PPFLWAGYEL	414	10	64	100	0.0002	5364
POL	HPDKWTVPQI	424	10	53	83	0.0012	5365
POL	DPKDLIAEI	512	10	26	41	0.0002	5366
POL	LPIQKETWEA	583	10	15	23		5367
POL	PPLVKLWYQL	612	10	53	83	0.0002	5368
POL	EPVGAETFY	624	10	21	33	0.0002	5369
POL	QPIKSESELV	701	10	37	58	0.0002	5370
POL	LPIVVAKEIV	780	10	26	41		5371
POL	LPIVVAKEIV	780	10	27	42	0.0002	5372
POL	PIVVAKEIVA	781	10	25	39		5373
POL	PIVVAKEIVA	781	10	28	44	0.0066	5374
POL	IPAEIGQETA	841	10	58	91	0.0002	5375
POL	IPYNPOSGV	893	10	63	98	0.0023	5376
POL	DHWKGPAPKL	984	10	35	55		5377
POL	DPLWKGPAKL	984	10	15	23	0.0001	5378
POL	VPTNFPQITL	79	11	01	17		5379
POL	FPQITLWQRIPL	87	11	60	63	0.0001	5380
POL	KPKMGIGIGF	130	11	40	94	0.0001	5381
POL	TPVNIQGNLL	167	11	26	41	0.0002	5382
POL	TPVNIQGNML	167	11	24	38		5383
POL	FPISMETVIV	186	11	55	86	0.0067	5384
POL	WPLTEEKIKAL	211	11	54	84	0.0001	5385
POL	GPENFYNTIRF	240	11	24	38		5386
POL	GPENFYNTIVF	240	11	38	59	0.0001	5387
POL	IPAGLKKKKS	285	11	50	78	0.0001	5388
POL	IPSINNETVGI	321	11	31	48		5389
POL	IPSTNNETVGI	321	11	11	17		5390
POL	TPGIRYQYNVL	328	11	51	80	0.0015	5391
POL	LPQGWKGSFAI	338	11	58	92	0.0002	5392
POL	EPFRKQNPDI	338	11	14	22		5393
POL	EPFLWAGYE	413	11	63	98	0.0001	5394
POL	HPDKWTVPQI	424	11	12	19		5395
POL	QPIQPEKDSW	431	11	13	20		5396
POL	QPIVLPKDSW	431	11	13	20		5397
POL	IPLTEEALEL	482	11	11	17		5398
POL	VPLTEEALEL	482	11	19	30		5399
POL	EPFKNLTKG	536	11	45	70	0.0001	5400
POL	LPIQKETWEA	583	11	13	23		5401
POL	LPIQKETWET	583	11	42	42		5402
POL	TPPLVKLWYQ	611	11	53	83	0.0001	5403
POL	EPVGAETFYV	624	11	21	33		5404
POL	LPIVVAKEIVA	780	11	25	39		5405

Table XI
IIIY B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	LPFVVAKEIVA	780	11	27	42	0.0001	5406
POL	IPAEITQETAY	841	11	58	91	0.0001	5407
POL	IPYNPOSQGVV	893	11	59	92	0.0120	5408
POL	NPOSQGVVES	896	11	53	83	0.0001	5409
POL	DIWKGFPAKLL	984	11	34	53		5410
POL	DPLWKGPAKL	981	11	14	22		5411
REV	SPEGTIRQA	3	8	13	20		5412
REV	RPAEPVPL	70	8	20	31		5413
REV	VPLQLPPI	75	8	11	17		5414
REV	VPLQLPPL	75	8	36	56	0.0490	5415
REV	PLERLTL	80	8	19	30	0.0001	5416
REV	LPLERLTL	79	9	19	30	0.3100	5417
REV	QFQGTETGV	100	9	05	18		5418
REV	PFSPECTRQA	100	10	12	19		5419
REV	RPAEPVPLQL	70	10	20	31		5420
REV	EPVPLQLPPI	73	10	11	17	0.0023	5421
REV	EPVPLQLPPL	73	10	34	53		5422
REV	PFSPECTRQA	29	11	12	19		5423
REV	VPLQLPPIERL	75	11	11	17		5424
REV	VPLQLPPIERL	75	11	34	53	0.0001	5425
TAT	IKGSQPKTA	16	9	26	41	0.0007	5426
TAT	IKGSQPKTA	16	9	16	16		5427
TAT	IKGSQPKTA	16	9	13	20		5428
TAT	EPVDPNLEPW	2	10	14	22		5429
TAT	EPVDPNLEPW	2	10	13	20	0.0001	5430
VIF	IKPKISSEV	48	8	13	20		5431
VIF	IKPKVSSEV	48	8	19	30		5432
VIF	IKPKISSEV	48	8	13	20		5433
VIF	IKPKISSEV	48	8	14	22		5434
VIF	IKPKISSEV	48	8	20	31		5435
VIF	IKPKISSEV	48	8	19	30		5436
VIF	IKPKISSEV	48	8	19	30		5437
VIF	IKPKISSEV	48	8	21	33	0.0008	5438
VIF	IKPKISSEV	48	9	11	17		5439
VIF	IKPKISSEV	48	9	19	30		5440
VIF	IKPKISSEV	48	9	19	30	0.0002	5441
VIF	IKPKISSEV	48	9	19	30		5442
VIF	IKPKISSEV	48	9	10	16		5443
VIF	IKPKISSEV	48	9	21	33		5444
VIF	IKPKISSEV	48	9	14	22		5445
VIF	IKPKISSEV	48	10	13	20		5446
VIF	IKPKISSEV	48	10	13	20		5447
VIF	IKPKISSEV	48	10	13	20	0.0330	5448
VIF	IKPKISSEV	48	10	10	16		5449
VIF	IKPKISSEV	48	10	20	31		5450
VIF	IKPKISSEV	48	11	18	28		5451
VPR	EPYNEWTL	13	8	30	47		5452
VPR	EPYNEWTL	13	9	10	16		5453
VPR	EPYNEWTL	13	9	24	38		5454
VPR	EPYNEWTL	13	10	37	58	0.0001	5455

Table XI
HIV D07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	U*0702	SEQ ID NO.
VPR	EPYNEWTLLEL	13	10	29	45	0.0054	5456
VPR	RIWLIIGLGQY	36	10	10	16		5457
VPR	EPYNEWTLLEL	13	11	29	45		5458
VPR	RIWLIIGLGQII	36	11	12	19		5459
VPU	APWDVDIDL	99	8	12	19		5460

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	KKLWTLVL	9	8	01	50	5461
ENV	RKSWSLYL	9	8	01	50	5462
ENV	WRWGTLEL	15	8	01	50	5463
ENV	WRWGTMLL	15	8	01	50	5464
ENV	EKLWVTYV	43	8	09	15	5465
ENV	WKEATITL	56	8	23	36	5466
ENV	MIHEDISL	117	8	29	45	5467
ENV	IKNCSFNI	182	8	13	20	5468
ENV	IKVSFEPI	251	8	30	47	5469
ENV	LKCNDRKF	272	8	13	20	5470
ENV	AKTIIVQL	330	8	14	22	5471
ENV	QRGPGRAF	360	8	01	33	5472
ENV	KKKKTGYI	374	8	01	50	5473
ENV	IKQALICNI	381	8	17	27	5474
ENV	IKQINMIW	489	8	33	52	5475
ENV	IKQVNMW	489	8	13	21	5476
ENV	QRVGGQNT	497	8	11	17	5477
ENV	FRPGGDNI	546	8	43	67	5478
ENV	WRSELYKY	557	8	54	84	5479
ENV	YKYKVVIE	562	8	13	20	5480
ENV	YKYKVVKI	562	8	29	45	5481
ENV	ARQLLSGI	627	8	38	59	5482
ENV	VRQLLSGI	627	8	10	16	5483
ENV	LKLTWVGI	652	8	13	20	5484
ENV	EKNEQDLL	749	8	17	27	5485
ENV	EKNEQELL	749	8	18	28	5486
ENV	LRIFAVL	790	8	17	27	5487
ENV	LRIFAVL	790	8	28	44	5488
ENV	VRQYSIPL	803	8	56	88	5489
ENV	IRLVNGFL	843	8	11	17	5490
ENV	IRLVSGFL	843	8	13	20	5491
ENV	YIIRLDPI	865	8	13	20	5492
ENV	YIIRLDLL	865	8	15	23	5493
ENV	IRLRDILL	866	8	13	20	5494
ENV	GRRGWEAL	884	8	13	20	5495
ENV	LKGLRLGW	890	8	09	15	5496
ENV	LKGLQIGW	890	8	12	40	5497
ENV	LRIGWIEGL	893	8	05	17	5498
ENV	LKYLWNLL	900	8	10	32	5499
ENV	LKYWVNLL	900	8	14	22	5500
ENV	LKNSAINL	914	8	14	22	5501
ENV	LKNSAISL	914	8	10	16	5502
ENV	LKNSAVSL	914	8	10	16	5503
ENV	PRRIROGF	951	8	13	20	5504
ENV	PRRIROGL	951	8	11	17	5505
ENV	GKDLWVTIV	42	9	26	41	5506
ENV	EKLWVTIVY	43	9	01	33	5507
ENV	WKEATITLF	56	9	09	15	5508
ENV	WKNMVEQM	109	9	23	36	5509
ENV			9	35	55	5510

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	MIHDIISLW	117	9	29	45	5511
ENV	GKNEINDTY	218	9	01	20	5512
ENV	IIYCAPAGF	261	9	27	42	5513
ENV	IIYCTPAGF	261	9	10	16	5514
ENV	IKPVSTQL	298	9	33	52	5515
ENV	IRPVSTQL	298	9	26	41	5516
ENV	CRIKQIINM	487	9	30	47	5517
ENV	CRIKQIVNM	487	9	12	19	5518
ENV	GKAMYAPPI	501	9	23	36	5519
ENV	GRAMYAPPI	501	9	12	19	5520
ENV	MRDNWRSEL	553	9	40	63	5521
ENV	YKVKIEPL	564	9	25	39	5522
ENV	EREKRAVGI	590	9	11	17	5523
ENV	QIILLKLTW	649	9	13	20	5524
ENV	QIILLQLTW	649	9	34	53	5525
ENV	QIMLQLTW	649	9	10	16	5526
ENV	IKQLQARVL	659	9	40	63	5527
ENV	ARVLAVERY	664	9	33	52	5528
ENV	ERYLKDOQL	670	9	30	47	5529
ENV	ERYLRDOQL	670	9	18	28	5530
ENV	LKDOQLLGI	673	9	27	42	5531
ENV	LRDQQLGI	673	9	19	30	5532
ENV	DKWASLWNW	759	9	26	41	5533
ENV	TKWLWYIKI	771	9	15	23	5534
ENV	LRNLCLFSY	857	9	16	25	5535
ENV	LRSLCLFSY	857	9	35	55	5536
ENV	YIIRLRDL	865	9	13	20	5537
ENV	YIIRLRDLL	865	9	13	20	5538
ENV	IIRLRDLL	866	9	11	17	5539
ENV	LKNSAVSLL	914	9	11	17	5540
ENV	IKQGLEKAL	954	9	34	53	5541
ENV	KKLWTLYLAM	9	10	01	50	5542
ENV	AKSWSLYAM	9	10	01	50	5543
ENV	WRWGTFLGM	15	10	01	50	5544
ENV	WRWGTMLLGM	15	10	01	50	5545
ENV	GKDLWTVYY	42	10	01	33	5546
ENV	LKHCVKLTPL	129	10	55	86	5547
ENV	VKLTLVCVTL	133	10	52	81	5548
ENV	PKVSFEPPI	231	10	30	47	5549
ENV	IKPVVSTQLL	298	10	33	52	5550
ENV	IRPVVSTQLL	298	10	26	41	5551
ENV	MIISFNCGGEF	433	10	13	20	5552
ENV	THISFNCGGEF	433	10	22	34	5553
ENV	THISFNCGGEF	433	10	13	20	5554
ENV	THISFNCGGEF	433	10	30	47	5555
ENV	CRIKQINMW	487	10	12	19	5556
ENV	IKCSSNITGL	513	10	12	19	5557
ENV	MRDNWRSELY	553	10	40	63	5558
ENV	KRAVGIGAVF	593	10	11	17	5559
ENV	LRAIEAQHIL	642	10	45	70	5560

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Seq ID NO.
ENV	ARVLAVERYL	664	10	33	52	5561
ENV	ERYLKDQQL	670	10	29	45	5562
ENV	ERYLRDQQL	670	10	17	27	5563
ENV	LKDQQLGIW	673	10	27	42	5564
ENV	LRDQQLGIW	673	10	19	30	5565
ENV	EKNEQDLAL	749	10	17	27	5566
ENV	EKNEQELLEI	749	10	13	20	5567
ENV	DKWASLWNWF	759	10	26	41	5568
ENV	TKWLWYIKIF	771	10	12	19	5569
ENV	LRIFAVLSI	790	10	14	22	5570
ENV	LRIFAVLSI	790	10	19	30	5571
ENV	NIYRQGYSP	801	10	52	81	5572
ENV	VRQGYSPISF	803	10	48	75	5573
ENV	PRGPRPEGI	820	10	12	19	5574
ENV	IRLVSGFLAL	833	10	11	17	5575
ENV	YIIRLDLLI	865	10	11	17	5576
ENV	LKLGWEGLY	893	10	09	29	5577
ENV	LKYWNLLQY	900	10	14	22	5578
ENV	IRQGLERALL	954	10	33	52	5579
ENV	WRWGTILFLGML	15	11	01	50	5580
ENV	WRWGTMLLGML	15	11	01	50	5581
ENV	YRLNCNTSAI	235	11	15	24	5582
ENV	IHYCAPAGEAI	261	11	27	42	5583
ENV	IRPVVSTQLLL	298	11	33	52	5584
ENV	IRPVVSTQLLL	298	11	26	41	5585
ENV	TRPNNTRKSI	346	11	12	19	5586
ENV	QRGPGRAFVTI	360	11	01	33	5587
ENV	MIISFNCGEFF	433	11	13	20	5588
ENV	THSFNCRGEFF	433	11	21	33	5589
ENV	THSFNCRGEFF	433	11	13	20	5590
ENV	IRCSSNITGLL	513	11	10	16	5591
ENV	YKYKVVKIETL	562	11	25	39	5592
ENV	EKRAVGIGAVF	592	11	10	16	5593
ENV	KRAVGIGAVFL	593	11	11	17	5594
ENV	LRAEAAQHILL	642	11	44	69	5595
ENV	QIILLKLTWVGI	649	11	13	20	5596
ENV	QIILLKLTWVGI	649	11	34	53	5597
ENV	LKLTWVGKQL	652	11	13	20	5598
ENV	GKLICTTAVPW	686	11	19	30	5599
ENV	GKLICTTNVW	686	11	17	27	5600
ENV	GKLICTTVPW	686	11	12	19	5601
ENV	TKWLWYIKIFI	771	11	12	19	5602
ENV	IKIFIMIVGGL	777	11	38	59	5603
ENV	LKGLRLGWEG	890	11	08	27	5604
ENV	LRIGWEGIKYL	893	11	09	29	5605
ENV	LKYWNLLQYV	900	11	14	22	5606
ENV	LIIPRRIRKQL	948	11	12	19	5607
ENV	RRIRQGLERAL	952	11	16	25	5608
ENV	TRIRQGLERAL	952	11	11	17	5609
GAG	DKWEKIRL	14	8	18	28	5610

Table XII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
GAG	KYKLIKII	28	8	10	16	5611
GAG	KYKLIKII	28	8	16	25	5612
GAG	YKLIKIIW	30	8	13	20	5613
GAG	YRLKILVW	30	8	17	27	5614
GAG	CRQILGQL	59	8	15	23	5615
GAG	IKDTKEAL	96	8	10	16	5616
GAG	VKDTKEAL	96	8	33	52	5617
GAG	VRDTKEAL	96	8	10	16	5618
GAG	TKEALDKI	99	8	33	52	5619
GAG	TKEALEKI	99	8	10	16	5620
GAG	GIQAAAMQM	214	8	61	95	5621
GAG	KRWILGL	287	8	55	86	5622
GAG	PKEPRDY	313	8	63	98	5623
GAG	FRDYVDRF	317	8	64	100	5624
GAG	CKTILKAL	354	8	28	44	5625
GAG	CKTILKAL	354	8	18	28	5626
GAG	ARVLAELAM	384	8	57	89	5627
GAG	IKGRPGNF	477	8	23	37	5628
GAG	NKGRPGNF	477	8	14	23	5629
GAG	SKGRPGNF	477	8	11	18	5630
GAG	LKDKEMPL	535	8	01	25	5631
GAG	ERTENSLY	537	8	01	25	5632
GAG	EKEEKGLY	538	8	01	25	5633
GAG	GKLDWELI	11	9	17	27	5634
GAG	LRPGKKKY	21	9	35	55	5635
GAG	KRYRLKII	27	9	13	20	5636
GAG	SRELEIFAL	39	9	22	34	5637
GAG	ERFALNPL	44	9	15	23	5638
GAG	ERFALNPL	44	9	15	23	5639
GAG	VKVEEKAF	177	9	24	38	5640
GAG	VKVEEKAF	177	9	28	44	5641
GAG	ERAFSPFI	182	9	48	75	5642
GAG	GIQAAAMQML	214	9	61	95	5643
GAG	LIIPVILAGPI	236	9	22	34	5644
GAG	VHPVILAGPI	236	9	14	22	5645
GAG	MREPRGSDI	249	9	44	69	5646
GAG	YKRWILGL	286	9	55	86	5647
GAG	VRMYSPFSI	298	9	14	22	5648
GAG	VRMYSPFSI	298	9	40	63	5649
GAG	IKQGPKEPI	309	9	20	31	5650
GAG	IRQGPKEPI	309	9	42	66	5651
GAG	FRDYVDRFF	317	9	35	55	5652
GAG	FRDYVDRFY	317	9	29	45	5653
GAG	VKNWMTDTL	337	9	16	25	5654
GAG	VKNWMTETL	337	9	16	25	5655
GAG	SIKGRPGNF	476	9	23	37	5656
GAG	IKGRPGNFI	477	9	09	15	5657
GAG	NKGRPGNFI	477	9	01	50	5658
GAG	NKGRPGNFI	477	9	01	50	5659
GAG	DKDKELYPL	536	9	01	25	5660

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HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SiQ ID NO.
GAG	GKKYRLKIL	25	10	12	19	5661
GAG	KYRLKILVW	28	10	10	16	5662
GAG	KYRLKILVW	28	10	16	25	5663
GAG	KIIVWASREL	33	10	21	33	5664
GAG	KIIVWASREL	33	10	36	56	5665
GAG	ERFALNPGLL	44	10	15	23	5666
GAG	ERFALNPGLL	44	10	15	23	5667
GAG	VIQALSPRTL	164	10	27	42	5668
GAG	VIQALSPRTL	164	10	11	17	5669
GAG	VRMYSPTSL	298	10	14	22	5670
GAG	VRMYSPTSL	298	10	40	63	5671
GAG	VRMYSPTSL	298	10	16	25	5672
GAG	VRMYSPTSL	337	10	36	56	5673
GAG	VRMYSPTSL	337	10	16	25	5674
GAG	IKARVLAFAAM	382	10	57	89	5675
GAG	IKARVLAFAAM	438	10	53	83	5676
GAG	WRAPRKKGCW	447	10	46	72	5677
GAG	WRAPRKKGCW	447	10	54	84	5678
GAG	ERQANFLGKI	464	10	23	37	5679
GAG	SHKGRGNFL	476	10	01	50	5680
GAG	TRKETAPPL	491	10	12	19	5681
GAG	QKQEPHDKEL	530	10	01	25	5682
GAG	EKEKGLYPL	538	10	13	21	5683
GAG	IKELYPLASL	541	10	10	16	5684
GAG	DKELYPLTSL	541	10	12	19	5685
GAG	LKSLFGNDPL	552	10	11	17	5686
GAG	ARASVLSGGIEL	3	11	28	44	5687
GAG	ARASVLSGGIEL	3	11	16	25	5688
GAG	GKLDWEXIRL	11	11	33	52	5689
GAG	IKLRPGGKKY	19	11	10	16	5690
GAG	LRPGGKKYKL	21	11	16	25	5691
GAG	LRPGGKKYKL	21	11	13	20	5692
GAG	KKKYRLKILVW	27	11	21	33	5693
GAG	KKKYRLKILVW	32	11	22	34	5694
GAG	KIIVWASREL	32	11	13	20	5695
GAG	LKSLYNTVATL	77	11	16	25	5696
GAG	VRDTREALDKI	96	11	30	48	5697
GAG	PRTLNAAVKKVI	170	11	48	75	5698
GAG	EKAFSPVIM	182	11	22	34	5699
GAG	DRVIPVHAGPI	234	11	14	22	5700
GAG	DRVIPVHAGPI	234	11	17	27	5701
GAG	VIAGPIACQM	239	11	17	27	5702
GAG	VIAGPIACQM	239	11	55	86	5703
GAG	KRWILGLNKI	287	11	35	55	5704
GAG	GIKARVLAFAAM	381	11	19	30	5705
GAG	GIKARVLAFAAM	381	11	50	78	5706
GAG	MKDCTERQANF	456	11	54	84	5707
GAG	ERQANFLGKIW	464	11	12	19	5708
GAG	QKQEPHDKELY	530	11	01	25	5709
GAG	LKDKETPLASL	535	11	01	25	5710
GAG	ERTENSLYPPL	537	11	01	25	5711

Table XII
IIIY B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	GKWSKSSI	3	8	18	28	5711
NEF	SKSSVOW	6	8	20	31	5712
NEF	EKGGLDGL	121	8	26	41	5713
NEF	EKGGLGL	121	8	34	53	5714
NEF	SKKQEL	177	8	25	39	5715
NEF	KRODILD	181	8	18	28	5716
NEF	KROEILD	181	8	32	50	5717
NEF	ARELIPEF	322	8	11	17	5718
NEF	ARELIPEY	322	8	24	38	5719
NEF	EKGGLDGLI	121	9	23	36	5720
NEF	EKGGLGLI	121	9	27	42	5721
NEF	KKROEILD	179	9	25	39	5722
NEF	KKROEILD	179	9	12	19	5723
NEF	KROEILDW	181	9	18	28	5724
NEF	KROEILDW	181	9	32	50	5725
NEF	IRYPLTFGW	214	9	13	20	5726
NEF	TRPPLTFGW	214	9	12	19	5727
NEF	LIPICQIGM	258	9	10	16	5728
NEF	LIPMSQIGM	258	9	12	19	5729
NEF	ARELIPEFY	322	9	11	17	5730
NEF	ARELIPEY	322	9	21	33	5731
NEF	SIDLEKIGAI	50	10	14	22	5732
NEF	VAPQVPLRPM	97	10	47	73	5733
NEF	LRPMYKGF	103	10	12	19	5734
NEF	SHFLKEKGL	115	10	29	45	5735
NEF	LKEKGGDGL	118	10	26	42	5736
NEF	LKEKGLGL	118	10	21	33	5737
NEF	EKGGLGLY	121	10	21	33	5738
NEF	EKGGLGLY	121	10	19	30	5739
NEF	SKKROEILD	177	10	25	39	5740
NEF	KKROEILDW	179	10	25	39	5741
NEF	QKRODILDW	179	10	12	19	5742
NEF	YHITQGFYFDW	193	10	14	22	5743
NEF	YHITQGFYFDW	193	10	25	39	5744
NEF	GKWSKSSVGV	3	11	18	28	5745
NEF	LKEKGLDGLI	118	11	23	37	5746
NEF	LKEKGLDGLI	118	11	24	39	5747
NEF	SKKROEILDW	177	11	25	39	5748
NEF	KKRODILDWVY	181	11	16	25	5749
NEF	KKROEILDWVY	181	11	29	45	5750
NEF	TRPPLTFGWCF	214	11	10	16	5751
POL	TRRELQVW	43	8	13	20	5752
POL	GKWKPKMI	127	8	41	64	5753
POL	GRWKPKMI	127	8	16	25	5754
POL	VRQYDQIL	143	8	21	33	5755
POL	IKKAGTVL	156	8	20	31	5756
POL	KKKAGTVL	156	8	29	45	5757
POL	GRNLLTQI	173	8	21	33	5758
POL	GRNMLTQI	173	8	19	30	5759
POL	GRNMLTQI	173	8	11	17	5760

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PKVKQWPL	206	8	51	80	5761
POL	KKKDSIKW	253	8	57	89	5762
POL	NKRTQDFW	270	8	57	89	5763
POL	KKKSIVTL	291	8	50	78	5764
POL	RKYTAFTI	314	8	62	97	5765
POL	IRYQYNVL	311	8	53	81	5766
POL	WKGSIATF	342	8	59	92	5767
POL	FRQNPDII	360	8	16	25	5768
POL	IRAKIEEL	387	8	26	41	5769
POL	IRTKIEEL	387	8	22	34	5770
POL	LRHLLKW	394	8	17	27	5771
POL	LRQHLLRW	394	8	15	23	5772
POL	EIILLKWGF	396	8	14	22	5773
POL	QHLLRWGF	396	8	12	19	5774
POL	KIQKEPIF	409	8	62	97	5775
POL	QKEPPELW	411	8	63	98	5776
POL	DKWTVQNI	426	8	54	84	5777
POL	VKQLCKLL	465	8	28	44	5778
POL	VKQLCKLL	465	8	19	30	5779
POL	TKALTEVI	475	8	11	17	5780
POL	SKDLIAEI	514	8	27	42	5781
POL	QKQGQDQW	522	8	16	25	5782
POL	QKQGQDQW	522	8	24	38	5783
POL	QRIATESI	565	8	14	22	5784
POL	GKTRFKFL	576	8	17	27	5785
POL	GKTPKFL	576	8	30	47	5786
POL	QKETWEAW	586	8	15	23	5787
POL	QKETWETW	586	8	27	42	5788
POL	TKIGKAGY	642	8	10	16	5789
POL	TKLGRAGY	642	8	36	56	5790
POL	GRQKVVS	634	8	24	38	5791
POL	QKTELIHAI	667	8	12	19	5792
POL	QKTELOAI	667	8	42	66	5793
POL	IKKEKVYL	718	8	35	55	5794
POL	DKLVSAHI	741	8	16	25	5795
POL	DKLVSSGI	741	8	29	45	5796
POL	YIINWWRAM	767	8	10	16	5797
POL	YIISNWRAM	767	8	39	61	5798
POL	WRAMASDF	771	8	43	67	5799
POL	THLEGKII	818	8	35	55	5800
POL	THLEGKVI	818	8	26	41	5801
POL	VIIIVASGYI	829	8	53	83	5802
POL	GRWPKVTI	858	8	13	21	5803
POL	GRWPKVTI	858	8	22	35	5804
POL	NKELKII	907	8	57	89	5805
POL	VROQAEIIL	917	8	48	75	5806
POL	VROQAEIIL	917	8	13	20	5807
POL	RKGGIGGY	939	8	59	92	5808
POL	TKELQKQI	962	8	47	75	5809
POL	YRDSRDP	979	8	35	55	5810

Table XI1
IIIY B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YRDSRDPL	979	8	14	22	5811
POL	WGPAAKLL	987	8	59	92	5812
POL	PRKAKII	1014	8	50	78	5813
POL	PRKVKII	1014	8	11	17	5814
POL	IKDYGKQM	1021	8	11	17	5815
POL	IRDYGRQM	1021	8	50	78	5816
POL	QRPLVTIKI	94	9	14	22	5817
POL	QRPLVTIKI	94	9	12	19	5818
POL	WKPKNIIGGI	129	9	60	94	5819
POL	IKVHQYDQI	141	9	41	64	5820
POL	VRQYDQILI	143	9	20	31	5821
POL	VRQYDQIIM	143	9	13	20	5822
POL	GIUKAIGTIVL	155	9	20	31	5823
POL	GKKAIGTIVL	155	9	29	45	5824
POL	EKIKALTEI	216	9	28	44	5825
POL	EKIKALVEI	216	9	15	23	5826
POL	EKEGKISKI	231	9	36	56	5827
POL	SKIGPENPY	237	9	42	66	5828
POL	SRIGPENPY	237	9	11	17	5829
POL	IKKKDSTKW	252	9	57	89	5830
POL	TKWHKLVDF	258	9	59	92	5831
POL	IKKLVDFREL	261	9	63	98	5832
POL	KKKKSVTVL	290	9	50	78	5833
POL	FRKYTAFTI	313	9	61	97	5834
POL	IKQNIPDIVI	361	9	14	22	5835
POL	QIURAKIEEL	386	9	26	41	5836
POL	QIURKIEEL	386	9	22	34	5837
POL	KKIHQKEPFF	408	9	60	94	5838
POL	KIHQKEPFL	409	9	62	97	5839
POL	QKEPPELWM	411	9	63	98	5840
POL	QKLVGKLNW	447	9	62	97	5841
POL	GKLNWASQI	451	9	61	95	5842
POL	IKVKQLCKL	463	9	29	45	5843
POL	IKVRQLCKL	463	9	18	28	5844
POL	LKEPVIIGVY	502	9	45	70	5845
POL	FKNLKTGKY	538	9	10	16	5846
POL	YKNLKTGKY	541	9	19	30	5847
POL	LKTGKYAKM	541	9	13	20	5848
POL	LKTGKYARM	541	9	46	72	5849
POL	AIITNDVKQL	552	9	15	23	5850
POL	QKETWEAWW	586	9	27	42	5851
POL	QKETWETWW	586	9	12	19	5852
POL	QKTELQAIY	667	9	20	32	5853
POL	KKEKVYLAW	719	9	13	21	5854
POL	KKEKVYLSW	719	9	50	78	5855
POL	RKVLFDGI	749	9	10	16	5856
POL	DIIEKYIISNW	763	9	20	31	5857
POL	EIEKYIISNW	763	9	13	20	5858
POL	EIEKYIISNW	763	9	31	50	5859
POL	THLEGGKIL	818	9	31	48	5860

Table XII
 IIIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	THLEQKVL	818	9	23	36	5861
POL	IHTDNGSNF	865	9	42	66	5862
POL	IKQEGIPY	887	9	26	41	5863
POL	EHLKTAQOM	922	9	57	89	5864
POL	KRKGIGGY	938	9	59	92	5865
POL	TKELQKHL	962	9	10	16	5866
POL	IKIQNFRVY	970	9	12	19	5867
POL	TKIQNFRVY	970	9	37	58	5868
POL	YRDSRDPW	979	9	35	55	5869
POL	YRDSRDPW	979	9	14	22	5870
POL	WKGPAKLLW	987	9	59	92	5871
POL	WKGPAKLLW	995	9	61	95	5872
POL	WKGPAKLLW	1016	9	41	64	5873
POL	PKMIGGIGF	131	10	62	97	5874
POL	IKVIRYDQIL	141	10	21	33	5875
POL	KKDKTKWKIL	254	10	58	91	5876
POL	WRKLVDFREL	260	10	63	98	5877
POL	LKKKSVTVL	289	10	49	78	5878
POL	DKDFRYTAF	310	10	18	28	5879
POL	FRQNPDIVI	360	10	14	22	5880
POL	IKQNPDIIVY	361	10	14	22	5881
POL	AKIELREHL	389	10	13	20	5882
POL	TKIEELRQHL	389	10	14	22	5883
POL	LRHILLKWGF	394	10	14	22	5884
POL	LRQHILLRWGF	394	10	12	19	5885
POL	DKKIQKEPFF	407	10	60	94	5886
POL	KKIQKEPFFL	409	10	62	97	5887
POL	KKIQKEPFFL	409	10	28	44	5888
POL	DKWTVQHIQL	426	10	12	19	5889
POL	DKWTVQHIQL	426	10	41	64	5890
POL	EKDSWTVDNI	437	10	60	94	5891
POL	GKLNWASQIY	451	10	28	44	5892
POL	IKVQLCKLL	463	10	18	28	5893
POL	IKVQLCKLL	463	10	25	39	5894
POL	CKLLRGAKAL	469	10	24	38	5895
POL	CKLLRGAKAL	469	10	22	34	5896
POL	LRGAKALTDI	472	10	17	27	5897
POL	AKALTDIIVPL	475	10	11	17	5898
POL	TKALTEVIFL	475	10	39	61	5899
POL	LKEPVIQVY	502	10	15	23	5900
POL	QKQGQDQWY	522	10	24	38	5902
POL	QKQGQDQWY	522	10	14	22	5903
POL	QKQIATESVI	565	10	17	27	5904
POL	GKTPKFLPI	576	10	29	45	5905
POL	GKTPKFLPI	576	10	20	32	5906
POL	FKLPIQKETW	581	10	26	41	5907
POL	FKLPIQKETW	581	10	18	28	5908
POL	DRGRQKVVSL	652	10	15	23	5909
POL	QKTELQAIHL	667	10	12	19	5910
POL	QKTELQAIYL	667	10	12	19	5910

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	IIILALQDSGL	674	10	15	23	5911
POL	IKKEKVVYLA	718	10	20	31	5912
POL	IKKEKVVYLA	718	10	13	20	5913
POL	IRKVLFLDGI	748	10	49	77	5914
POL	DKAQEEIERK	758	10	25	39	5915
POL	DKAQEEIERK	758	10	15	23	5916
POL	EKYIISNWRAM	765	10	28	44	5917
POL	EKYIISNWRAM	765	10	10	16	5918
POL	WRAMASDFNL	771	10	41	64	5919
POL	DKCOLKGEM	793	10	44	69	5920
POL	VKAACWVAGI	878	10	31	48	5921
POL	LKTAVQMAVF	924	10	57	89	5922
POL	IIINFKRKGGI	934	10	58	91	5923
POL	FKRKGIGGY	937	10	59	92	5924
POL	QKQIKIQNF	966	10	12	19	5925
POL	QKQIKIQNF	966	10	34	53	5926
POL	IKIQNFRVYY	970	10	12	19	5927
POL	IKIQNFRVYY	970	10	37	58	5928
POL	RRKAKIRIDY	1015	10	41	64	5929
POL	TRANSITRREL	32	11	11	17	5930
POL	ERAIISPATREL	25	11	01	50	5931
POL	SRANSPISKIDL	25	11	01	50	5932
POL	TRANSPTSREL	34	11	01	33	5933
POL	TRANSPTTREL	36	11	01	33	5934
POL	IKIGQLKEAL	100	11	19	30	5935
POL	GRWKPKMIGGI	127	11	41	64	5936
POL	GRWKPKMIGGI	127	11	16	25	5937
POL	IKMIGGIGGFI	131	11	62	97	5938
POL	IKVRQYDQILI	141	11	20	31	5939
POL	IKVRQYDQIPI	141	11	13	20	5940
POL	VRQYDQILIEI	143	11	20	31	5941
POL	VRQYDQILIEI	143	11	12	19	5942
POL	VKQWPLTEFKI	208	11	52	81	5943
POL	IKALVEICTEM	218	11	15	23	5944
POL	KKKDKTKWRKL	253	11	57	89	5945
POL	FRELNRKTQDF	266	11	57	89	5946
POL	KRTQDFWEVQL	271	11	52	81	5947
POL	RKYTAFTIISI	314	11	37	58	5948
POL	FRKQNPDIYIY	360	11	14	22	5949
POL	AKIEELREIILL	389	11	13	20	5950
POL	TKIEELRQIILL	389	11	14	22	5951
POL	DKKHQKEPFL	407	11	60	94	5952
POL	KKHQKEPFLW	408	11	60	94	5953
POL	KKHQKEPFLWM	409	11	62	97	5954
POL	QKEPFLWMGY	411	11	63	98	5955
POL	LHPDKWTVQPI	423	11	53	83	5956
POL	LRGTKALTEVI	472	11	11	17	5957
POL	VKQLTEAVQKI	557	11	30	47	5958
POL	QKIATESIWIW	565	11	14	22	5959
POL	EKEPIVQNETF	622	11	16	25	5960

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	NRETKLGKAGY	639	11	28	44	5961
POL	DKSESELVNOI	703	11	18	28	5962
POL	DKSESELVSOI	703	11	19	30	5963
POL	MHGQVDCSPGI	802	11	52	81	5964
POL	LKTAQMAVFI	974	11	56	88	5965
POL	ERIDIASDI	950	11	12	19	5966
POL	ERIDIASDI	950	11	29	45	5967
POL	ERIDIASDI	950	11	11	17	5968
POL	ERIDIASDI	950	11	10	16	5969
POL	TKELQKQIKI	962	11	31	49	5970
POL	TKELQKQIKI	962	11	51	80	5971
POL	IKVVPKAKAI	1010	11	11	17	5972
POL	IKVVPKAKAI	1010	11	41	64	5973
POL	PRKAKIIRDIY	1014	11	42	66	5974
POL	AKHIDYQKQM	1018	11	18	28	5975
REV	VRIKILY	18	8	21	33	5976
REV	IKNNRRRW	42	8	40	63	5977
REV	IKNNRRRW	42	8	36	56	5978
REV	WRARQRQI	49	8	11	17	5979
REV	WRERQRQI	49	8	11	17	5980
REV	ERLSTCL	61	8	18	28	5981
REV	ARNNRRRW	41	9	39	61	5982
REV	ARNNRRRW	41	9	10	16	5983
REV	ARQRQIISI	51	9	20	31	5984
REV	GRPAEPVPL	69	9	12	19	5985
REV	GRSAEPVPL	69	9	17	27	5986
REV	GRSGDSDEEL	3	10	25	39	5987
REV	IKILYQSNPY	21	10	34	53	5988
REV	RRWRARQRQI	47	10	11	17	5989
REV	RRWRERQRQI	47	10	16	25	5990
REV	GRSGDSDEEL	3	11	34	53	5991
REV	RRWRARQRQI	46	11	11	17	5992
REV	RRWRERQRQI	46	11	10	16	5993
REV	WILARQRQIISI	49	11	20	31	5994
REV	GRPAEPVPLQI	69	11	12	19	5995
REV	GRSAEPVPLQI	69	11	15	23	5996
TAT	KKGLGISY	43	8	14	22	5997
TAT	KKGLGISY	43	8	14	30	5998
TAT	TKGLGISY	43	8	19	30	5999
VIF	DRMKIRTW	14	8	12	19	6000
VIF	DRMRIRTW	14	8	10	16	6001
VIF	DRMRIRTW	14	8	32	50	6002
VIF	ARLVITY	64	8	11	17	6003
VIF	LITGERDW	74	8	22	34	6004
VIF	GHGVSEW	85	8	31	48	6005
VIF	GHGVSEW	85	8	47	73	6006
VIF	GHGVSEW	85	8	47	75	6007
VIF	NKVGSLQY	145	8	19	30	6008
VIF	PKKIKPPL	161	8	13	21	6009
VIF	KKLTEDRW	176	8	23	39	6010
VIF	GHIGSHITM	191	8	25	39	6011
VIF	NRWQVLIVW	3	9	10	16	6012

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	NRWQVMIIV	3	9	42	66	6011
VIF	MKIRTWNSL	16	9	12	19	6012
VIF	MRIRTWNSL	16	9	15	23	6013
VIF	MRIRTWNSL	16	9	15	23	6014
VIF	WKSIVKIHIM	21	9	18	28	6015
VIF	WKSIVKIHIM	21	9	10	16	6016
VIF	PKISSEVIII	49	9	15	23	6017
VIF	PKISSEVIII	49	9	20	31	6018
VIF	PKISSEVIII	49	9	15	23	6019
VIF	ARLVITYYW	64	9	11	17	6020
VIF	WILGIGVSI	82	9	23	36	6021
VIF	WILGIGVSI	82	9	26	41	6022
VIF	IIILYDFCF	112	9	16	25	6023
VIF	IIILYDFCF	112	9	15	23	6024
VIF	NKVGSLQYL	145	9	47	75	6025
VIF	NKVGSLQYL	175	9	13	20	6026
VIF	WKSIVKIHIM	21	10	18	28	6027
VIF	AKGWFYRIHY	35	10	10	16	6028
VIF	VIIPLGDARL	55	10	13	20	6029
VIF	VIIPLGDARL	55	10	20	31	6030
VIF	LIITGERDWII	74	10	21	33	6031
VIF	GIIGVSIWRL	85	10	15	23	6032
VIF	GIIGVSIWRL	143	10	47	73	6033
VIF	IKPKKIKITL	159	10	10	16	6034
VIF	TKGIRGSIITM	189	10	18	29	6035
VIF	DRMKIRTWNSL	14	11	12	19	6036
VIF	DRMKIRTWNSL	14	11	15	23	6037
VIF	DRMKIRTWNSL	14	11	15	23	6038
VIF	WKSIVKIHIMYI	21	11	11	17	6039
VIF	RIIPKVSSEVIII	47	11	16	25	6040
VIF	PKISSEVIIIPL	49	11	14	22	6041
VIF	PKISSEVIIIPL	49	11	19	30	6042
VIF	PKISSEVIIIPL	49	11	13	20	6043
VIF	ARLVITYWGL	64	11	11	17	6044
VIF	WILGIGVSIW	82	11	23	36	6045
VIF	WILGIGVSIW	82	11	26	41	6046
VIF	GIIGVSIWRL	143	11	47	73	6047
VIF	NKVGSLQYLAL	145	11	46	73	6048
VPR	QREPYNEW	11	8	38	59	6049
VPR	VRIIFRIW	31	8	14	22	6050
VPR	VRIIFRIW	31	8	34	53	6051
VPR	RIIFPRIWL	32	8	14	22	6052
VPR	RIIFPRIWL	32	8	34	53	6053
VPR	PRPWLIISL	35	8	10	16	6054
VPR	PRPWLIISL	35	8	24	38	6055
VPR	LIIGLQIHI	39	8	20	31	6056
VPR	IRILQIILL	61	8	45	70	6057
VPR	CRISIRIGI	77	8	11	17	6058
VPR	QISIRIGI	78	8	16	25	6059
VPR	LKNEAVRIIF	26	9	18	28	6060

Table XII
HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	LKQEAVERIF	26	9	11	17	6061
VPR	LKSEAVRIIF	26	9	15	23	6062
VPR	VRIFPRWIL	31	9	14	22	6063
VPR	VRIFPRPWL	31	9	34	33	6064
VPR	LHGLGQHLY	39	9	20	31	6065
VPR	IRILQQLIF	61	9	44	69	6066
VPR	QREYNEWTIL	11	10	30	47	6067
VPR	IRILQQLLEI	61	10	36	56	6068
VPR	FRIGCQHSRI	73	10	44	69	6069
VPR	FRIGCRHSRI	73	10	12	19	6070
VPR	RHPRWLIHSL	32	11	10	16	6071
VPR	RHPRWLIHSL	32	11	24	38	6072
VPR	RPWLIHGLQY	35	11	10	16	6073
VPR	QHYYETGDTW	44	11	17	27	6074
VPR	QHYYNTYGDITW	44	11	13	20	6075
VPR	QRKIDRLI	49	8	21	33	6076
VPU	AKVDYRVI	6	9	01	33	6077
VPU	RKILRQKI	44	9	13	21	6078
VPU	LQKIDRL	47	9	17	27	6079
VPU	YRKILRQKI	42	10	13	21	6080
VPU	AKKLLKQKKI	43	10	01	50	6081
VPU	LRQKIDRLI	47	10	15	24	6082
VPU	RKIDRLIDRI	51	10	12	19	6083
VPU	QRKIDRLIDRI	49	11	12	19	6084

Table XIII
HIV BS8 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Site ID No.
ENV	NTSPSRV	376	8	01	33	6085
ENV	NTSPSRVAY	376	10	01	33	6086
ENV	TAGNRSRAAY	376	10	01	33	6087
ENV	TSNNSNSTPI	160	11	01	33	6088
ENV	GTAGNRSRAAY	375	11	01	33	6089
ENV	ITTEGNITL	478	8	01	50	6090
ENV	NANITPCRI	478	10	01	50	6091
ENV	STRTHREKNAV	586	11	01	50	6092
ENV	DSSNSTGNY	218	9	01	20	6093
ENV	STNGTET	537	8	01	17	6094
ENV	NTETNKTET	537	10	01	17	6095
ENV	NTIGNTTET	537	10	01	17	6096
ENV	CSNGTET	538	9	02	18	6097
ENV	NTRKSIRI	331	8	10	16	6098
ENV	SSLKGLRL	886	8	10	16	6099
ENV	SSLKGLRLGW	886	10	10	16	6100
ENV	CTPAGCAI	264	8	10	16	6101
ENV	QSSGGDPEI	423	9	10	16	6102
ENV	QSSGGDPEIV	423	10	10	16	6103
ENV	WSQELKNSAV	910	10	10	16	6104
ENV	FAIKCNDKKF	269	11	10	16	6105
ENV	RAVGIGAVE	594	9	11	17	6106
ENV	RAVGIGAVFL	594	10	11	17	6107
ENV	AARTVELL	876	8	11	17	6108
ENV	GTRDVIEV	932	8	11	17	6109
ENV	LALDKWASL	736	9	11	17	6110
ENV	LAARTVELL	874	9	11	17	6111
ENV	VSLNATAI	919	9	11	17	6112
ENV	YATGDIIGDI	368	10	11	17	6113
ENV	TTNVPWNSSW	691	10	11	17	6114
ENV	LALDKWASLW	736	10	11	17	6115
ENV	ISNLWYIKI	770	10	11	17	6116
ENV	RSIRLVNGFL	841	10	11	17	6117
ENV	CTTNVWVNSSW	690	11	11	17	6118
ENV	ISNLWYIKIF	770	11	11	17	6119
ENV	SAVSLNATAI	917	11	11	17	6120
ENV	VSLNATAIAY	919	11	11	17	6121
ENV	RAVGIGAV	594	8	12	19	6122
ENV	EAQQILLKL	646	9	12	19	6123
ENV	EAQQILLKLTV	646	11	12	19	6124
ENV	RANVAPH	502	8	12	19	6125
ENV	GALFLGFL	601	8	12	19	6126
ENV	IAARTVEL	874	8	12	19	6127
ENV	PTIRIQGL	931	8	12	19	6128
ENV	ATGDIIGDI	369	9	12	19	6129
ENV	RSIRLVNGF	841	9	12	19	6130
ENV	MTWMEWGREI	731	10	12	19	6131
ENV	RAILMIPRI	945	10	12	19	6132
ENV	PTDPNPQEVVL	89	11	12	19	6133
ENV	TSVITQACPKV	242	11	12	19	6134

Table XIII
 HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GTGPKNVSTV	281	11	12	19	6135
ENV	TTISFNCGEF	432	11	12	19	6136
ENV	CSGKLCITTV	684	11	12	19	6137
ENV	ITKWLWYKIF	770	11	12	19	6138
ENV	PSYHRLDLL	863	11	12	19	6139
ENV	LAFEEVVI	312	8	13	20	6140
ENV	GAMFLGFL	601	8	13	20	6141
ENV	RSIRLVSGF	841	9	13	20	6142
ENV	PTDIPNQEVS	89	10	13	20	6143
ENV	SATQACPKV	243	10	13	20	6144
ENV	GSLAEDEVVI	310	10	13	20	6145
ENV	SSGGDPEVM	424	10	13	20	6146
ENV	RSIRLVSGFL	841	10	13	20	6147
ENV	TSATQACPKV	863	11	13	20	6148
ENV	PSYHRLRDEL	863	11	13	20	6149
ENV	NAKTIIVQL	329	9	14	22	6150
ENV	QAMYPPI	502	8	14	22	6151
ENV	ISNWLWYI	770	8	14	22	6152
ENV	GSLAEDEVV	310	9	14	22	6153
ENV	ITNWLWYIKI	770	10	14	22	6154
ENV	PSYHRLDLL	863	10	14	22	6155
ENV	IAVAEGTDIV	927	10	14	22	6156
ENV	ITNWLWYKIF	770	11	14	22	6157
ENV	IAVAEGTDIVI	927	11	14	22	6158
ENV	ITKWLWYIKI	770	10	14	22	6159
ENV	ITLPCRIRKQI	483	11	15	23	6160
ENV	IAVAEGTDRII	927	11	15	23	6161
ENV	GSLAEDEV	310	8	16	25	6162
ENV	SSGGDLEI	424	8	16	25	6163
ENV	ITKWLWYI	770	8	16	25	6164
ENV	VAEGTDIV	929	8	16	25	6165
ENV	ISFNCRGIEF	434	9	16	25	6166
ENV	VSGFLALAW	846	9	16	25	6167
ENV	VAEGTDIVI	929	9	16	25	6168
ENV	ISFNCRGIEF	434	10	16	25	6169
ENV	IAVAEGTDRI	927	10	16	25	6170
ENV	TTISFNCGEF	432	11	16	25	6171
ENV	ISFNCRGIEFF	434	11	16	25	6172
ENV	GTGPKNV	281	8	17	27	6173
ENV	DAKAYDTEV	70	9	17	27	6174
ENV	ASLWNWFDI	762	9	17	27	6175
ENV	KAYDTEVINV	72	10	17	27	6176
ENV	VAPTKARRV	574	10	17	27	6177
ENV	WASLWNWFDI	761	10	17	27	6178
ENV	ASDAKAYDTEV	68	11	17	27	6179
ENV	KAYDTEVINVW	72	11	17	27	6180
ENV	VAPTKARRV	574	11	17	27	6181
ENV	CSGKLCITTV	684	11	17	27	6182
ENV	SSGGDPEIV	424	9	18	28	6183
ENV						6184

Table XIII
HIV D58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO.
ENV	FSYIHLRDF	863	9	18	28	6185
ENV	VAEGTDRII	929	9	18	28	6186
ENV	DTEVINVW	75	8	19	30	6187
ENV	SSNITGLL	516	8	19	30	6188
ENV	ITNVLWYI	770	8	19	30	6189
ENV	VAEGTDRI	929	8	19	30	6190
ENV	CSSNITGLL	515	9	19	30	6191
ENV	SSNITGLL	516	9	19	30	6192
ENV	CSSNITGLLL	515	10	19	30	6193
ENV	CSGKLCTTAV	684	11	19	30	6194
ENV	LALAWDDLRL	850	11	19	30	6195
ENV	LAWDDLRLSL	852	9	20	31	6196
ENV	LAWDDLRLSL	852	11	20	31	6197
ENV	CSSNITGL	515	8	21	33	6198
ENV	PTDIPNQEY	89	9	21	33	6199
ENV	ETFRNGGDM	544	10	21	33	6200
ENV	PTKAKIRV	576	8	22	34	6201
ENV	GAVFLGFL	601	8	22	34	6202
ENV	PTKAKRRV	576	9	22	34	6203
ENV	KAMYAPPI	502	8	23	36	6204
ENV	FSYIHLRDL	863	9	23	36	6205
ENV	SSGGDIPI	424	8	24	38	6206
ENV	LALAWDDL	850	8	25	39	6207
ENV	PTDIPNQEI	89	9	25	39	6208
ENV	ITLPCIKIKOI	483	10	25	39	6209
ENV	LSGIVQQNNL	631	11	25	39	6210
ENV	CTIIGIRPV	294	8	26	41	6211
ENV	QSNLLRAI	638	8	26	41	6212
ENV	CTIIGIRPV	294	9	26	41	6213
ENV	ITLTVQARQL	631	10	27	42	6214
ENV	ITLTVQARQLL	631	11	27	42	6215
ENV	VSFEPIIHY	253	10	28	44	6216
ENV	YSPLSFQTL	807	9	29	46	6217
ENV	CAPAGFAL	264	8	29	45	6218
ENV	ITQACTKVSF	264	9	29	45	6219
ENV	VSFEPII	253	10	29	45	6220
ENV	WASLWNWF	761	8	30	47	6221
ENV	QACPKVSFEM	248	11	30	47	6222
ENV	FAVLSIVNRV	794	10	31	48	6223
ENV	RSCLFSYIHL	858	11	31	48	6224
ENV	CTIIGIKPV	294	9	32	50	6225
ENV	LSGIVQQSNL	631	11	32	50	6226
ENV	CTIIGIKPV	294	8	33	52	6227
ENV	QARVLAVERY	663	10	33	52	6228
ENV	QARVLAVERYL	663	11	33	52	6229
ENV	EAQILLQLTV	646	11	34	54	6230
ENV	VTENFMW	102	8	34	53	6231
ENV	AAGSTMGAASI	611	11	34	53	6232
ENV	LSIVNRVQGY	797	11	34	53	6233
ENV						6234

Table XIII
IIIY B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	EAQQIILLQL	646	9	35	56	6235
ENV	ISLCLEFY	858	8	35	55	6236
ENV	ISFNCGGEEF	434	10	35	55	6237
ENV	ISFNCGGEEF	434	11	35	55	6238
ENV	AASITLV	618	8	36	56	6239
ENV	ISFNCGGEEF	434	9	36	56	6240
ENV	GAASITLV	617	9	36	56	6241
ENV	LTVOARQLL	623	9	36	56	6242
ENV	ITQACPKV	245	8	37	58	6243
ENV	LTQARQL	623	8	38	59	6244
ENV	QARQLISGI	626	9	38	59	6245
ENV	QARQLISGI	626	10	38	59	6246
ENV	STMGAASI	614	8	39	61	6247
ENV	STMGAASI	613	9	39	61	6248
ENV	STMGAASITL	614	10	39	61	6249
ENV	STMGAASITL	613	11	39	61	6250
ENV	QACPKVSF	248	8	40	63	6251
ENV	CASDAKAY	67	8	42	66	6252
ENV	RAIEAQHILL	643	10	44	69	6253
ENV	RAIEAQHILL	643	9	45	70	6254
ENV	ISLWDQSL	122	8	48	75	6255
ENV	QSLKPCVKL	127	9	48	75	6256
ENV	RSELYKYKV	558	10	49	77	6257
ENV	RSELYKYKV	558	9	50	78	6258
ENV	STVQCTIIGI	289	9	51	80	6259
ENV	STVQCTIIGI	288	10	51	80	6260
ENV	LTPLCVTL	135	8	54	84	6261
ENV	VTVYGVV	47	9	55	86	6262
ENV	VTVYGVV	47	10	55	86	6263
ENV	STQLLNGSL	303	10	57	89	6264
ENV	STQLLNGSL	302	11	57	89	6265
ENV	LTVWGIKQL	654	9	59	92	6266
GAG	TAPPPEF	508	8	01	33	6267
GAG	ETIDKIDLY	337	8	01	25	6268
GAG	PTAPPPEF	507	9	01	33	6269
GAG	TAPPPEF	508	10	01	33	6270
GAG	ETIDKIDLY	517	10	01	25	6271
GAG	RTENSLYPL	518	10	01	25	6272
GAG	AAAMMOKSNF	405	11	01	25	6273
GAG	SATIMMQRUNF	405	11	01	25	6274
GAG	PTAPPPEF	507	11	01	33	6275
GAG	GAATAIDSNI	123	10	01	50	6276
GAG	AADKGVSNQY	130	10	01	50	6277
GAG	AAGTGNSSQV	130	10	01	50	6278
GAG	GANSIPVGD	276	10	01	50	6279
GAG	SAQDILKGGY	393	10	01	50	6280
GAG	TAQDILKGGY	393	10	01	50	6281
GAG	GANSIPVGD	276	11	01	50	6282
GAG	ASAQDILKGGY	392	11	01	50	6283
GAG	ATAQDILKGGY	392	11	01	50	6284

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	PAEPTAPPAEI	492	11	01	50	6285
GAG	TAPPAESF	508	8	02	67	6286
GAG	PTAPPAESF	507	9	02	67	6287
GAG	TAPPAESRF	508	10	02	67	6288
GAG	PTAPPAESRF	507	11	02	67	6289
GAG	GTRPGNY	480	8	02	100	6290
GAG	AADKGRVSNY	129	11	02	18	6291
GAG	EADGKVSQNY	129	10	04	36	6292
GAG	AAMMOKSNF	406	10	06	15	6293
GAG	TTPSOKQEH	522	10	09	45	6294
GAG	GASLEMM	364	8	10	16	6295
GAG	DIKEALEKI	98	9	10	16	6296
GAG	TAPPAESGF	496	10	10	16	6297
GAG	QALSPRTLNAW	166	11	10	16	6298
GAG	PTAPPAESFGF	495	11	10	16	6299
GAG	ATIMNIQGNF	406	10	11	28	6300
GAG	PSOKQEH	528	8	11	18	6301
GAG	SSKGRPGNF	476	9	11	18	6302
GAG	TTSTLQEQIAW	260	11	11	17	6303
GAG	QALSPRTL	166	8	11	17	6304
GAG	ASQEVKNW	333	9	11	17	6305
GAG	ASVLSGEL	3	9	11	17	6306
GAG	QASQEVKNW	332	9	11	17	6307
GAG	ASQEVKNWM	333	9	11	17	6308
GAG	NANPDKSI	349	9	11	17	6309
GAG	IASVLSGGEL	4	10	11	17	6310
GAG	QASQEVKNWM	332	10	11	17	6311
GAG	NANPDKSIL	349	10	11	17	6312
GAG	PSSKGRPGNF	475	10	11	17	6313
GAG	QTGSEELRSL	71	10	12	19	6314
GAG	GSEELKSL	73	8	12	19	6315
GAG	GTEELKSL	73	8	12	19	6316
GAG	ATPQDLNM	200	8	12	19	6317
GAG	LTSLSLF	549	8	12	19	6318
GAG	GSEELKSLY	73	9	12	19	6319
GAG	GATPQDLNM	199	9	12	19	6320
GAG	ATPQDLNM	200	9	12	19	6321
GAG	STLQEQIAW	262	9	12	19	6322
GAG	RAEQASQEV	329	9	12	19	6323
GAG	KSLFGNDYL	533	9	12	19	6324
GAG	ATLYCVIQQI	85	10	12	19	6325
GAG	GATPQDLNM	199	10	12	19	6326
GAG	ATPQDLNMML	200	10	12	19	6327
GAG	TSTLQEQIAW	261	10	12	19	6328
GAG	STLQEQIAWM	262	10	12	19	6329
GAG	VATLYCVIQQI	84	11	12	19	6330
GAG	GATPQDLNMML	199	11	12	19	6331
GAG	TSTLQEQIAWM	261	11	12	19	6332
GAG	TSNPPVGEI	272	11	12	19	6333
GAG	LTSLSLF	549	8	13	20	6334

Table XIII
 IIIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	YSPISILDI	301	9	13	20	6335
GAG	PSLQTGSEEL	68	10	13	20	6336
GAG	NSQVSONY	144	9	14	31	6337
GAG	NSQVSONYPI	144	11	14	31	6338
GAG	TSEGCROIL	55	9	14	22	6339
GAG	ETSEGCROIL	54	10	14	22	6340
GAG	AAEWDRVHPV	230	10	14	22	6341
GAG	PSNKGRPGNF	475	10	14	22	6342
GAG	TAPPEESFRF	496	10	14	22	6343
GAG	EAAEWDRVHPV	229	11	14	22	6344
GAG	PTAPPEESFRF	495	11	14	22	6345
GAG	SSQVSONY	145	8	15	31	6346
GAG	SSQVSONYHI	145	10	15	31	6347
GAG	SSQVSONYPIV	145	11	15	31	6348
GAG	RSLYNTVATL	78	10	15	24	6349
GAG	RSLYNTVATLY	78	11	15	24	6350
GAG	EAAEWDRV	229	8	15	23	6351
GAG	ATQDVKNW	333	8	15	23	6352
GAG	TAPPEESF	496	8	15	23	6353
GAG	LASLKSFL	549	8	15	23	6354
GAG	RAEQATQDV	329	9	15	23	6355
GAG	QATQDVKNW	332	9	15	23	6356
GAG	ATQDVKNWAM	333	9	15	23	6357
GAG	PTAPPEESF	495	9	15	23	6358
GAG	ATLYCVHIQRI	85	10	15	23	6359
GAG	QATQDVKNWAM	332	10	15	23	6360
GAG	VATLYCVHIQRI	84	11	15	23	6361
GAG	FAVNPGLL	46	8	16	25	6362
GAG	TSEGCROI	55	8	16	25	6363
GAG	GSEELRSL	73	8	16	25	6364
GAG	TSNPPIV	272	8	16	25	6365
GAG	PAATLEEM	363	8	16	25	6366
GAG	AATLEEMM	364	8	16	25	6367
GAG	LSGCKLDAAW	8	9	16	25	6368
GAG	ETSEGCROI	54	9	16	25	6369
GAG	MTSNPIV	271	9	16	25	6370
GAG	KALGPAATL	359	9	16	25	6371
GAG	PAATLEEMM	363	9	16	25	6372
GAG	DAWEKIRL	14	8	17	27	6373
GAG	LSPRTLNAW	168	9	17	27	6374
GAG	ASRELERFAV	38	10	17	27	6375
GAG	LSPRTLNAWV	168	10	17	27	6376
GAG	IAGPIPPQGM	240	10	17	27	6377
GAG	WASRELERFAV	37	11	17	27	6378
GAG	ATQEVKNW	333	8	18	28	6379
GAG	QATQEVKNW	332	9	18	28	6380
GAG	ATQEVKNWAM	333	9	18	28	6381
GAG	IAGPIPPQGM	240	10	18	28	6382
GAG	QATQEVKNWAM	332	10	18	28	6383
GAG	PSIIKARVL	380	8	19	30	6384

Table XIII
HIV-158 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	TAPPAESF	496	8	20	31	6385
GAG	MTNPPIPV	271	9	20	31	6386
GAG	PTAPPAESF	495	9	20	31	6387
GAG	FALNPGLL	46	8	22	34	6388
GAG	ASRELERFAL	38	10	22	34	6389
GAG	ETINEEAIEW	224	10	22	34	6390
GAG	WASRELERFAL	37	11	22	34	6391
GAG	PSIKGRPGNF	475	10	23	36	6392
GAG	PSIKGRPGNFI	475	11	23	36	6393
GAG	QAAMQMLKETI	217	10	26	41	6394
GAG	TSTLQEQIGW	260	11	26	41	6395
GAG	TSTLQEQIGW	262	9	27	43	6396
GAG	RAEQATQEV	329	9	27	42	6397
GAG	TSTLQEQIGW	261	10	27	42	6398
GAG	TSTLQEQIGWM	262	10	27	42	6399
GAG	TSTLQEQIGWM	261	11	27	42	6400
GAG	VSONYHVQNL	149	11	28	48	6401
GAG	ASVLSGGKL	5	9	28	44	6402
GAG	RASVLSGGKL	4	10	28	44	6403
GAG	QAISPTL	166	8	29	45	6404
GAG	GATLEEMM	364	8	29	45	6405
GAG	QAISPTLNAW	166	11	29	45	6406
GAG	RTLNAAVVKVI	171	10	30	47	6407
GAG	RTLNAAVVKVV	171	10	31	48	6408
GAG	DTINEEAIEW	224	10	31	48	6409
GAG	DTKEALDKI	98	9	31	48	6410
GAG	QAAMQMLKDIH	217	10	32	50	6411
GAG	QAAMQMLKDIH	216	11	33	52	6412
GAG	AAEWDRLLIPV	230	10	33	52	6413
GAG	EAAEWDRLLIPV	229	11	34	53	6414
GAG	LAEMSQV	387	8	34	53	6415
GAG	ISPTLNAW	168	9	36	57	6416
GAG	ISPTLNAWV	168	10	36	56	6417
GAG	EAAEWDRLL	229	8	36	56	6418
GAG	YSIVSILDI	301	9	39	61	6419
GAG	NTVATILYV	82	9	40	63	6420
GAG	ATPQDLNTM	200	9	41	64	6421
GAG	GATPQDLNTM	199	10	42	66	6422
GAG	GATPQDLNTML	200	10	42	66	6423
GAG	GATPQDLNTML	199	11	42	66	6424
GAG	TSTLQEQI	260	9	45	71	6425
GAG	NANPCKTI	349	9	45	70	6426
GAG	GTTSTLQEQI	259	10	45	70	6427
GAG	NANPCKTIL	349	10	45	70	6428
GAG	ASRELERF	38	8	46	72	6429
GAG	WASRELERF	37	9	46	72	6430
GAG	TSTLQEQI	261	8	47	73	6431
GAG	NTVGHQAAM	210	10	47	73	6432
GAG	GSDIAGTTSTL	234	11	47	73	6433

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	VSQNPVIV	149	8	48	83	6435
GAG	IAQTSTL	237	8	48	75	6436
GAG	KAFSEVI	183	8	50	78	6437
GAG	KAFSEVIM	183	10	50	78	6438
GAG	KAFSEVIMF	183	11	50	78	6439
GAG	RAPKKGCV	439	9	53	83	6440
GAG	FSPEVIM	185	8	54	84	6441
GAG	FSPEVIMF	185	9	54	84	6442
GAG	CTEQANF	439	8	55	87	6443
GAG	CTEQANFL	439	9	55	87	6444
GAG	QANFLGKI	466	8	57	89	6445
GAG	KARVLAEM	383	9	57	89	6446
GAG	QANFLGIW	466	9	57	89	6447
GAG	LSEGATPDIL	196	10	58	91	6448
GAG	RTLNAWVKV	171	9	61	95	6449
GAG	QAEPAAGV	34	9	01	33	6450
NEF	QTEPAAGV	32	9	01	17	6451
NEF	RAEPAAGV	32	9	01	17	6452
NEF	RTEPAAGV	32	9	01	17	6453
NEF	QAEPAAGV	33	9	01	17	6454
NEF	QAPTAAGV	33	9	01	17	6455
NEF	RAQAEPAAGV	32	11	01	17	6456
NEF	GAFDLSEF	110	8	10	16	6457
NEF	GAFDLSEFL	110	9	10	16	6458
NEF	MARELIPEY	321	9	10	16	6459
NEF	MARELIPEYY	321	10	10	16	6460
NEF	AADGVGAV	42	8	11	18	6461
NEF	PAADGVGAV	41	9	11	17	6462
NEF	VSRLDKIIGAI	49	11	11	17	6463
NEF	ATNADCAW	71	8	12	22	6464
NEF	ATNADCAW	70	9	12	22	6465
NEF	ATNADCAWL	71	9	12	22	6466
NEF	ATNADCAWL	70	10	12	22	6467
NEF	PAAEGVGAV	106	9	12	19	6468
NEF	MYKGAFLD	106	9	12	19	6469
NEF	NTQGYFPDW	194	9	12	19	6470
NEF	TAATNADCAW	69	10	12	19	6471
NEF	GTRFLTFGW	213	10	12	19	6472
NEF	NTAATNADCAW	68	11	12	19	6473
NEF	TAATNADCAWL	69	11	12	19	6474
NEF	GTRFLTF	213	8	13	20	6475
NEF	YTPGRTRE	207	9	13	20	6476
NEF	YTPGRTREPL	207	11	13	20	6477
NEF	HTQGFDPW	194	9	14	22	6478
NEF	EAQEEEV	82	8	16	25	6479
NEF	EAQEEEVGF	82	10	16	25	6480
NEF	YTPGIGIYPL	207	11	16	25	6481
NEF	AAEGVGAV	42	8	17	28	6482
NEF	YTPGIGIY	207	9	17	27	6483
NEF	WSKSSIVGW	5	9	20	31	6484

Table XIII
HIV-158 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	YSKKRQEI	176	8	22	34	6485
NEF	YSKKRQEI	176	9	22	34	6486
NEF	LSFELKEGGL	114	11	22	34	6487
NEF	YSKKRQEIHL	176	11	22	34	6488
NEF	HTQYFFDW	194	9	25	39	6489
NEF	LSIFLKEGGL	114	11	27	42	6490
NEF	LTFGWCFKL	221	10	35	55	6491
NEF	LTFGWCFKL	221	9	39	61	6492
POL	NSPTSREL	34	8	01	33	6493
POL	PTSHLOV	36	8	01	33	6494
POL	GTLCNQI	80	8	01	33	6495
POL	PTFNPTQI	80	8	01	33	6496
POL	STNSPTSREL	32	10	01	33	6497
POL	NSPTSRELQV	34	10	01	33	6498
POL	RANSPTSREL	35	10	01	33	6499
POL	GTLCNQITL	80	10	01	33	6500
POL	PTFNPTQITL	80	10	01	33	6501
POL	NSPTSREL	31	11	01	33	6502
POL	GTLCNQITLW	80	11	01	33	6503
POL	PTFNPTQITLW	80	11	01	33	6504
POL	NSPTSREL	37	8	01	50	6505
POL	NSPTSREL	39	8	01	50	6506
POL	PTSHLOV	39	8	01	50	6507
POL	NSPTSRELQV	37	10	01	50	6508
POL	RANSPTSREL	37	10	01	50	6509
POL	NSPTSRELQV	39	10	01	50	6510
POL	GADRGIV	70	8	01	20	6511
POL	GSGRAVH	70	8	01	20	6512
POL	GADRGIVSF	70	10	01	20	6513
POL	GSGRAVPICL	70	10	01	20	6514
POL	GTILNFPQI	79	9	01	17	6515
POL	GAISLSLPQI	79	10	01	17	6516
POL	GTILNFPQITF	79	11	01	17	6517
POL	PSLSHPQI	79	8	01	33	6518
POL	PSLSHPQITI	79	10	02	33	6519
POL	PSLSHPQITLW	79	11	02	33	6520
POL	SSFSFQI	82	8	03	30	6521
POL	SSFSFQITL	82	10	03	30	6522
POL	SSFSFQITLW	82	11	03	30	6523
POL	VSFSFQITLW	78	11	07	15	6524
POL	VSFSFQI	78	8	08	17	6525
POL	VSFSFQITL	78	8	08	17	6526
POL	ETWWTDYW	591	10	10	16	6527
POL	RANSPTSREL	26	10	10	16	6528
POL	ETWETWTDY	588	10	10	16	6529
POL	ETWETWTEY	588	10	10	16	6530
POL	QTKELQKH	961	10	10	16	6531
POL	LAPQGEAREF	6	11	10	16	6532
POL	RSATINDVKQL	550	11	10	16	6533
POL	EAVQKIATESI	562	11	10	16	6534

Table XIII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	ETWETWTDYVW	588	11	10	16	6515
POL	RTAITNDV	550	8	11	17	6516
POL	WAGIQQEF	884	8	11	17	6537
POL	WTVKIGQQL	98	9	11	17	6538
POL	STNNETPGI	323	9	11	17	6539
POL	GTKALTEVI	474	9	11	17	6540
POL	GSNFTSTV	870	9	11	17	6541
POL	GADDTVLHEM	114	10	11	17	6542
POL	ISIRIGPENPY	236	10	11	17	6543
POL	PSTNNETPGI	322	10	11	17	6544
POL	TAITNDYKQL	551	10	11	17	6545
POL	WAGIQQETGI	884	10	11	17	6546
POL	STNNETGIRY	323	11	11	17	6547
POL	ESWTVDIQKL	439	11	11	17	6548
POL	GTKALTEVHPL	474	11	11	17	6549
POL	ESWTVDNIH	439	8	12	19	6550
POL	KTELQAIY	668	8	12	19	6551
POL	KTELQAIYL	668	9	12	19	6552
POL	NSPTRELOQVW	28	11	12	19	6553
POL	ITNOKTELHAI	664	11	12	19	6554
POL	KTELQAIYLAL	668	11	12	19	6555
POL	GAVVIQINSEI	999	11	12	19	6556
POL	KTGKYARM	542	8	13	21	6557
POL	WTVQHIVL	428	8	13	20	6558
POL	PTRELOQVW	30	9	13	20	6559
POL	DTVLEDINL	117	9	13	20	6560
POL	NSPTRELOQV	28	10	13	20	6561
POL	LAGRWPKTI	856	10	13	20	6562
POL	RAKIELREIL	388	11	13	20	6563
POL	IATESIVI	567	8	14	22	6564
POL	IATESIVW	567	9	14	22	6565
POL	NSPTRELOQ	28	8	14	22	6566
POL	PTRELOQV	30	8	14	22	6567
POL	FSFQITLW	85	9	14	22	6568
POL	DTVLEEINL	117	9	14	22	6569
POL	WTDYWOATW	594	9	14	22	6570
POL	SAGERIVDI	947	9	14	22	6571
POL	ASDIQYKEL	957	9	14	22	6572
POL	WTDYWOATWI	594	10	14	22	6573
POL	TSTIVKAACW	874	10	14	22	6574
POL	YSAGERIVDI	946	10	14	22	6575
POL	SAGERIVDII	947	10	14	22	6576
POL	IASDIQYKEL	956	10	14	22	6577
POL	RTKIELRQNIL	388	11	14	22	6578
POL	FTSTIVKAACW	873	11	14	22	6579
POL	TSTIVKAACWW	874	11	14	22	6580
POL	YSAGERIVDII	946	11	14	22	6581
POL	KALVEICTEM	219	10	15	24	6582
POL	FSFQITL	85	8	15	23	6583
POL	LTQLGCTL	177	8	15	23	6584

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Sl:Q ID NO.
POL	RSATINDV	550	8	15	23	6585
POL	VSAGIRKV	744	8	15	23	6586
POL	SAGIRKVL	745	8	15	23	6587
POL	ITVKAACW	876	8	15	23	6588
POL	KTELOAHIL	668	9	15	23	6589
POL	VSAGIRKVL	744	9	15	23	6590
POL	SAGIRKVL	745	9	15	23	6591
POL	STTVKAACW	875	9	15	23	6592
POL	ITVKAACW	876	9	15	23	6593
POL	GADDTVLEDI	114	10	15	23	6594
POL	LTLQCTLNF	177	10	15	23	6595
POL	LTEEKIKALV	213	10	15	23	6596
POL	VSAGIRKVL	744	10	15	23	6597
POL	SAGIRKVL	745	10	15	23	6598
POL	STTVKAACW	875	10	15	23	6599
POL	KTELOAHIL	668	11	15	23	6600
POL	VSAGIRKVL	744	11	15	23	6601
POL	KAQEEHRY	759	9	16	23	6602
POL	YSAGIRV	946	8	16	25	6603
POL	KALTEVIPL	476	9	16	25	6604
POL	KANSPTREL	26	10	16	25	6605
POL	SATINDVKQL	551	10	16	25	6606
POL	NSPTREL	28	8	17	27	6607
POL	VTIKGGQL	98	9	17	27	6608
POL	KTPKFLPI	577	9	17	27	6609
POL	GAKALTDIVPL	474	11	17	27	6610
POL	FSVPLDKDF	305	9	18	28	6611
POL	YAGIKVKQL	460	9	18	28	6612
POL	GADDTVLEH	114	10	18	28	6613
POL	ITLWQRPLVTI	90	11	18	28	6614
POL	KTGKYAKM	542	8	19	30	6615
POL	GTKALTEV	474	8	19	30	6616
POL	ATESIVIV	568	8	19	30	6617
POL	GAITINDVKQL	551	10	19	30	6618
POL	KSESELVNQI	704	10	19	30	6619
POL	KSESELVSQI	704	10	19	30	6620
POL	ITLWQRPLVTI	90	11	19	30	6621
POL	LTDITNOKTEL	661	11	19	30	6622
POL	KSESELVNQI	704	11	19	30	6623
POL	KSESELVSQI	704	11	19	30	6624
POL	VSQIEQL	710	8	20	31	6625
POL	VSQIEQLI	710	9	20	31	6626
POL	MASDFNLPIIV	774	11	20	31	6627
POL	ESELVSQI	706	8	21	33	6628
POL	WAGIKQEF	884	8	21	33	6629
POL	KALTDIVPL	476	9	21	33	6630
POL	ESELVSQI	706	9	21	33	6631
POL	ASDFNLPIIV	775	10	21	33	6632
POL	WAGIKQEF	884	10	21	33	6633
POL	LAWVPATIKGI	725	10	22	34	6634

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	MASDFNLPII	774	10	22	34	6635
POL	LAGRWPKVVI	856	10	22	34	6636
POL	ASDFNLPII	775	9	23	36	6637
POL	CTHLEKGVIL	817	10	23	36	6638
POL	CTHLEKGVILV	817	11	23	36	6639
POL	GAKALTDIV	474	9	24	38	6640
POL	WTEYWQATW	594	9	24	38	6641
POL	WTEYWQATWI	594	10	24	38	6642
POL	PTIPVNIQRNM	166	11	24	38	6643
POL	GAKALTDI	474	8	25	39	6644
POL	DSGSEVNI	680	8	25	39	6645
POL	DSGSEVNI	680	9	25	39	6646
POL	ASDFNLPIV	775	9	25	39	6647
POL	LALQDSGSEV	676	10	25	39	6648
POL	SSGIRKVLFL	745	10	25	39	6649
POL	MASDFNLPIV	774	10	25	39	6650
POL	ASDFNLPIVV	775	10	25	39	6651
POL	LTETTNQKTEL	664	11	25	39	6652
POL	VSSGIRKVLFL	744	11	25	39	6653
POL	MASDFNLPIVV	774	11	25	39	6654
POL	ASQIYAGIKV	456	10	26	41	6655
POL	VSSGIRKV	744	8	26	41	6656
POL	SSGIRKVL	745	8	26	41	6657
POL	CTHLEKGV	817	8	26	41	6658
POL	PSKDLIAEI	513	9	26	41	6659
POL	DTTNQKTEL	663	9	26	41	6660
POL	VSSGIRKVL	744	9	26	41	6661
POL	SSGIRKVLV	745	9	26	41	6662
POL	CTHLEKVI	817	9	26	41	6663
POL	GSNFTSAAV	870	9	26	41	6664
POL	VSSGIRKVLV	744	10	26	41	6665
POL	ETGQETAYFL	844	10	26	41	6666
POL	PTIPVNIQRNL	166	11	26	41	6667
POL	WASQIYAGIKV	455	11	26	41	6668
POL	ETGQETAYFLL	844	11	26	41	6669
POL	ASQIYAGI	456	8	27	43	6670
POL	KAEHEIEKY	759	9	27	43	6671
POL	ASQIYPGIKV	456	10	27	43	6672
POL	LALQDSGL	676	8	27	42	6673
POL	ESELVNQI	706	8	27	42	6674
POL	TAYFLKL	849	8	27	42	6675
POL	WASQIYAGI	455	9	27	42	6676
POL	ESELVNOH	706	9	27	42	6677
POL	ETAYFLKL	848	9	27	42	6678
POL	CTEMEKEGKI	225	10	27	42	6679
POL	LALQDSGLFV	676	10	27	42	6680
POL	TSAAVKAACW	874	10	27	42	6681
POL	WASQIYPGIKV	455	11	27	42	6682
POL	FTSAAVKAACW	873	11	27	42	6683
POL	TSAAVKAACWW	874	11	27	42	6684

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WTVQPIQL	428	8	28	44	6685
POL	DSGLEVNI	680	8	28	44	6686
POL	AAVKAACW	876	8	28	44	6687
POL	DSGLEVNIV	680	9	28	44	6688
POL	SAAVKAACW	875	9	28	44	6689
POL	AAVKAACWW	876	10	28	44	6690
POL	VTDRGRQKV	650	10	28	44	6691
POL	SAAVKAACWW	875	10	28	44	6692
POL	ASQIYPCI	456	8	29	46	6693
POL	WASQNYGI	455	9	29	45	6694
POL	KTPKFRLEI	577	9	29	45	6695
POL	ETTNQKTEL	663	9	29	45	6696
POL	AAARETKL	637	8	30	47	6697
POL	GAARETKL	636	9	30	47	6698
POL	VTDRGRQKV	650	9	30	47	6699
POL	LAGRWPKV	856	9	30	47	6700
POL	KAACWWAGI	879	9	31	49	6701
POL	ETAYFILKL	848	9	31	48	6702
POL	PSINNETWGI	322	10	31	48	6703
POL	CTHLECKIL	817	10	31	48	6704
POL	ETGQETAYFI	844	10	31	48	6705
POL	CTHLECKILV	817	11	31	48	6706
POL	ETGQETAYFIL	844	11	31	48	6707
POL	TAYFILKL	849	8	32	50	6708
POL	AAACWWAGI	880	8	32	50	6709
POL	IISNWRAMASDF	768	11	32	50	6710
POL	SSMTKILEPF	351	10	33	52	6711
POL	QSSMTKILEPF	350	11	33	52	6712
POL	LTEAVQKI	560	8	34	53	6713
POL	CTHLECKI	817	8	35	55	6714
POL	ETKLCKAGIY	641	9	35	55	6715
POL	CTHLECKII	817	9	35	55	6716
POL	ATDIQTKEL	957	9	35	55	6717
POL	ETKLCKAGIYV	641	10	35	55	6718
POL	IATIDIQTKEL	956	10	35	55	6719
POL	ITKIQNFRV	969	9	36	57	6720
POL	ITKIQNFRVY	969	10	36	57	6721
POL	ITKIQNFRVY	969	11	36	57	6722
POL	PAIFQSSMTKI	346	11	36	56	6723
POL	QAQPKDSIESEL	699	11	36	56	6724
POL	TAFTIPI	317	8	37	58	6725
POL	YTAFTIPI	316	9	37	58	6726
POL	LTEEALEL	484	9	37	58	6727
POL	LSWVTAIKGI	725	10	37	58	6728
POL	GAVVIQDINSDI	999	11	37	58	6729
POL	QSSMTKIL	350	8	38	59	6730
POL	KAKIRDY	1017	8	41	64	6731
POL	RAMASDFNL	772	9	41	64	6732
POL	SAGERIIDI	947	9	41	64	6733
POL	LTQIGCTLNF	177	10	41	64	6734

Table XIII
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YSAGERIIDI	946	10	41	64	6735
POL	SAGERIIDI	947	10	41	64	6736
POL	YSAGERIIDI	946	11	41	64	6737
POL	LTOIGCTL	177	8	42	66	6738
POL	PAIQSSM	346	8	42	66	6739
POL	YSAGERII	946	8	42	66	6740
POL	ISKIGPENPY	236	10	42	66	6741
POL	GSPAIFQSSM	344	10	42	66	6742
POL	WTYOIQEFP	529	10	42	66	6743
POL	TTNQKTELOAI	664	11	42	66	6744
POL	DSWTVNDI	439	8	43	67	6745
POL	ASCDKCCQL	790	8	43	67	6746
POL	VASCDKCCQL	789	9	43	67	6747
POL	DSWTVNDIQKL	439	11	43	67	6748
POL	MTKILEFF	353	8	44	69	6749
POL	QIKELQKQI	961	9	46	72	6750
POL	ITLWQRPL	90	8	47	73	6751
POL	ITLWQRPLV	90	9	47	73	6752
POL	KAIGTVLV	157	8	48	75	6753
POL	ITNDVKKQL	553	8	49	77	6754
POL	PAGLKKKKS	286	10	50	78	6755
POL	QATWPEWEFV	599	11	51	81	6756
POL	KSVTVLDV	293	8	51	80	6757
POL	IITDNGSNF	866	8	51	80	6758
POL	ATWPEWEFV	600	10	51	80	6759
POL	ETVPVKLKFGM	192	11	51	80	6760
POL	ETPGIRYQNV	327	11	51	80	6761
POL	QATWPEWEF	599	10	52	83	6762
POL	ETPGIRYQY	327	9	52	81	6763
POL	ATWPEWEF	600	9	52	81	6764
POL	VASGYIEAEV	831	10	52	81	6765
POL	VASGYIEAEVI	831	11	52	81	6766
POL	ASGYIEAEV	832	9	53	83	6767
POL	QSQQGVVESM	894	9	53	83	6768
POL	GTVLVGTPV	160	10	53	83	6769
POL	RTQDFWEVQL	272	10	53	83	6770
POL	VAVIIVASGYI	827	10	53	83	6771
POL	ASGYIEAEVI	832	10	53	83	6772
POL	ESMKNELKKI	904	10	53	83	6773
POL	ISPIETVPVKL	188	11	53	83	6774
POL	ESMKNELKKII	904	11	53	83	6775
POL	QATWPEW	599	8	54	86	6776
POL	RTQDFWEV	272	8	55	86	6777
POL	DAYESVPL	302	8	55	86	6778
POL	TTNQKTEL	664	8	55	86	6779
POL	ISPIETVPV	188	9	56	88	6780
POL	LTEERIKAL	213	9	56	88	6781
POL	VTVLVDGDAY	295	10	56	88	6782
POL	KIATVQMAVFI	925	10	56	88	6783
POL	VTVLVDGDAYF	295	11	56	88	6784

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PAETGOETAYF	842	11	56	88	6785
POL	LAENREIL	492	8	57	89	6786
POL	NTPLVLKL	610	8	57	89	6787
POL	CSPGIWOL	808	8	57	89	6788
POL	KTAVQNAV	925	8	57	89	6789
POL	NTPLVLKLW	610	9	57	89	6790
POL	ETGOETAYF	844	9	57	89	6791
POL	KTAVQMAVF	925	9	57	89	6792
POL	NTPLVLKLWY	610	10	57	89	6793
POL	FAKKKIDSTKW	250	11	57	89	6794
POL	QAEILKTAVQM	920	11	57	89	6795
POL	STKWRKLVDF	257	10	58	91	6796
POL	VIDSQYALGI	688	10	58	91	6797
POL	PAETGOETAY	842	10	58	91	6798
POL	DSTKWRKLVDF	256	11	58	91	6799
POL	VIDSQYALGII	688	11	58	91	6800
POL	DSTKWRKL	256	8	59	92	6801
POL	STKWRKLV	257	8	59	92	6802
POL	VIDSQYAL	688	8	59	92	6803
POL	DSQYALGI	690	8	59	92	6804
POL	ETGOETAY	844	8	59	92	6805
POL	DSTKWRKLV	256	9	59	92	6806
POL	DSQYALGII	690	9	59	92	6807
POL	VAVIVASGY	827	9	59	92	6808
POL	QAEILKTAV	920	9	59	92	6809
POL	TAVQMAVFI	926	9	59	92	6810
POL	MAVFIINF	930	8	60	94	6811
POL	CTLNFIPII	182	10	60	94	6812
POL	TAVQMAVF	928	8	61	95	6813
POL	DTGADDTVL	112	9	61	95	6814
POL	WTVNDIQKLV	441	10	61	95	6815
POL	WTVNDIQKL	441	9	62	97	6816
POL	DTGADDTV	112	8	63	98	6817
REV	RAIQRQIISI	50	10	10	16	6818
REV	GYOQVGSQI	97	10	11	18	6819
REV	RSAPVPVL	70	8	12	19	6820
REV	SAEPVPLQL	71	9	12	19	6821
REV	RSAPVPLQL	70	10	12	19	6822
REV	RSQDSDELL	4	10	16	25	6823
REV	QARKNRRRW	40	10	16	25	6824
REV	RSQDSDEEL	4	9	17	27	6825
REV	GTSGTQGV	94	8	21	33	6826
REV	PAEPVPLQL	71	9	21	33	6827
REV	QARRNRRRW	40	10	38	59	6828
TAT	PTGPKESKKV	88	11	12	19	6829
VIF	KSLVKYIM	22	8	10	16	6830
VIF	FSDSAIRKAI	120	10	10	16	6831
VIF	YSTQIDFDL	99	9	11	17	6832
VIF	YSTQVDI'GL	99	9	11	17	6833
VIF	STQVDI'GL	100	8	11	17	6834

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	KSLVKIHHIYI	22	10	11	17	6835
VIF	VSIEWRLRRY	88	10	11	17	6836
VIF	FSFAIRKAIL	120	11	11	17	6837
VIF	GSLOYLALKAL	148	11	11	17	6838
VIF	STQIDPIL	100	8	12	19	6839
VIF	ESAIRNAI	122	8	12	19	6840
VIF	SAIRNAIL	123	8	12	19	6841
VIF	QIGERDWIIL	75	9	12	19	6842
VIF	FSAIRNAIL	122	9	12	19	6843
VIF	KTKPLPSV	164	9	12	19	6844
VIF	FSFAIRKAI	120	10	12	19	6845
VIF	FSFAIRNAI	120	10	12	19	6846
VIF	GSLOYLALAAL	148	11	12	19	6847
VIF	LADQLHHIY	107	10	13	20	6848
VIF	ESRIHKVSSEV	45	11	13	20	6849
VIF	LADQLHHIYF	107	11	13	20	6850
VIF	PSVKKLTEDRW	173	11	13	20	6851
VIF	NSLVKHHIYV	22	10	14	22	6852
VIF	LADQLHHIYY	107	10	14	22	6853
VIF	RTWKSLSVKHHUM	19	11	14	22	6854
VIF	LADQLHHIYF	107	11	14	22	6855
VIF	LADQLHHIY	107	9	15	23	6856
VIF	LADQLHHIY	107	11	15	23	6857
VIF	KTKGIIRGSITM	188	11	15	23	6858
VIF	ESAIRKAIL	122	9	16	25	6859
VIF	LADQLHHI	107	8	17	27	6860
VIF	ESAIRKAI	122	8	17	27	6861
VIF	KSLVKHHUM	22	8	18	28	6862
VIF	KSLVKHHUMY	72	9	18	28	6863
VIF	DSAIRKAI	122	9	19	30	6864
VIF	HYGERDWIIL	75	8	20	31	6865
VIF	NSLVKHHUMY	22	9	21	33	6866
VIF	RTWNSLSVKHHUM	19	11	24	38	6867
VIF	LADQLHHI	107	8	25	39	6868
VIF	NSLVKHHUM	22	8	27	42	6869
VIF	ISSEVHHPL	51	9	27	42	6870
VIF	VSSEVHHPL	51	9	27	42	6871
VIF	GSLOYLALAL	148	11	31	48	6872
VIF	SAIRKAIL	123	8	35	55	6873
VIF	QAGINKVGS	141	10	38	59	6874
VIF	SSEVHHPL	52	8	38	59	6875
VIF	GSLOYLAL	148	8	55	86	6876
VIF	WALELLEEL	18	9	58	91	6877
VPR	ETYGDTWTGV	48	10	09	15	6878
VPR	EAVRIHFRI	29	9	11	17	6879
VPR	EAVRIHFRIW	29	10	14	22	6880
VPR	EAVRIHFRIWL	29	11	14	22	6881
VPR	KSEAVRIIF	27	8	15	23	6882
VPR	WAGVEAIIRI	54	10	15	23	6883
VPR						6884

Table XIII
IIIY B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	WAGVEAIRIL	54	11	15	23	6885
VPR	WAGVEAI	54	8	16	23	6886
VPR	DTWAGVEAI	52	9	16	23	6887
VPR	ETYGDTWAGV	48	10	16	23	6888
VPR	NTYGDTWAGV	48	10	16	23	6889
VPR	DTWAGVEAI	52	10	16	23	6890
VPR	DTWEGVEAI	52	10	19	30	6891
VPR	DTWEGVEAI	52	9	20	31	6892
VPR	EAIRILQQL	58	10	33	52	6893
VPR	EAIRILQQL	58	11	33	52	6894
VPR	EAVRIHFPFW	29	10	34	53	6895
VPR	EAVRIHFPFW	29	11	34	53	6896
VPR	WLELLEEL	14	9	42	69	6897
VPU	LAKVDYRI	5	8	01	25	6898
VPU	LAKVDYRL	5	8	01	25	6899
VPU	LAKVDYRIV	5	9	01	25	6900
VPU	LAKVDYRIV	5	10	01	25	6901
VPU	LAKVDYRLGV	5	10	01	25	6902
VPU	LAKVDYRIV	5	11	01	25	6903
VPU	VTLLSSKL	94	9	01	50	6904
VPU	LAIVALVV	13	8	12	20	6905
VPU	WTIVFIEY	34	8	12	19	6906
VPU	ESGQDEEL	75	9	13	20	6907
VPU	ESGQDEEL	75	9	13	20	6908
VPU	IAIVVWTIV	28	9	20	31	6909
VPU	IAIVVWTI	28	8	23	36	6910

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHD ID NO.
ENV	GIGPGQTF	360	8	01	33	6911
ENV	SIGSQAF	360	8	01	33	6912
ENV	KLRIKQF	405	8	01	25	6913
ENV	EPDRMERI	823	8	01	33	6914
ENV	PPDRPEGI	823	8	01	33	6915
ENV	GIGPGQTF	360	9	01	33	6916
ENV	SIGSQAFY	360	9	01	33	6917
ENV	SIGSQAFYV	360	10	01	33	6918
ENV	QLYATVY	34	8	01	50	6919
ENV	QLYATVYAGV	34	10	01	50	6920
ENV	QLYATVYSGV	34	11	01	50	6921
ENV	TIGAMFLGF	599	9	03	27	6922
ENV	MLGAMFLGF	599	9	04	36	6923
ENV	SLRGLOHGW	889	9	05	18	6924
ENV	RLGWEGKLYLW	894	11	07	23	6925
ENV	RLGWEGKLY	894	9	09	29	6926
ENV	GLRLQWEGKLY	892	11	09	29	6927
ENV	LILGLVII	21	8	09	15	6928
ENV	IPRRIRQGF	950	9	10	16	6929
ENV	ALFYKLIV	202	8	10	16	6930
ENV	IMLQLTW	630	8	10	16	6931
ENV	DTNWLWY	769	8	10	16	6932
ENV	DIRQAICNV	380	9	10	16	6933
ENV	LPCRKQIV	485	9	10	16	6934
ENV	MLQLVWGH	651	9	10	16	6935
ENV	DTNWLWYI	769	9	10	16	6936
ENV	SOELKNSAV	911	9	10	16	6937
ENV	PIIYCTPAGF	260	10	10	16	6938
ENV	TLPCRKQIV	484	10	10	16	6939
ENV	PIIYCTPAGF	259	11	10	16	6940
ENV	RYGOAMYAPPI	498	11	10	16	6941
ENV	WMEWERIDNY	723	11	10	16	6942
ENV	ALDKWASLWNW	757	11	10	16	6943
ENV	SLKGLRLGW	889	9	11	39	6944
ENV	GIGAVFLGF	598	9	11	18	6945
ENV	KLWVTYY	44	8	11	17	6946
ENV	AVGIGAVE	595	8	11	17	6947
ENV	KLWVTYYGV	44	8	11	17	6948
ENV	AVGIGAVFLGF	595	10	11	17	6949
ENV	RIGPGQTF	357	11	11	17	6950
ENV	NITLPCR	482	8	11	17	6951
ENV	WORVGQAM	496	8	11	17	6952
ENV	QIRCSSNI	512	8	11	17	6953
ENV	ALFYRLDVV	202	9	11	17	6954
ENV	GPCTNVSTV	283	9	11	17	6955
ENV	RIGPGQTFY	357	9	11	17	6956
ENV	WQRYGQAMY	496	9	11	17	6957
ENV	GOIRCSSNI	511	9	11	17	6958
ENV	ALDKWASLW	757	9	11	17	6959
ENV	AVSLNATAI	918	10	11	17	6960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NITLPCRIKQI	482	11	11	17	6961
ENV	VVEREKIYVGI	588	11	11	17	6962
ENV	LLALDKWASLIW	735	11	11	17	6963
ENV	NNAWKNDIMV	107	8	12	19	6964
ENV	ALFYRLIV	202	8	12	19	6965
ENV	RIKQIVNM	488	8	12	19	6966
ENV	KLICITTV	687	8	12	19	6967
ENV	WMEWEREI	723	8	12	19	6968
ENV	ILKCNIDKKF	271	9	12	19	6969
ENV	RIKQIVNMW	488	9	12	19	6970
ENV	LICTTVPW	688	9	12	19	6971
ENV	GQELKNSAI	911	9	12	19	6972
ENV	AILIIPRI	946	9	12	19	6973
ENV	AILKCNIDKKF	270	10	12	19	6974
ENV	KLICITTVPW	687	10	12	19	6975
ENV	NMTWMEWEREI	720	11	12	19	6976
ENV	IVGGLIGLRH	783	11	12	19	6977
ENV	ELYKYKVVEI	560	10	13	21	6978
ENV	DPNIQEVV	91	8	13	20	6979
ENV	ILLKLTW	650	8	13	20	6980
ENV	NVPWNSSW	693	8	13	20	6981
ENV	EWDMNTW	716	8	13	20	6982
ENV	SIRLVNCF	842	8	13	20	6983
ENV	SIRLVSGF	842	8	13	20	6984
ENV	RLRIDLLI	867	8	13	20	6985
ENV	ILHIFRII	947	8	13	20	6986
ENV	EIKNCSFNI	181	9	13	20	6987
ENV	AIHQACTKV	244	9	13	20	6988
ENV	SLAEFVVI	311	9	13	20	6989
ENV	QQHILKLTIV	648	9	13	20	6990
ENV	LLKLTWGI	651	9	13	20	6991
ENV	AQHILKLTIV	647	10	13	20	6992
ENV	QQHILKLTIV	648	10	13	20	6993
ENV	ILKLTWGI	650	10	13	20	6994
ENV	EQELLEDKW	752	10	13	20	6995
ENV	VPTDPNIQEVV	88	11	13	20	6996
ENV	VMIISFNGGIEF	432	11	13	20	6997
ENV	NITLPCRIKQI	482	11	13	20	6998
ENV	AQHILKLTIV	647	11	13	20	6999
ENV	SLAEFVVI	311	8	14	22	7000
ENV	NITLPCRI	482	8	14	22	7001
ENV	SLLNATAI	920	8	14	22	7002
ENV	DPEIVMISF	428	9	14	22	7003
ENV	GQAMYAPPI	501	9	14	22	7004
ENV	RIIFAVLSI	791	9	14	22	7005
ENV	AVAEQTDIV	928	9	14	22	7006
ENV	EQDLALDKW	752	10	14	22	7007
ENV	RIIFAVLSIV	791	10	14	22	7008
ENV	SLLNATAIV	920	10	14	22	7009
ENV	AVAEQTDIV	928	10	14	22	7010

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	VITQACPKVSF	244	11	14	22	7011
ENV	GLRIEAVLSI	789	11	14	22	7012
ENV	AIATAEGTDRV	926	11	14	22	7013
ENV	RLNCNTSAI	236	10	15	24	7014
ENV	GLIGLRRI	786	8	15	23	7015
ENV	IFFAVLSI	792	8	15	23	7016
ENV	GPRPEGI	822	8	15	23	7017
ENV	LINCNTSAI	237	9	15	23	7018
ENV	VITQACPKV	244	9	15	23	7019
ENV	GPCKNVSTV	283	9	15	23	7020
ENV	DIRQAHCNI	380	9	15	23	7021
ENV	GLIGLRIF	786	9	15	23	7022
ENV	IFFAVLSI	792	9	15	23	7023
ENV	LLNATAIAV	921	9	15	23	7024
ENV	SVITQACPKV	243	10	15	23	7025
ENV	TLPCRIKQII	484	10	15	23	7026
ENV	NMWQEVGKAM	494	10	15	23	7027
ENV	AVAEGTDRII	928	10	15	23	7028
ENV	NMWQEVGKAMY	494	11	15	23	7029
ENV	GLIGLRIFAV	786	11	15	23	7030
ENV	LIGLRIF	787	8	16	25	7031
ENV	VVQREKRAV	588	9	16	25	7032
ENV	AVAEGTDRI	928	9	16	25	7033
ENV	RVVQREKRAV	587	10	16	25	7034
ENV	LIGLRIFAV	787	10	16	25	7035
ENV	LVSGFLALAW	845	10	16	25	7036
ENV	DLRNLCLFSY	836	10	16	25	7037
ENV	LLNGSLAEVEV	307	11	16	25	7038
ENV	ELDKWASLWNW	757	11	16	25	7039
ENV	RLVSGFLALAW	844	11	16	25	7040
ENV	AIATAEGTDRI	926	11	16	25	7041
ENV	VQREKRAV	589	8	17	27	7042
ENV	IINMWQEV	492	8	17	27	7043
ENV	KLICTINV	687	8	17	27	7044
ENV	SLWNWFDI	763	8	17	27	7045
ENV	DLRNLCLF	856	8	17	27	7046
ENV	QIINMWQEV	491	9	17	27	7047
ENV	LICTINVPW	688	9	17	27	7048
ENV	RPNNTRKSI	347	10	17	27	7049
ENV	KQIINMWQEV	490	10	17	27	7050
ENV	EIRPGGQDM	544	10	17	27	7051
ENV	KLICTINVPW	687	10	17	27	7052
ENV	RIVFAVLSI	791	10	17	27	7053
ENV	GVAPTAKRRV	573	11	17	27	7054
ENV	WQEVGKAM	496	8	18	28	7055
ENV	GLRIEAV	789	8	18	28	7056
ENV	WQEVGKAMY	496	9	18	28	7057
ENV	ELDKWASLW	757	9	18	28	7058
ENV	IVFAVLSI	792	9	18	28	7059
ENV	YLRDQQLGI	672	10	18	28	7060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	LPCKRIQIIM	485	11	18	28	7061
ENV	EVGKAMYAPPI	498	11	18	28	7062
ENV	YLRDQQLGHW	672	11	18	28	7063
ENV	LEFLDKWASLW	755	11	18	28	7064
ENV	CLFSYIIRLDF	861	11	18	28	7065
ENV	KLICITAV	687	8	19	30	7066
ENV	LICTTAVPW	688	9	19	30	7067
ENV	RIVEAVLSI	791	9	19	30	7068
ENV	KLICITAVPW	687	10	19	30	7069
ENV	GLRIVFAVLSI	789	11	19	30	7070
ENV	ELLELDKW	754	8	20	31	7071
ENV	IVFAVLSI	792	8	20	31	7072
ENV	LPCKRIKQII	485	9	20	31	7073
ENV	NMVEQMIHEDI	112	10	20	31	7074
ENV	NMVEQMIHEDI	112	11	20	31	7075
ENV	DLALADKW	754	8	21	33	7076
ENV	DELETTISF	428	9	21	33	7077
ENV	VPTDPNPQEV	88	10	21	33	7078
ENV	LIGLRIVEAV	787	10	21	33	7079
ENV	CVPTDPNPQEV	87	11	21	33	7080
ENV	GLIGLRIVEAV	786	11	21	33	7081
ENV	APTAKRRV	575	9	22	34	7082
ENV	IVELLGRGW	879	10	22	34	7083
ENV	PWKEATITLF	54	11	22	34	7084
ENV	EQMIHEDISLW	115	11	22	34	7085
ENV	TVQCTHIGIRPV	290	11	22	34	7086
ENV	RIVELLGRGW	878	11	22	34	7087
ENV	ELLGRGW	881	8	23	34	7088
ENV	MVEQMIHEDI	113	9	23	37	7089
ENV	VVKIEPLGV	566	9	23	36	7090
ENV	MVEQMIHEDI	113	10	23	36	7091
ENV	KVKIEPLGV	565	10	23	36	7092
ENV	EQMIHEDI	115	8	24	38	7093
ENV	VVEREKRAV	588	9	25	39	7094
ENV	VPTDPNPQEI	88	10	25	39	7095
ENV	VQCTHIGIRPV	292	10	25	39	7096
ENV	RVEREKRAV	587	10	25	39	7097
ENV	QQNNLLRAI	636	10	25	39	7098
ENV	CVPTDPNPQEI	87	11	25	39	7099
ENV	VQCTHIGIRPV	292	11	25	39	7100
ENV	VQQNNLLRAI	635	11	25	39	7101
ENV	TLCKRIKQI	484	9	26	41	7102
ENV	QQNNLLRAI	637	9	26	41	7103
ENV	QQSNLLRAI	637	9	26	41	7104
ENV	QQSNLLRAI	636	10	26	41	7105
ENV	IPILIYCAPAGE	259	11	26	41	7106
ENV	VQQSNLLRAI	635	11	26	41	7107
ENV	MIYIYCAPAGE	260	10	27	42	7108
ENV	YLRDQQLLGI	672	10	27	42	7109
ENV						7110

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	YLKDDQLLGW	672	11	27	42	7111
ENV	KVSFERMITY	232	11	28	44	7112
ENV	TVQCTIGIKPV	290	11	28	44	7113
ENV	ELYKYKVVKI	560	10	29	46	7114
ENV	LIGLRIVF	787	8	29	45	7115
ENV	GLRIVFAV	789	8	29	45	7116
ENV	GLIGLRIVF	786	9	29	45	7117
ENV	QMIEDISLW	116	10	29	45	7118
ENV	RIKQINNM	488	8	30	47	7119
ENV	TOACPVSF	247	9	30	47	7120
ENV	CPKVSFEPI	250	9	30	47	7121
ENV	KVSFERPI	252	9	30	47	7122
ENV	RIKQINMW	488	9	30	47	7123
ENV	NMWKNNMVEQM	107	11	30	47	7124
ENV	CPKVSFEPI	250	11	30	47	7125
ENV	IVGGLIGLRIV	783	11	30	47	7126
ENV	LPCRUKOI	485	8	31	48	7127
ENV	AVLSVNRV	795	9	31	48	7128
ENV	VOCTIGIKPVV	292	11	31	48	7129
ENV	KIFMIVGGLI	778	11	31	48	7130
ENV	GLIGLRIV	786	8	32	50	7131
ENV	VOCTIGIKPV	292	10	32	50	7132
ENV	LOARVLAV	662	8	33	52	7133
ENV	RYLAVERY	665	8	33	52	7134
ENV	QLQARVLAV	661	9	33	52	7135
ENV	KQLQARVLAV	660	10	33	52	7136
ENV	LQARVLAVERY	662	11	33	52	7137
ENV	NLWVTYYGV	44	10	34	54	7138
ENV	NVTENFM	101	8	34	53	7139
ENV	NMWKNNMV	107	8	34	53	7140
ENV	IILLQLTVW	650	8	34	53	7141
ENV	NVTENFMW	101	9	34	53	7142
ENV	QQIILLQLTV	648	9	34	53	7143
ENV	LQLTVWGI	651	9	34	53	7144
ENV	AQIILLQLTV	647	10	34	53	7145
ENV	QQIILLQLTVW	648	10	34	53	7146
ENV	IILLQLTVWGI	650	10	34	53	7147
ENV	AQIILLQLTVW	647	11	34	53	7148
ENV	NLWVTYY	44	8	35	56	7149
ENV	IMIVGGLI	781	8	35	56	7150
ENV	FIMIVGGLI	780	9	35	55	7151
ENV	DLKSLCFY	856	10	35	55	7152
ENV	VQARQLLSGI	625	10	36	56	7153
ENV	SIVNRVQQY	798	10	36	56	7154
ENV	TMGAAITLTV	615	11	36	56	7155
ENV	TVQARQLLSGI	624	11	36	56	7156
ENV	VQARQLLSGIV	625	11	36	56	7157
ENV	MIVGGILGLRI	782	11	36	56	7158
ENV	DMRDNRSELY	552	11	37	58	7159
ENV	VLSIVNRV	796	8	38	59	7160

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
ENV	DLRLCLF	856	8	38	59	7161
ENV	IVNRVROGY	799	9	38	59	7162
ENV	RPOGDMRDNW	547	11	38	59	7163
ENV	YIKIFIMV	776	9	39	61	7164
ENV	GIKQLOARV	658	9	40	63	7165
ENV	TLFCASDAKAY	64	11	40	63	7166
ENV	IVGLIGLRI	783	10	42	66	7167
ENV	YIKIFIMI	776	8	43	67	7168
ENV	WLWYIKIFIM	773	10	43	67	7169
ENV	WLWYIKIFIMI	773	11	43	67	7170
ENV	LQLTWVGI	652	8	44	69	7171
ENV	SLWDQSLKPCV	123	11	47	75	7172
ENV	RVRQGSPLSF	802	11	47	75	7173
ENV	RQGYSPLSF	804	9	48	75	7174
ENV	GIWGCCKLI	680	10	48	75	7175
ENV	KQLLSGIV	628	8	49	77	7176
ENV	NVWATIACV	80	9	49	77	7177
ENV	WLWYIKIFI	773	9	49	77	7178
ENV	DQSLKPCV	126	8	50	78	7179
ENV	WLWYIKIF	773	8	50	78	7180
ENV	TVQCTHGI	290	8	51	80	7181
ENV	DQQLGIW	675	8	51	80	7182
ENV	NVSTVOCTHGI	287	11	51	80	7183
ENV	KICVKLTPLCV	130	11	54	84	7184
ENV	TVYYGVV	48	8	55	86	7185
ENV	TVYYGVVW	48	9	55	86	7186
ENV	CVKLTPLCV	132	9	55	86	7187
ENV	FLGAAGSTM	608	9	55	86	7188
ENV	WVTVYGVV	46	10	55	86	7189
ENV	WVTVYGVVW	46	11	56	89	7190
ENV	ELYKRVV	360	8	58	91	7191
ENV	WVTVYGVV	46	8	58	91	7192
GAG	PPPIESRF	510	8	01	33	7193
GAG	EMDKELY	537	9	01	33	7194
GAG	APPPIESRF	509	9	01	25	7195
GAG	KQETIDKELY	535	10	01	25	7196
GAG	EPLTALRSLF	547	10	01	25	7197
GAG	PPLASLSLF	547	10	01	33	7198
GAG	PPLISLSLF	547	10	01	33	7199
GAG	EPTAPPESF	506	10	01	33	7200
GAG	EPTAPPESF	506	10	01	33	7201
GAG	PPAESRF	510	10	01	50	7202
GAG	APPPIESRF	509	9	02	67	7203
GAG	PPLASLSLF	546	10	04	24	7204
GAG	YPLASLSLF	545	10	07	15	7205
GAG	YPLASLSLF	545	10	08	17	7206
GAG	NIMMQRCNF	407	9	10	17	7207
GAG	TIQKQKEFI	527	9	10	17	7208
GAG	NPIPIVVDI	277	9	10	16	7209
						7210

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	NPIPVGDIY	277	10	10	16	7211
GAG	QGNWMTSNPI	267	11	10	16	7212
GAG	KLDKWEKI	12	8	10	16	7213
GAG	GPVAPGQM	242	8	10	16	7214
GAG	PIPVGDI	278	8	10	16	7215
GAG	PIAESFGF	498	8	10	16	7216
GAG	PIPVGDIY	278	9	10	16	7217
GAG	APPAESFGF	497	9	10	16	7218
GAG	ALSPRTLNAW	167	10	10	16	7219
GAG	ALSPRTLNAWV	167	11	10	16	7220
GAG	IPVGDYKRWI	280	11	10	16	7221
GAG	VQNAFDCKSI	347	11	10	16	7222
GAG	PIPVGDIY	279	8	11	17	7223
GAG	SQEVKNWMI	314	8	11	17	7224
GAG	IMMOKSNF	408	8	11	17	7225
GAG	PQDLNMLNI	202	10	11	17	7226
GAG	IPVGDYKRW	280	10	11	17	7227
GAG	EQASQEVKNV	311	10	11	17	7228
GAG	TPQDLNMLNI	201	11	11	17	7229
GAG	PQDLNMLNIV	202	11	11	17	7230
GAG	IVGGIIQAAMQM	211	11	11	17	7231
GAG	TLRAEQATQDV	327	11	11	17	7232
GAG	EQASQEVKNVM	311	11	11	17	7233
GAG	WPSSKGRIGNF	474	11	11	17	7234
GAG	EPIDKELY	533	8	12	19	7235
GAG	KQEPIDKELY	531	10	12	19	7236
GAG	TPQDLNMM	201	8	12	19	7237
GAG	DLNMLNI	204	8	12	19	7238
GAG	TLQEQIAW	263	8	12	19	7239
GAG	TYCVIHKI	86	9	12	19	7240
GAG	DLNMLNIV	204	9	12	19	7241
GAG	IVGGIIQAAM	211	9	12	19	7242
GAG	TLQEQIAWM	263	9	12	19	7243
GAG	PLTSLKSLF	548	9	12	19	7244
GAG	PLTSLKSLF	548	9	12	19	7245
GAG	NIVGGIIQAAM	210	10	12	19	7246
GAG	TLRAEQASQEV	327	11	12	19	7247
GAG	TIMMQRGNF	407	9	13	22	7248
GAG	SPTSILDI	302	8	13	20	7249
GAG	RMYSPTSILDI	299	11	13	20	7250
GAG	LQEQIAWM	264	8	14	22	7251
GAG	RMYSPTSI	299	8	14	22	7252
GAG	VQNAQQQMV	156	9	14	22	7253
GAG	IVQNAQQQMV	155	10	14	22	7254
GAG	RVIPVILAGPI	235	10	14	22	7255
GAG	IVRMYSPTSI	297	10	14	22	7256
GAG	PIVQNAQQQMV	154	11	14	22	7257
GAG	KIVRMYSPTSI	296	11	14	22	7258
GAG	WISNKGRIQNF	474	11	14	22	7259
GAG	KVSQNYPI	148	8	15	27	7260

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
GAG	KVSQNYPIV	148	9	15	27	7261
GAG	TQDVKNWM	334	8	15	23	7262
GAG	PPEESPIF	498	8	15	23	7263
GAG	ELASLYNTV	76	9	15	23	7264
GAG	TLVCYIQR	86	9	15	23	7265
GAG	APPEESRF	497	9	15	23	7266
GAG	PLASLKSIF	548	9	15	23	7267
GAG	VLSGKLDIAW	7	10	15	23	7268
GAG	SLFNIVATLY	79	10	15	23	7269
GAG	LQGMVIGAI	159	10	15	23	7270
GAG	EQATQDVKNW	331	10	15	23	7271
GAG	EPTAPPEEF	494	10	15	23	7272
GAG	SVLSGKLDIAW	6	11	15	23	7273
GAG	NLQGMVIGAI	158	11	15	23	7274
GAG	EQATQDVKNWM	331	11	15	23	7275
GAG	WMTSNPII	270	8	16	25	7276
GAG	GPAATLEEM	362	9	16	25	7277
GAG	WMTSNPIIV	270	10	16	25	7278
GAG	GPAATLEEM	362	10	16	25	7279
GAG	LLETSICROI	52	11	16	25	7280
GAG	ALGPAATLEEM	360	11	16	25	7281
GAG	GPIIPGQM	242	11	17	27	7282
GAG	DIYKRRII	284	8	17	27	7283
GAG	PVGDIYKRWI	281	10	17	27	7284
GAG	PVGDIYKRWI	281	11	17	27	7285
GAG	ALGPGATLEEM	360	11	17	27	7286
GAG	QIGWMTNPII	267	11	18	29	7287
GAG	KLDWKEI	12	8	18	28	7288
GAG	TQEVKNWM	334	8	18	28	7289
GAG	PVGDIYKRW	281	9	18	28	7290
GAG	GPGATLEEM	362	9	18	28	7291
GAG	EQATQEVKNW	331	10	18	28	7292
GAG	GPGATLEEM	362	10	18	28	7293
GAG	EQATQEVKNWM	331	11	18	28	7294
GAG	GPIIPGQM	242	8	19	30	7295
GAG	GPIIPGQM	379	8	19	30	7296
GAG	DIKQPKPEF	308	10	19	30	7297
GAG	IVWASRELERF	35	11	19	30	7298
GAG	GVGTSIIKARV	376	11	19	30	7299
GAG	WMTNPII	270	8	20	31	7300
GAG	WMTNPIIIV	270	10	20	31	7301
GAG	EPTAPPEEF	494	10	20	31	7302
GAG	YPIVQNAQGM	153	11	21	31	7303
GAG	VIEKAFSPEV	179	11	21	31	7304
GAG	VQNAQGM	156	8	21	33	7305
GAG	KQPKPEF	310	8	21	33	7306
GAG	IVQNAQGM	155	9	21	33	7307
GAG	PIVQNAQGM	154	10	21	33	7308
GAG	KQPKPEFRDY	310	11	21	33	7309
GAG	SQVSQNYPI	146	9	22	44	7310

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	SOVSONYPIV	146	10	22	44	7311
GAG	WMTDTLLV	340	8	22	34	7312
GAG	SLYNTVATLY	79	10	22	34	7313
GAG	RLIIPVHAGPI	235	10	22	34	7314
GAG	WPSIIGRPGNF	474	11	23	36	7315
GAG	KVIEEKAF	178	8	24	38	7316
GAG	WVKVIEKAF	176	10	24	38	7317
GAG	TLRAEQATQEV	327	11	24	38	7318
GAG	LVWASKELERF	35	11	25	39	7319
GAG	MQMLKETI	219	8	26	41	7320
GAG	AMQMLKETI	218	9	26	41	7321
GAG	QVSONYPI	148	8	27	48	7322
GAG	QVSONYPIV	148	9	27	48	7323
GAG	TLQEQIGW	263	8	27	42	7324
GAG	IMMQRGNF	408	8	27	42	7325
GAG	TLQEQIGWM	263	9	27	42	7326
GAG	GMVHIOAI	161	8	28	44	7327
GAG	KVIEEKAF	178	8	28	44	7328
GAG	WVKVIEKAF	176	10	28	44	7329
GAG	VVEEKAFPEV	179	11	28	44	7330
GAG	EPERDYVDIRFY	315	11	28	44	7331
GAG	VQNLOGQM	156	8	29	45	7332
GAG	LOEQIGWM	264	8	29	45	7333
GAG	IVQNLOGQM	155	9	29	45	7334
GAG	VQNLOGQM	156	9	29	45	7335
GAG	PIVQNLOGQM	154	10	29	45	7336
GAG	IVQNLOGQM	155	10	29	45	7337
GAG	AIPTLTNAW	167	10	29	45	7338
GAG	YIIVQNLOGQM	153	11	29	45	7339
GAG	PIVQNLOGQM	154	11	29	45	7340
GAG	AIPTLTNAWV	167	11	30	45	7341
GAG	TLNAWVKVI	172	9	30	47	7342
GAG	TLNAWVKV	172	9	31	48	7343
GAG	MQMLKDTI	219	8	31	52	7344
GAG	AMQMLKDTI	218	9	31	52	7345
GAG	VLAEMASQV	386	9	33	52	7346
GAG	NPIPVGEI	277	9	33	52	7347
GAG	NPIPVGEI	277	10	34	54	7348
GAG	RLRPGGKKY	20	10	34	54	7349
GAG	IPVGEIYKRW	280	10	34	53	7350
GAG	IPVGEIYKRW	279	11	34	53	7351
GAG	IPVGEIYKRWI	280	11	34	53	7352
GAG	RPGGKKY	22	8	35	55	7353
GAG	PIPVGEI	278	8	35	55	7354
GAG	PIPVGEI	279	8	35	55	7355
GAG	PIPVGEI	278	9	35	55	7356
GAG	EPERDYVDRFF	315	11	35	55	7357
GAG	GIPIHARV	379	11	35	55	7358
GAG	GVGGPIHARV	376	11	36	56	7359
GAG						7360

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	WMETLLV	340	8	37	58	7361
GAG	IIPVHAGPI	237	8	38	59	7362
GAG	RMYSVPVSLDI	299	11	38	59	7363
GAG	EYKRWII	284	8	39	61	7364
GAG	PVGEIYKRWII	281	11	39	61	7365
GAG	KIVRMYSVPVSI	296	11	39	61	7366
GAG	RMYSVPVSI	299	8	40	63	7367
GAG	SPVSILDI	302	8	40	63	7368
GAG	PVGEIYKRW	281	9	40	63	7369
GAG	PVGEIYKRWI	281	10	40	63	7370
GAG	IIVRMYSVPVSI	297	10	40	63	7371
GAG	TVATLYCV	83	8	41	64	7372
GAG	KIVRMYSVP	296	9	41	64	7373
GAG	DIRQGPKEPF	308	10	41	64	7374
GAG	PQDLNTMLNTV	202	11	41	64	7375
GAG	THQDLNTM	201	8	42	66	7376
GAG	IIVRMYSVP	297	8	42	66	7377
GAG	ROGPKEPF	310	8	42	66	7378
GAG	DLNTMLNTV	204	9	42	66	7379
GAG	ROGPKEPF	310	11	42	66	7380
GAG	QMRPEPGSDI	248	10	44	69	7381
GAG	QMRPEPGSDI	247	11	44	69	7382
GAG	VQNANPDCSTI	347	11	45	70	7383
GAG	TVGGIIQAAM	211	9	47	73	7384
GAG	TVGGIIQAAMQ	211	11	47	73	7385
GAG	TINEAAEW	225	9	53	83	7386
GAG	SPNEVIMF	186	8	53	86	7387
GAG	APRKKGCV	440	8	55	86	7388
GAG	SPRTLNAWVKV	169	11	55	86	7389
GAG	RQANFLGKI	465	9	56	88	7390
GAG	RQANFLGIW	465	10	56	88	7391
GAG	ILGLNKIVRM	290	11	56	88	7392
GAG	SPRTLNAW	169	8	56	88	7393
GAG	ILGLNKI	290	8	57	89	7394
GAG	SPRTLNAWV	169	9	57	89	7395
GAG	WIHLGLNKI	289	9	57	89	7396
GAG	ILGLNKIV	290	9	57	89	7397
GAG	WIHLGLNKIV	289	10	57	89	7398
GAG	ILGLNKIVRM	291	10	57	89	7399
GAG	ILGLNKIVRMV	291	11	57	89	7400
GAG	ILGLNKIV	291	8	58	91	7401
GAG	EMMTACQGV	369	9	59	92	7402
GAG	GLNKIVRM	293	8	60	94	7403
GAG	MMITACQGV	370	8	60	94	7404
GAG	GLNKIVRMV	293	9	60	94	7405
GAG	TLNAWVKV	172	8	61	95	7406
GAG	GPKEPRDY	312	9	63	98	7407
GAG	GPKEPRDYV	312	10	63	98	7408
GAG	EPFRDYVDRF	315	10	63	98	7409
NEF	APTAAKGV	34	8	01	33	7410

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	APTAAGVGAV	34	11	01	33	7411
NEF	KQAEPAAGV	32	10	01	17	7412
NEF	ROAPTAAGV	32	10	01	17	7413
NEF	AQAEPAAGV	33	10	01	17	7414
NEF	EPAAAGVGAV	40	10	04	15	7415
NEF	VPLRPMTF	101	8	10	16	7416
NEF	IIPICQIGM	259	8	10	16	7417
NEF	QVPLRPMTF	100	9	10	16	7418
NEF	POVPLRPMTF	99	10	10	16	7419
NEF	LLIPIQIGM	357	10	10	16	7420
NEF	IIMARELIPEY	320	10	10	16	7421
NEF	RPQVPLRPMTF	98	11	10	16	7422
NEF	CLLIIPMSQIGM	256	11	10	16	7423
NEF	IIMARELIPEY	320	11	10	16	7424
NEF	WQNYTPGCV	204	10	11	17	7425
NEF	VPIVPIREV	230	8	11	17	7426
NEF	LVPVPIREV	229	9	11	17	7427
NEF	KLPVPIREV	228	10	11	17	7428
NEF	PMTYKGAF	105	8	12	19	7429
NEF	IIPMSQIGM	259	8	12	19	7430
NEF	RPMTYKGAF	104	9	12	19	7431
NEF	LLIIPMSQIGM	257	10	12	19	7432
NEF	PLKPMYKGAF	102	11	12	19	7433
NEF	SQKRQDILDW	177	11	12	19	7434
NEF	WVYIITQGF	191	8	13	20	7435
NEF	TPGPGTRF	208	8	13	20	7436
NEF	GIRYPLTF	213	8	13	20	7437
NEF	WVYIITQGF	191	9	13	20	7438
NEF	DLWVYIITQGF	188	10	13	20	7439
NEF	GPTRPLTF	210	10	13	20	7440
NEF	GIRYPLTFGW	213	10	13	20	7441
NEF	DLWVYIITQGF	188	11	13	20	7442
NEF	DLKIKGAI	57	8	14	22	7443
NEF	WLEAQEEEEV	79	10	15	24	7444
NEF	AQEEEEVG	83	9	17	27	7445
NEF	AQEEEEVGFPV	83	11	17	27	7446
NEF	TPGPGIRY	208	8	17	27	7447
NEF	FPLTFGWCF	217	9	17	27	7448
NEF	TQOFFPDWQNY	195	11	17	27	7449
NEF	WQNYTPGPI	204	10	18	29	7450
NEF	LIYSKKRQEI	174	10	18	29	7451
NEF	GLYSKKRQEI	173	11	18	28	7452
NEF	DILDWVY	185	8	20	31	7453
NEF	RQDILDWV	182	9	20	31	7454
NEF	RQDILDWVY	182	10	20	31	7455
NEF	WVYIITQGY	191	8	21	33	7456
NEF	WVYIITQGY	191	9	21	33	7457
NEF	DLWVYIITQGY	188	10	21	33	7458
NEF	DLWVYIITQGY	188	11	21	33	7459
NEF	DLWVYIITQGY			21	33	7460

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	TQGFDPW	195	8	22	34	7461
NEF	YPLTFGWCF	217	9	24	38	7462
NEF	RODILDLW	182	8	25	39	7463
NEF	RQERDLWVY	182	10	32	50	7464
NEF	EILDWVY	185	8	33	52	7465
NEF	RQERDLWV	182	9	35	55	7466
NEF	PLTFGWCF	219	11	35	55	7467
NEF	RQGVFLRPMTY	98	11	36	56	7468
NEF	TQGVFLRPMTY	195	11	36	56	7469
NEF	RQERDLW	182	8	37	58	7470
NEF	TQGVFLRPW	195	8	37	58	7471
NEF	EVGFVPRQV	91	10	40	63	7472
NEF	PLTFGWCF	219	8	43	67	7473
NEF	POVPLRPMTY	99	10	45	70	7474
NEF	VPLRPMTY	101	8	46	73	7475
NEF	QVPLRPMTY	100	9	46	72	7476
NEF	RQVPLRPMTY	98	9	47	73	7477
NEF	PVPLRPMTY	95	11	47	73	7478
NEF	POVPLRPMTY	99	8	56	88	7479
POL	SPTSRELOV	35	9	01	33	7480
POL	ALSLSLQI	80	9	01	33	7481
POL	SPTSRELOV	38	9	01	33	7482
POL	OPERALS	70	8	01	20	7483
POL	VPTFNFPQI	79	9	01	17	7484
POL	EPGEDRELSV	69	10	01	17	7485
POL	GROGTVSLSF	69	11	01	17	7486
POL	PQGEAREF	9	8	10	16	7487
POL	PQGEAREF	8	9	10	16	7488
POL	LIEICGHKAI	150	10	10	16	7489
POL	AVQKIATESI	563	10	10	16	7490
POL	MLTQLGCTLNF	176	11	10	16	7491
POL	AVQKIATESI	563	11	10	16	7492
POL	AVKACVWAGI	877	11	10	16	7493
POL	IQTKELQKQII	960	11	10	16	7494
POL	RIGFNIV	238	8	11	17	7495
POL	YQLETEPI	619	8	11	17	7496
POL	AQEDIEKY	760	8	11	17	7497
POL	GIQDEFGL	886	8	11	17	7498
POL	KVPRRKV	1011	8	11	17	7499
POL	VPRRKVKI	1013	8	11	17	7500
POL	VPRRKVKI	1012	9	11	17	7501
POL	VPRRKVKII	1013	9	11	17	7502
POL	IKDYGKQM	1020	9	11	17	7503
POL	GIQDEFGL	886	10	11	17	7504
POL	KVPRRKVKI	1011	10	11	17	7505
POL	VPRRKVKII	1012	10	11	17	7506
POL	KIKDYGKQM	1019	10	11	17	7507
POL	KISRIGFNIV	235	11	11	17	7508
POL	IPSTNNETPGI	321	11	11	17	7509
POL	KLWYQLETEPI	616	11	11	17	7510

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KVPRRKVKII	1011	11	11	17	7511
POL	KQIKQNF	967	9	12	19	7512
POL	IKIQNFV	969	9	12	19	7513
POL	IKIQNFVY	969	10	12	19	7514
POL	IKIQNFVY	967	11	12	19	7515
POL	IKIQNFVYY	969	11	12	19	7516
POL	RPLVTVKI	95	8	12	19	7517
POL	EINLPKW	122	8	12	19	7518
POL	QIKQNF	968	8	12	19	7519
POL	VIQDSEI	1003	8	12	19	7520
POL	RQILLRWGF	395	9	12	19	7521
POL	NQKTELIAT	666	9	12	19	7522
POL	IDIASDI	952	9	12	19	7523
POL	IVDIATDI	952	9	12	19	7524
POL	VVIQDSEI	1002	9	12	19	7525
POL	IQDNSEIKV	1004	9	12	19	7526
POL	WQRIPLTVKI	93	10	12	19	7527
POL	ROYDQPIEI	144	10	12	19	7528
POL	GODQWTYQIY	525	10	12	19	7529
POL	RMRGALTNDV	548	10	12	19	7530
POL	NQKTELAIV	666	10	12	19	7531
POL	RIDIASDI	951	10	12	19	7532
POL	RVIDIATDI	951	10	12	19	7533
POL	QIKIQNFV	968	10	12	19	7534
POL	AVVIQDSEI	1000	10	12	19	7535
POL	VIQDSEIKV	1003	10	12	19	7536
POL	IQDNSEIKV	1004	10	12	19	7537
POL	VLEEINLPKW	119	11	12	19	7538
POL	ELRQILLRWGF	393	11	12	19	7539
POL	IIPDKWTVQPIV	424	11	12	19	7540
POL	IQKQGQDQWTY	521	11	12	19	7541
POL	LQKQIKQNF	965	11	12	19	7542
POL	QIKIQNFV	968	11	12	19	7543
POL	VVIQDSEIKV	1002	11	12	19	7544
POL	VIQDSEIKV	1003	11	12	19	7545
POL	ELQKQIKI	964	9	13	21	7546
POL	NLKTGKYARM	540	10	13	21	7547
POL	DINLPKW	122	8	13	20	7548
POL	ROYDQPI	144	8	13	20	7549
POL	QLPEKDSW	434	8	13	20	7550
POL	VLPEKDSW	434	8	13	20	7551
POL	LQKQIKI	965	8	13	20	7552
POL	IQLEKDSW	433	9	13	20	7553
POL	IVLEKDSW	433	9	13	20	7554
POL	IQKQGQDQW	521	9	13	20	7555
POL	GQDQWTYQI	525	9	13	20	7556
POL	SPTRRELQVW	29	10	13	20	7557
POL	KVROYDQPI	142	10	13	20	7558
POL	LIEIGKKAI	150	10	13	20	7559
POL	PIQLPEKDSW	432	10	13	20	7560

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SFQ ID NO.
POL	PIVLPEKDSW	412	10	13	20	7561
POL	QLPEKDSWTV	434	10	13	20	7562
POL	VLPKDSWTV	434	10	13	20	7563
POL	EIQKQDQW	520	10	13	20	7564
POL	EQAEHLKTAV	919	10	13	20	7565
POL	VLEDINLPKW	119	11	13	20	7566
POL	ILIEKCKKAI	149	11	13	20	7567
POL	QIQLPEKDSW	431	11	13	20	7568
POL	QIVLPEKDSW	431	11	13	20	7569
POL	IQLPEKDSWTV	433	11	13	20	7570
POL	IVLPEKDSWTV	433	11	13	20	7571
POL	KQKQDQWTYQI	523	11	13	20	7572
POL	LIKKKRVYLSW	717	11	13	20	7573
POL	KLACGRWPVKTI	855	11	13	20	7574
POL	RPLVTIKI	95	8	14	22	7575
POL	KQNPDIIV	362	8	14	22	7576
POL	KIATIESIV	566	8	14	22	7577
POL	YOLEKIP	619	8	14	22	7578
POL	SPTRRELQV	29	9	14	22	7579
POL	KQNPDIIV	362	9	14	22	7580
POL	VOKIATESI	564	9	14	22	7581
POL	KIATIESIV	566	9	14	22	7582
POL	WORPLVTIKI	93	10	14	22	7583
POL	VOKIATESIV	564	10	14	22	7584
POL	KIATIESIV	566	10	14	22	7585
POL	TIITIDGNSNF	864	10	14	22	7586
POL	EPFRKQNPDIIV	358	11	14	22	7587
POL	KQNPDIIVQY	362	11	14	22	7588
POL	ELREIILLKWGF	393	11	14	22	7589
POL	VOKIATESIV	564	11	14	22	7590
POL	KLWYQLKEDPH	616	11	14	22	7591
POL	LVEICTEM	221	8	15	24	7592
POL	KIKALVEI	217	8	15	23	7593
POL	TOLGCTLNF	178	9	15	23	7594
POL	ALVEICTEM	220	9	15	23	7595
POL	ELRQILLRW	393	9	15	23	7596
POL	IQKQGGQW	521	9	15	23	7597
POL	KQKQDQWTY	523	9	15	23	7598
POL	IQKETWEAW	585	9	15	23	7599
POL	LVSAGIRKV	743	9	15	23	7600
POL	LPGRWPKMI	125	10	15	23	7601
POL	EIQKQGGQW	520	10	15	23	7602
POL	PIKETWEAW	584	10	15	23	7603
POL	IQKETWEAW	585	10	15	23	7604
POL	QVDKLVSAIGI	739	10	15	23	7605
POL	KLVSAGIRKV	742	10	15	23	7606
POL	TOLGCTLNEPI	178	11	15	23	7607
POL	PLTEKIKALV	212	11	15	23	7608
POL	IQKQGGQWTY	521	11	15	23	7609
POL	LPIKETWEAW	583	11	15	23	7610

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SSEQ ID NO.
POL	PIQETWEAWW	584	11	15	23	7611
POL	ILALQDSGLEV	675	11	15	23	7612
POL	EQVDKLVSAIG	738	11	15	23	7613
POL	LVSAGIRKVLV	743	11	15	23	7614
POL	QLGCTLNF	179	8	16	25	7615
POL	QLEKEPIV	620	8	16	25	7616
POL	AQEEHRY	760	8	16	25	7617
POL	LNGRWKPKM	125	9	16	25	7618
POL	YQLEKEPIV	619	9	16	25	7619
POL	IQQEGIPY	887	9	16	25	7620
POL	QLGCTLNPI	179	10	16	25	7621
POL	EPHKKQNPDI	358	10	16	25	7622
POL	TPKFKLPI	578	8	17	27	7623
POL	NPDIIVQY	364	9	17	27	7624
POL	ELREHLLKW	393	9	17	27	7625
POL	NPDIIVQYM	364	10	17	27	7626
POL	MLTOIGCTLNF	176	11	17	27	7627
POL	NLTKYKAKI	540	10	18	29	7628
POL	SVPLDKDF	306	8	18	28	7629
POL	DIVIVQYM	366	8	18	28	7630
POL	TLWQRPLVTY	91	10	18	28	7631
POL	HGRNMLTQI	171	10	18	28	7632
POL	VPLDKDFRY	307	10	18	28	7633
POL	NIGRNMLTQI	170	11	18	28	7634
POL	SVPLDKDFRY	306	11	18	28	7635
POL	LLRGTKALTEV	471	11	18	28	7636
POL	ELVNQIEQLI	708	11	18	28	7637
POL	AMASDFNLPI	773	11	18	28	7638
POL	PLWKGPAKLLW	985	11	18	28	7639
POL	PLDKIDFRKY	308	9	19	30	7640
POL	WQRPLVTY	93	8	19	30	7641
POL	EICGIKAI	152	8	19	30	7642
POL	LVNQIEQLI	709	10	19	30	7643
POL	LVSQIEQLI	709	10	19	30	7644
POL	EICGHKAGTV	152	11	19	30	7645
POL	ELVSQIEQLI	708	11	19	30	7646
POL	QQEFGIPY	888	8	20	32	7647
POL	ROYDQILI	144	8	20	31	7648
POL	SQIEQLI	711	8	20	31	7649
POL	KLPIQETW	582	9	20	31	7650
POL	KVROYDQILI	142	10	20	31	7651
POL	ROYDQILIEI	144	10	20	31	7652
POL	DLEIGQIRTKI	381	11	20	31	7653
POL	LIKKKVVYLAW	717	11	20	31	7654
POL	TVKAAACWVAGI	877	11	20	31	7655
POL	KVIHTDNGSNF	863	11	21	33	7656
POL	WORPLVTI	93	8	21	33	7657
POL	EIGQIRTKI	383	9	21	33	7658
POL	EPVGAETP	624	9	21	33	7659
POL	TLWQRPLVTI	91	10	21	33	7660

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	HGRNLLTQI	171	10	21	33	7661
POL	EMVGAETFY	624	10	21	33	7662
POL	NIGRNLLTQI	170	11	21	33	7663
POL	LLTQIGCTLNF	176	11	21	33	7664
POL	EPVGAETFYV	624	11	21	33	7665
POL	IQWTYQY	527	8	22	34	7666
POL	GKQIEGI	886	8	22	34	7667
POL	GKQIEGIPY	886	10	22	34	7668
POL	LLRGAKALTDI	471	11	22	34	7669
POL	YLAWVPALIKGI	724	11	22	34	7670
POL	KLGRWPVKVI	855	11	22	34	7671
POL	NPEVIYQY	364	9	23	36	7672
POL	ILEGRVILV	819	9	23	36	7673
POL	KVILVAVIIV	823	9	23	36	7674
POL	NPEVIYQYM	364	10	23	36	7675
POL	EICGRKAITV	152	11	23	36	7676
POL	ILEGRVILVAV	819	11	23	36	7677
POL	EICGRKAI	152	8	24	38	7678
POL	NPYNTPIF	243	8	24	38	7679
POL	EIVYQYM	366	8	24	38	7680
POL	NQIEQLI	711	8	24	38	7681
POL	VILVAVIIV	824	8	24	38	7682
POL	TVKAAACWV	877	8	24	38	7683
POL	IPVNIIGRNM	168	9	24	38	7684
POL	TPVNIIGRNM	167	10	24	38	7685
POL	GPENPYNTPI	240	10	24	38	7686
POL	NPYNTPIAI	243	10	24	38	7687
POL	GQGQWTYQY	525	10	24	38	7688
POL	VHITDINGSNF	864	10	24	38	7689
POL	GPENPYNTPIF	240	11	24	38	7690
POL	LQDSGSEV	678	8	25	39	7691
POL	LLKLAGRW	853	8	25	39	7692
POL	KQGQGWYTY	523	9	25	39	7693
POL	GQGQWTYQI	525	9	25	39	7694
POL	ALQDSGSEV	677	9	25	39	7695
POL	FLKLAGRW	852	9	25	39	7696
POL	LQDSGSEVNI	678	10	25	39	7697
POL	LLKLAGRWIV	853	10	25	39	7698
POL	KQGQGWYTYQI	523	11	25	39	7699
POL	ALQDSGSEVNI	677	11	25	39	7700
POL	LQDSGSEVNI	678	11	25	39	7701
POL	AMASDFNLPIV	773	11	25	39	7702
POL	FLKLAGRWFPV	852	11	25	39	7703
POL	QLDCTHLEGKV	814	11	26	41	7704
POL	PIVAKEIV	782	8	26	41	7705
POL	RIQIRAKI	383	9	26	41	7706
POL	RLPIQKETW	582	9	26	41	7707
POL	LVSSGIRKV	743	9	26	41	7708
POL	PIVAKEIV	781	9	26	41	7709
POL	DPSKDLIAEI	512	10	26	41	7710

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KLVSSGIRKV	742	10	26	41	7711
POL	NLPVVAKEI	779	10	26	41	7712
POL	LPIVVAKEI	780	10	26	41	7713
POL	DLEIGQIRAKI	381	11	26	41	7714
POL	LVSSGIRKVLV	743	11	26	41	7715
POL	NLPVVAKEIV	779	11	26	41	7716
POL	QIVAGIKV	458	8	27	43	7717
POL	QIVTGIKV	458	8	27	43	7718
POL	LQDSGLEV	678	8	27	42	7719
POL	AQHEIEKY	760	8	27	42	7720
POL	PIVVAKEI	781	8	27	42	7721
POL	SOIYAGIKV	457	9	27	42	7722
POL	SOIYRGIKV	457	9	27	42	7723
POL	IQKETWETW	585	9	27	42	7724
POL	ALQDSGLEV	677	9	27	42	7725
POL	LPIVVAKEI	780	9	27	42	7726
POL	PIQKETWETW	584	10	27	42	7727
POL	IQKETWETW	585	10	27	42	7728
POL	LQDSGLEVNI	678	10	27	42	7729
POL	NLPVVAKEI	779	10	27	42	7730
POL	LPIVVAKEIV	780	10	27	42	7731
POL	PIQKETWETW	583	11	27	42	7732
POL	PIQKETWETWW	584	11	27	42	7733
POL	YVTDGRQKVV	649	11	27	42	7734
POL	ALQDSGLEVNI	677	11	27	42	7735
POL	LQDSGLEVNI	678	11	27	42	7736
POL	NLPVVAKEIV	779	11	27	42	7737
POL	KQEFQIPY	888	8	28	44	7738
POL	KIKALTEI	217	8	28	44	7739
POL	PIVGAETF	625	8	28	44	7740
POL	IVGAETFY	626	8	28	44	7741
POL	OLIKKEKV	716	8	28	44	7742
POL	PVVAKEIV	782	8	28	44	7743
POL	PIVGAETFY	625	9	28	44	7744
POL	IVGAETFYV	626	9	28	44	7745
POL	IQIKKEKV	715	9	28	44	7746
POL	OLIKKEKVY	716	9	28	44	7747
POL	LPIVVAKEI	780	9	28	44	7748
POL	PIVVAKEIV	781	9	28	44	7749
POL	PIVGAETFYV	625	10	28	44	7750
POL	EQIKKEKVY	715	10	28	44	7751
POL	IIQLIKKEKV	713	11	28	44	7752
POL	PIVVAKEI	781	8	29	45	7753
POL	IIIIATDI	952	8	29	45	7754
POL	YVTDGRQKVV	649	10	29	45	7755
POL	QVDKLVSSGI	739	10	29	45	7756
POL	RIIDIIATDI	951	10	29	45	7757
POL	EQVDKLVSSGI	738	11	29	45	7758
POL	TPKFRLLPI	578	8	30	47	7759
POL	IILVAIIV	824	8	30	47	7760

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	KILVAVIIV	823	9	30	47	7761
POL	KLGRWPVKV	853	10	30	47	7762
POL	GOWTYQIY	527	8	31	48	7763
POL	YOLEKEPI	619	8	31	48	7764
POL	GQETAYFI	846	8	31	48	7765
POL	IILEGRIILV	819	9	31	48	7766
POL	IPSINNETGI	321	11	31	48	7767
POL	GVYYDFSKDIL	508	11	31	48	7768
POL	KLWYQLEKEPI	616	11	31	48	7769
POL	IILEGRIILVAV	819	11	31	48	7770
POL	KQLTEAYQKI	538	10	32	51	7771
POL	AVKACACW	877	8	32	50	7772
POL	SINNETPGI	323	9	32	50	7773
POL	FILKLAGRW	852	9	32	50	7774
POL	EMEKEGKISKI	329	11	32	50	7775
POL	SINNETGIRY	323	11	32	50	7776
POL	FILKLAGRW	852	11	32	50	7777
POL	QLDCTIIEGKI	814	11	33	52	7778
POL	DVKQLTEAV	556	9	33	52	7779
POL	ELOKQITKI	964	9	34	54	7780
POL	KQITKIONF	967	9	34	54	7781
POL	KQITKIONFRV	967	11	34	54	7782
POL	ILKLAGRW	853	8	34	53	7783
POL	QLTEAVQKI	539	9	34	53	7784
POL	ILKLAGRW	853	10	34	53	7785
POL	LQKQITKIONF	965	11	34	53	7786
POL	RVYYRDSRDP	976	11	34	53	7787
POL	LIKKEKVV	717	8	35	55	7788
POL	QITKIONF	968	8	35	55	7789
POL	NLPCKWKPKM	124	10	35	55	7790
POL	QITKIONFRV	968	10	35	55	7791
POL	NLPCKWKPKMI	124	11	35	55	7792
POL	QITKIONFRV	968	11	35	55	7793
POL	PIWGPAPKLLW	985	11	35	55	7794
POL	KLGRAGYV	643	8	36	56	7795
POL	LQKQITKI	965	8	36	56	7796
POL	AIFQSSMTKI	347	10	36	56	7797
POL	AQPDKSESLV	700	11	36	56	7798
POL	VIQNSDI	1003	8	37	58	7799
POL	VVIQNSDI	1002	9	37	58	7800
POL	NPYNTPVFAI	243	10	37	58	7801
POL	QPDKSESLV	701	10	37	58	7802
POL	AVVIQNSDI	1000	10	37	58	7803
POL	VIQNSDIKV	1003	10	37	58	7804
POL	YLSWVFAIKGI	724	11	37	58	7805
POL	VVIQNSDIKV	1002	11	37	58	7806
POL	VIQNSDIKV	1003	11	37	58	7807
POL	NPYNTPVF	243	8	38	59	7808
POL	FQSSMTKI	349	8	38	59	7809
POL	IQDNSDIKV	1004	9	38	59	7810

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	GPENPYNTPV	240	10	38	59	7811
POL	IQDNSDIKVV	1004	10	38	59	7812
POL	GPENPYNTPVF	240	11	38	59	7813
POL	ILKEPVIIGVY	498	11	38	59	7814
POL	LPCKWKPKM	125	9	39	61	7815
POL	LPCKWKPKMI	125	10	39	61	7816
POL	LPCKWKPKMI	435	9	40	63	7817
POL	LPCKDKSWTV	498	10	40	63	7818
POL	ILKEPVIIGVY	497	11	40	63	7819
POL	ILKEPVIIGVY	142	8	41	64	7820
POL	KVROYDQI	179	8	41	64	7821
POL	QIGCTLNF	504	8	41	64	7822
POL	EPVIIGVY	178	9	41	64	7823
POL	QIGCTLNF	498	9	41	64	7824
POL	ILKEPVIIGV	140	10	41	64	7825
POL	FIKVRQYDQI	179	10	41	64	7826
POL	QIGCTLNF	497	10	41	64	7827
POL	ILKEPVIIGV	178	11	41	64	7828
POL	QIGCTLNF	235	11	41	64	7829
POL	KISKIGPENPY	571	11	41	64	7830
POL	SIVIWGKTPF	229	8	42	66	7831
POL	EMEKEGKI	345	9	42	66	7832
POL	SPAFQSSM	666	9	42	66	7833
POL	NQTELOAI	367	11	42	66	7834
POL	IVYQYMDL	531	8	43	67	7835
POL	YQIYQEPF	352	9	43	67	7836
POL	SMTKILEPF	1027	8	44	69	7837
POL	QMAAGDDCV	1026	9	44	69	7838
POL	KQAGDDCV	960	10	44	69	7839
POL	IQIKELQKI	959	11	44	69	7840
POL	DIQIKELQKI	536	11	45	70	7841
POL	EPFKNLTKGY	919	10	46	72	7842
POL	DQAEHLKTAV	583	8	47	73	7843
POL	LPIQKETW	573	9	47	73	7844
POL	VIWGTPTF	89	10	47	73	7845
POL	QITLWQPLV	572	10	47	73	7846
POL	IVWGTPTF	88	11	47	73	7847
POL	PQITLWQPLV	197	11	47	73	7848
POL	KLKPGMDGPKV	826	11	47	73	7849
POL	LVAVIIVASGYI	91	8	49	77	7850
POL	TLWQPLV	288	10	49	77	7851
POL	GLKKKSVTV	747	11	49	77	7852
POL	GIRKVLFDGI	750	8	50	78	7853
POL	KVLFDGI	1013	9	50	78	7854
POL	VPRRKAKII	1020	9	50	78	7855
POL	IIRDYGGQM	1012	10	50	78	7856
POL	VVPRRKAKII	1019	10	50	78	7857
POL	KIIRDYGGQM	285	11	50	78	7858
POL	HPAGLKKKSV	1011	11	50	78	7859
POL	KVPRRKAKII	238	8	51	80	7860
POL	KIGPENPY					

Table XIV
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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	VPRKAKI	1013	8	51	80	7861
POL	KPGMDGPKV	199	9	51	80	7862
POL	VVPRKAKI	1012	9	51	80	7863
POL	QMDGPKVKQW	201	10	51	80	7864
POL	TPGIRYQYNV	328	10	51	80	7865
POL	VYQYMDLLV	368	10	51	80	7866
POL	KVPRKAKI	1011	10	51	80	7867
POL	VLVGPITPVNI	162	11	51	80	7868
POL	VYQYMDLLV	368	11	51	80	7869
POL	WIPEWFEV	602	8	52	84	7870
POL	IONFRVYY	972	8	52	84	7871
POL	GLKKKKS	288	8	52	81	7872
POL	THGIRYQY	328	8	52	81	7873
POL	GIRYQYNV	330	8	52	81	7874
POL	KIONFRVY	971	8	52	81	7875
POL	KIONFRVY	971	9	52	81	7876
POL	LVGPTPVNII	163	10	52	81	7877
POL	WQATWPEWFEF	598	11	52	81	7878
POL	IIVASGYIEAEV	830	11	52	81	7879
POL	VLGPTTV	162	8	53	83	7880
POL	CQLKGEAM	795	8	53	83	7881
POL	SQGVVESM	899	8	53	83	7882
POL	TVLVGPTTV	161	9	53	83	7883
POL	AVIHVASYII	828	9	53	83	7884
POL	SMNKLKKI	905	9	53	83	7885
POL	VLVGPITPVNI	162	10	53	83	7886
POL	HPDKWTVQPI	424	10	53	83	7887
POL	ELFLAENKEI	489	10	53	83	7888
POL	LVAVIHVASY	826	10	53	83	7889
POL	POSQGVVESM	897	10	53	83	7890
POL	SMNKLKKII	905	10	53	83	7891
POL	GIGGHKVRQY	136	11	53	83	7892
POL	TVLVGPTPVNI	161	11	53	83	7893
POL	VLVGDGDAYESV	297	11	53	83	7894
POL	QLKGEAMIIQGV	796	11	53	83	7895
POL	ILVAVIHVASY	825	11	53	83	7896
POL	NPOSQGVVESM	896	11	53	83	7897
POL	FVNTPLV	608	8	54	86	7898
POL	FVNTPLV	608	11	54	86	7899
POL	GPTPVNII	165	8	54	84	7900
POL	LVGPTPVNI	163	9	54	84	7901
POL	DVGDAYESV	299	9	54	84	7902
POL	WQATWPEW	598	9	54	84	7903
POL	TVTVKLLKFGM	193	10	54	84	7904
POL	FPISPIETPV	186	11	55	86	7905
POL	TQDFWEVQLGI	273	11	55	86	7906
POL	SPITETPV	189	8	56	88	7907
POL	IPVKKLPGM	195	8	56	88	7908
POL	WPLTEEKI	211	8	56	88	7909
POL	FPISPIETV	186	9	56	88	7910

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPVKLPKGM	194	9	56	88	7911
POL	PISPIETVPV	187	10	56	88	7912
POL	KOWPLTEEKI	209	10	56	88	7913
POL	SVTVLDVGDAY	294	11	56	88	7914
POL	PISPIETV	187	8	57	89	7915
POL	ELAENREI	491	8	57	89	7916
POL	TPPLVKLW	611	8	57	89	7917
POL	PPLVKLWY	612	8	57	89	7918
POL	QVDCSPGI	805	8	57	89	7919
POL	ILKTAVQM	923	8	57	89	7920
POL	ELNKRITQDF	268	9	57	89	7921
POL	TVLDVGDAY	296	9	57	89	7922
POL	TPPLVKLWY	611	9	57	89	7923
POL	GOVIX'SPGI	804	9	57	89	7924
POL	QVDCSPGIW	805	9	57	89	7925
POL	ELKKIGQV	909	9	57	89	7926
POL	AIKKKDSIKW	251	10	57	89	7927
POL	ELNKRITQDFW	268	10	57	89	7928
POL	TVLDVGDAYF	296	10	57	89	7929
POL	QVDCSPGIW	804	10	57	89	7930
POL	ILKTAVQMAV	923	10	57	89	7931
POL	ILKTAVQMAVVF	923	11	57	89	7932
POL	GIGYSAGIERI	942	11	57	89	7933
POL	LPQGWKGSPIAI	338	11	57	89	7934
POL	YVGSDLFI	377	8	58	92	7935
POL	DLVGSDLFI	375	10	58	91	7936
POL	IVTDSQYALGI	687	11	58	91	7937
POL	IPAEITQETAY	841	11	58	91	7938
POL	FIHFKRKGGI	913	11	58	91	7939
POL	SOYALGII	691	8	58	92	7940
POL	GIGGNEQV	713	8	59	92	7941
POL	AVIVASGY	828	8	59	92	7942
POL	KLGRWTV	855	8	59	92	7943
POL	NPQSQGVV	896	8	59	92	7944
POL	PQGWKGSPIAI	339	10	59	92	7945
POL	EVNIVTDSQY	684	10	59	92	7946
POL	PQGWKGSPIAF	339	11	59	92	7947
POL	IPYNPQSQGVV	893	11	59	92	7948
POL	KLLWKGGGAVV	992	11	59	92	7949
POL	LLWKGGGAVVI	993	11	59	92	7950
POL	KPKMIGGI	130	8	60	94	7951
POL	VLDVGDAY	297	8	60	94	7952
POL	AVQMAVFI	927	8	60	94	7953
POL	VLDVGDAYF	297	9	60	94	7954
POL	ELHPDKWTV	422	9	60	94	7955
POL	KLNWASQIY	452	9	60	94	7956
POL	QMAVFIINF	929	9	60	94	7957
POL	VQMAVFIINF	928	10	60	94	7958
POL	KLLWKGGGAV	992	10	60	94	7959
POL	KPKMIGGIGGF	130	11	60	94	7960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WMGYELIPDKW	418	11	60	94	7961
POL	LVGKLNWASQI	449	11	60	94	7962
POL	AVQMAVFIINF	927	11	60	94	7963
POL	TLNFMISPI	183	9	61	97	7964
POL	YOYMDLILY	370	8	61	95	7965
POL	KLNWASQI	432	8	61	95	7966
POL	YOYMDLILY	370	9	61	95	7967
POL	TVNDIQKLV	442	9	61	95	7968
POL	LLWKGEQAVV	993	10	61	95	7969
POL	ALLDTGADITV	109	11	61	95	7970
POL	MIGGIGGF	133	8	62	97	7971
POL	KLVGKLNW	448	8	62	97	7972
POL	NIVTDSQY	686	8	62	97	7973
POL	KMIGGIGGF	132	9	62	97	7974
POL	MIGGIGGF	133	9	62	97	7975
POL	IQKEPFLW	410	9	62	97	7976
POL	LLWKGEQAVV	993	9	62	97	7977
POL	KMIGGIGGF	132	10	62	97	7978
POL	IQKEPFLW	410	10	62	97	7979
POL	IQKLVGKLNW	446	10	62	97	7980
POL	MIGGIGGF	133	11	62	97	7981
POL	DIQKLVGKLNW	445	11	62	97	7982
POL	WVTAIKGI	727	8	63	98	7983
POL	EPFLWMGY	413	9	63	98	7984
POL	LLDTGADITV	110	10	63	98	7985
POL	YOYNVLPQGW	333	10	63	98	7986
POL	IPYNPOSQGV	893	10	63	98	7987
POL	GIYNPOSQGV	892	11	63	98	7988
POL	GIGGFIK	136	8	64	100	7989
POL	IPFLWMGY	414	8	64	100	7990
REV	PQGTETGV	101	8	05	18	7991
REV	SQGTETGV	101	8	05	18	7992
REV	QPGTETGV	100	9	05	18	7993
REV	CLGRRAEV	67	9	10	16	7994
REV	TQGVGSQI	98	9	11	18	7995
REV	LLKTVRLI	12	8	11	17	7996
REV	RQRQHSI	52	8	11	17	7997
REV	VPLQLPPI	75	8	11	17	7998
REV	PVPLQLPPI	74	9	11	17	7999
REV	EPVPLQLPPI	73	10	11	17	8000
REV	AVRIKILY	17	9	13	20	8001
REV	RQARKNRNRW	39	11	16	25	8002
REV	IKILYQSNPY	20	11	18	28	8003
REV	KILYQSNPY	22	9	26	41	8004
REV	ILYQSNPY	23	8	27	42	8005
REV	RQARNNRNRW	39	11	38	59	8006
TAT	GPRESKKV	90	9	13	20	8007
TAT	EPVDRLEPW	2	10	13	20	8008
TAT	FLNKGIGI	41	8	14	22	8009
TAT	PVDRLEPW	3	9	14	22	8010

Table XIV
IIIY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
TAT	EPVDPNLEPW	2	10	14	22	R011
TAT	FLNKLGLISY	41	10	14	22	R012
TAT	PVDPNLEPW	3	9	20	31	R013
VIF	ALIKPKKI	157	8	10	16	R014
VIF	PLGEARLVI	58	9	10	16	R015
VIF	QVDRMRINTW	12	10	10	16	R016
VIF	IIPLGDAARLV	56	10	10	16	R017
VIF	IPLGEARLVI	57	10	10	16	R018
VIF	WQVDRMRINTW	11	11	10	16	R019
VIF	IIPLGEARLVI	56	11	10	16	R020
VIF	GVSIEVRLRRY	87	11	10	16	R021
VIF	QIDHDLARQLI	102	11	10	16	R022
VIF	PLGDARLV	58	8	11	17	R023
VIF	IPLGDARLV	57	9	11	17	R024
VIF	SIEWRLRRY	89	9	11	17	R025
VIF	GLADQLIIMIIY	106	11	11	17	R026
VIF	RLVITYW	65	8	12	19	R027
VIF	LQYGERDW	74	8	12	19	R028
VIF	KIRTWNSLV	17	9	12	19	R029
VIF	GLQTGERDW	73	9	12	19	R030
VIF	IYWQVDRMKI	9	10	12	19	R031
VIF	QVDRMKIINTW	12	10	12	19	R032
VIF	WQVDRMKIINTW	11	11	12	19	R033
VIF	RMKIRTWNSLV	15	11	12	19	R034
VIF	WQVDRMKI	11	8	13	20	R035
VIF	IIPKISSEV	48	8	13	20	R036
VIF	IIPRISSEV	48	8	13	20	R037
VIF	DQLIIMIIY	109	8	13	20	R038
VIF	DQLIIMIIYF	109	9	13	20	R039
VIF	IIPKISSEVIII	48	10	13	20	R040
VIF	IIPRISSEVIII	48	10	13	20	R041
VIF	SVKKLTEDRW	174	10	13	20	R042
VIF	QLIHLIYFDCF	110	11	13	20	R043
VIF	DQLIHLIY	109	8	14	22	R044
VIF	QLIHLIYF	110	8	14	22	R045
VIF	QLIHLIYF	110	8	14	22	R046
VIF	IVSPKCEY	133	8	14	22	R047
VIF	DQLIHLIYF	109	9	14	22	R048
VIF	QVDPGLADQLI	102	11	14	22	R049
VIF	QLIHLIYFDCF	110	11	14	22	R050
VIF	KISSEVIII	50	8	15	23	R051
VIF	RISSEVIII	50	8	15	23	R052
VIF	IIMIIYFDCF	113	8	15	23	R053
VIF	RIRTWNSLV	17	9	15	23	R054
VIF	RIRTWNSLV	17	9	15	23	R055
VIF	GLADQLIIM	106	9	15	23	R056
VIF	LIIMHYFDCF	111	10	15	23	R057
VIF	RMKIRTWNSLV	15	11	15	23	R058
VIF	RMKIRTWNSLV	15	11	15	23	R059
VIF	IILYYFDCF	113	8	16	25	R060

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	LIILYYFDCF	111	10	16	25	8061
VIF	LVKIHIMYI	24	8	19	30	8062
VIF	IIPKYSSEV	48	8	19	30	8063
VIF	PLGEARLV	58	8	19	30	8064
VIF	SLVKIHIMYI	23	9	19	30	8065
VIF	IPLGEARLV	57	9	19	30	8066
VIF	DPDLADQLI	104	9	19	30	8067
VIF	DPGLADQLI	104	9	19	30	8068
VIF	KIKPLPSV	164	9	19	30	8069
VIF	IIPKYSSEVIII	48	10	19	30	8070
VIF	IIPLGEARLV	56	10	19	30	8071
VIF	KYSSEVIII	50	8	20	31	8072
VIF	LVKIHIMYV	24	8	21	33	8073
VIF	SLVKIHIMYV	23	9	21	33	8074
VIF	GLITGERDW	73	9	22	34	8075
VIF	ILGHIGVSI	83	8	25	39	8076
VIF	ILGHIGVSI	83	10	25	39	8077
VIF	ILGQGVSI	83	8	25	39	8078
VIF	GGQVSIEW	83	8	26	41	8079
VIF	ILGQVSIEW	83	10	26	41	8080
VIF	SLQYLALTALI	149	11	26	41	8081
VIF	YALTALI	152	8	27	42	8082
VIF	LQYLALTALI	150	10	28	44	8083
VIF	QVDRMRIRTW	12	10	28	44	8084
VIF	WQVDRMRIRTW	11	11	31	48	8085
VIF	YQAGIINKV	140	8	31	48	8086
VIF	QVMIVQV	6	8	38	59	8087
VIF	WQVMIVQV	5	8	43	67	8088
VIF	QVMIVQVQVDRM	6	9	43	67	8089
VIF	MIVWQVDRMRI	8	11	43	67	8090
VIF	SLVKIHIMY	23	8	44	69	8091
VIF	MIVWQVDRM	7	10	44	69	8092
VIF	MIVWQVDRM	8	9	46	72	8093
VIF	IVWQVDRMRI	9	10	47	73	8094
VIF	WQVDRMRI	11	8	48	75	8095
VIF	IVWQVDRM	9	8	48	75	8096
VPR	RPWLIGLQY	36	10	59	92	8097
VPR	QQLLFVIF	65	8	10	16	8098
VPR	QQLLFVIF	64	9	10	16	8099
VPR	QQLLFVIFRI	66	9	10	16	8100
VPR	QQLLFVIFRI	65	10	10	16	8101
VPR	QKEAVRIIF	27	11	10	16	8102
VPR	WLHIGLOY	38	8	11	17	8103
VPR	RIGCRHSRGI	74	8	11	17	8104
VPR	RPWLIGLQCHI	36	11	11	17	8105
VPR	LLEVIIFRI	67	11	12	19	8106
VPR	RIGCRHSRI	74	8	12	19	8107
VPR	GOHIYNTY	43	9	12	19	8108
VPR	AVRIIFRI	30	8	13	20	8109
VPR			8	14	22	8110

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	GOYIYET	43	8	14	22	8111
VPR	AVRIIPRIW	30	9	14	22	8112
VPR	HIYNTYGDITW	45	10	14	22	8113
VPR	YIYETYGDTW	45	10	14	22	8114
VPR	ELKSEAVRIIF	25	10	15	23	8115
VPR	COHSRIGII	77	9	16	25	8116
VPR	LLEELKSEAV	22	10	16	25	8117
VPR	ELLEELKNEAV	21	11	16	25	8118
VPR	ELLEELKSEAV	21	11	16	25	8119
VPR	GQIHYET	43	8	17	27	8120
VPR	LLEELKNEAV	22	10	17	27	8121
VPR	ELKNEAVRIIF	25	10	17	27	8122
VPR	HIYETYGDTW	45	10	17	27	8123
VPR	WLIIGLCQIIF	38	9	20	31	8124
VPR	WLIIGLCQIIF	38	9	20	31	8125
VPR	IIRILOQLFI	60	11	33	52	8126
VPR	GVEAIRI	56	8	34	53	8127
VPR	AVRIIPRIW	30	9	34	53	8128
VPR	RILOQLLFIIIF	62	11	34	53	8129
VPR	RILOQLLFIIIF	62	10	35	55	8130
VPR	RILOQLFI	63	9	36	56	8131
VPR	POREPYNEW	10	8	37	58	8132
VPR	GQREPYNEW	9	9	37	58	8133
VPR	AIIRILOQLLF	59	10	37	58	8134
VPR	DQGIQREPY	7	11	38	59	8135
VPR	IIRILOQLLF	60	9	41	64	8136
VPR	QQLFIIF	65	8	41	64	8137
VPR	LLFIIFRI	67	8	44	69	8138
VPR	LOQLLFIIIF	64	9	44	69	8139
VPR	QQLFIIFRI	66	9	44	69	8140
VPR	QQLFIIFRI	65	9	44	69	8141
VPR	LOQLFIIFRI	64	10	44	69	8142
VPR	RILOQLLF	62	11	44	69	8143
VPR	COHSRIGI	77	8	45	70	8144
VPR	RIGCOHSRIGI	74	8	45	70	8145
VPR	RIGCOHSRIGI	74	11	45	70	8146
VPU	KVDYRIGI	7	8	01	33	8147
VPU	KVDYRLGV	7	8	01	33	8148
VPU	RIDYRLGV	7	8	01	33	8149
VPU	KVDYRIVIV	7	9	01	33	8150
VPU	KVDYRIVIVAF	7	9	01	33	8151
VPU	GVEMGHIIAPW	91	11	01	33	8152
VPU	RIKEIRDSY	64	10	01	50	8153
VPU	RIRERDSY	64	11	01	50	8154
VPU	LIAIVVW	26	8	01	50	8155
VPU	DQEELSALV	79	9	10	16	8156
VPU	ILAIVALV	12	9	11	18	8157
VPU	EMGHIIAPW	89	8	11	17	8158
VPU	ILAIVALV	12	8	12	19	8159
						8160

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPV	IVFIEYRKI	36	9	12	19	8161
VPV	VVWTVFIEY	31	10	12	19	8162
VPV	IVVWTVFIEY	30	11	12	19	8163
VPV	ILRQRKIDRLI	46	11	13	20	8164
VPV	AIIVVWTVF	29	9	14	22	8165
VPV	KIDRLIDRI	52	9	14	22	8166
VPV	AIIVVWTVFI	29	10	14	22	8167
VPV	IVVWTVFI	30	8	15	23	8168
VPV	VVWTVFI	31	8	15	23	8169
VPV	KILRQRKI	45	8	15	23	8170
VPV	IVVWTVFI	30	9	15	23	8171
VPV	RQRKIDRLI	48	9	17	27	8172
VPV	IIAIVVWTVI	27	10	20	31	8173
VPV	IIAIVVWTI	27	9	23	36	8174
VPV	AIIVVWTVI	29	8	29	45	8175

Table XV
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	IGSQAFY	361	8	01	25		R176
ENV	GKDLWTVY	42	9	01	33		R177
ENV	GKDLWTVY	42	10	01	33		R178
ENV	NTSPSRVAY	376	10	01	33		R179
ENV	GTAGNSRAA	375	11	01	33		R180
ENV	DSSNSTGNY	218	9	01	20		R181
ENV	TNSSTINDTY	458	10	01	17		R182
ENV	WFDTNWLW	767	10	10	16		R183
ENV	WMEWEREIDN	723	11	10	16		R184
ENV	EWEREIDNY	725	9	11	17		R185
ENV	NMWQEVGKA	494	11	15	23		R186
ENV	IISFNCRGEFFY	434	11	16	25		R187
ENV	WQEVGKAMY	496	9	18	28		R188
ENV	VSFEPIHLY	253	10	28	44		R189
ENV	KVSFEPIHLY	252	11	28	44		R190
ENV	SFEPIHLY	254	9	31	48		R191
ENV	LQARVLAVER	662	11	33	52		R192
ENV	LSVNRVRQGY	707	11	34	53		R193
ENV	RSCLFSY	858	8	35	55		R194
ENV	LRSLCLFSY	857	9	35	55		R195
ENV	IISFNCGGEFFY	434	11	35	55		R196
ENV	DMIDNWRSEL	552	11	37	58		R197
ENV	MIDNWRSELY	553	10	40	63		R198
ENV	CASDAKAY	67	8	42	66	0.0010	R199
ENV	FCASDAKAY	66	9	42	66		R200
ENV	WRSELYKY	557	8	54	84		R201
GAG	ETIDKDL	537	8	01	25		R202
GAG	EKEKGLY	538	8	01	25		R203
GAG	KQETIDKDL	535	10	01	25		R204
GAG	AADKGVSNY	130	10	01	25		R205
GAG	ASAOQDLKGG	392	11	01	50		R206
GAG	ATAQDLKGG	392	11	01	50		R207
GAG	AADKGVSNY	129	11	01	50		R208
GAG	EADKGVSNY	129	10	02	18		R209
GAG	GNSQVSQNY	140	10	04	36		R210
GAG	KQETIDKDL	531	10	12	23		R211
GAG	SEELRSLY	74	8	12	19		R212
GAG	GSEELRSLY	73	9	12	19		R213
GAG	TGSEELRSLY	72	10	12	19		R214
GAG	NSSQVSQNY	144	9	14	31		R215
GAG	SSQVSQNY	145	8	15	31		R216
GAG	RSLYNTVATL	78	11	15	24		R217
GAG	FRDYVDRFY	317	9	29	45		R218
GAG	PKEFRDY	313	8	63	98	0.0900	R219
NEF	IMARELIPEY	320	10	10	16		R220
NEF	IMARELIPEY	320	11	10	16		R221
NEF	ARELIPEFY	322	9	11	17		R222
NEF	YTPGPIRY	207	9	17	27		R223
NEF	RQDLDLVVY	182	10	20	31		R224
							R225

Table XX
HIV A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO.
NEF	ARELIPEYY	322	9	21	33		8226
NEF	ARELIPEY	322	8	24	38		8227
NEF	ROELDLWVY	182	10	32	50		8228
POL	TWETWTDY	589	9	10	16		8229
POL	TWETWTEY	589	10	10	16		8230
POL	ETWETWTD	588	10	10	16		8231
POL	ETWETWTE	588	10	10	16		8232
POL	AOEDIEKY	760	8	11	17		8233
POL	ISRIGPENY	236	10	11	17		8234
POL	KISRIKENPY	235	11	11	17		8235
POL	STINETPGIRY	323	11	11	17		8236
POL	KTELQAIY	668	8	12	19		8237
POL	GQDQWYQIY	535	10	12	19		8238
POL	DKAQEEIERV	758	10	15	23		8239
POL	AOEIEERY	760	8	16	25		8240
POL	NDIVIVYQY	364	9	17	27	0.0011	8241
POL	PLDKDFRKY	308	9	19	30		8242
POL	QOEFQIPY	888	8	20	32		8243
POL	NPEIVIVQY	364	9	23	36		8244
POL	DKAQEHIEKY	758	10	25	39		8245
POL	AOEIEIEKY	760	8	27	42		8246
POL	KQEKQIPY	888	8	28	44		8247
POL	NRETGLGKAG	639	11	28	44		8248
POL	ETKLGKAGY	641	9	35	55	0.0010	8249
POL	ITKIQNFRVY	969	10	36	57	0.0010	8250
POL	ITKIQNFRVY	969	11	36	57	0.0110	8251
POL	LKEPVIGVY	502	10	39	61	0.0010	8252
POL	LKEPVIGVY	502	9	41	64	0.0007	8253
POL	KKAKIRDY	1016	9	41	64		8254
POL	KISKIGPENPY	235	11	41	64		8255
POL	ISKIGPENPY	236	10	42	66	0.0130	8256
POL	NNETPGIRY	325	9	51	80	0.0007	8257
POL	NNETPGIRYQY	327	11	51	80	0.0004	8258
POL	ETPGIRYQY	327	10	52	81	0.0052	8259
POL	LVAVIVASGY	826	10	53	83	0.0390	8260
POL	VTVLVDVGDY	295	10	56	88	0.2800	8261
POL	NTPLPVKLWY	610	10	57	89	0.0041	8262
POL	PAETGOETAY	842	10	58	91	0.0130	8263
POL	IPAEIQTETAY	841	11	58	91		8264
POL	ETGOETAY	844	8	59	92		8265
POL	VLDVGDY	297	8	60	94		8266
POL	QKEPFLWMG	411	11	63	98	0.0004	8267
VIF	GVSEWRLRR	87	11	10	16		8268
VIF	SIEWRLRRY	89	9	11	17		8269
VIF	VSEWRLRRY	88	10	11	17		8270
VIF	GLADQLIIMII	106	11	11	17		8271
VIF	LADQLIIMIIY	107	10	13	20		8272
VIF	IVSPRCEY	133	8	14	22		8273
VIF	LADQLIILYY	107	10	14	22		8274
VIF	LADQLIILY	107	9	15	23		8275

Table XV
HIV Δ01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0101	SEQ ID NO.
VIF	KSLVKIIMMY	22	9	18	28		8276
VIF	WKSIVKIIIM	21	10	18	28		8277
VIF	NSLVKIIIMY	22	9	24	38		8278
VIF	WNSLVKIIIM	21	10	24	38		8279
VPR	PEDQGIQREPY	5	11	37	58		8280
VPU	WTIVFIEY	14	8	12	19		8281

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ ⁰ 01	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33		8282
ENV	SIGSQQAF	360	8	01	33		8283
ENV	IGPGQTFY	361	8	01	25		8284
ENV	IGSQQAFY	361	8	01	25		8285
ENV	GTAGNSSR	375	8	01	33		8286
ENV	TAGNSSRA	376	8	01	33		8287
ENV	KLREIRQF	405	8	01	25		8288
ENV	ADNLWVTVY	42	9	01	33		8289
ENV	GIGPGQTFY	360	9	01	33		8290
ENV	SIGSQQAFY	360	9	01	33		8291
ENV	IGPGQTFYA	361	9	01	25		8292
ENV	GTAGNSSRA	375	9	01	33		8293
ENV	NTSPRSRA	376	9	01	33		8294
ENV	TAGNSSRAA	376	9	01	33		8295
ENV	ADNLWVTVVY	42	10	01	33		8296
ENV	EGKNEINDY	217	10	01	33		8297
ENV	GIGPGQTFYA	360	10	01	33		8298
ENV	GTAGNSSRAA	375	10	01	33		8299
ENV	NTSPRSRAVY	376	10	01	33		8300
ENV	TAGNSSRAAY	376	10	01	33		8301
ENV	FGLGALFLGF	597	10	01	33		8302
ENV	VGLGAVFLGF	597	10	01	33		8303
ENV	TAGNSSRAA	375	11	01	25		8304
ENV	KLREIRQFENK	405	11	01	33		8305
ENV	QLYATVYA	34	8	01	50		8306
ENV	IINIHTII	584	8	01	50		8307
ENV	VISTRTHIR	584	8	01	50		8308
ENV	STRTHIREK	586	8	01	50		8309
ENV	NANITHCR	478	9	01	50		8310
ENV	IINIHTHIR	584	9	01	50		8311
ENV	ISTRTHIREK	585	9	01	50		8312
ENV	NIITHIREK	586	9	01	50		8313
ENV	STRTHIREKIR	586	9	01	50		8314
ENV	VISTRTHIREK	584	10	01	50		8315
ENV	ISTRTHIREK	585	10	01	50		8316
ENV	NIITHIREKRA	586	10	01	50		8317
ENV	STRTHIREKRA	586	10	01	50		8318
ENV	IITEGNTLQCR	478	11	01	50		8319
ENV	NANITHCRIR	478	11	01	50		8320
ENV	IINIHTHIREK	584	11	01	50		8321
ENV	VISTRTHIREKRA	584	11	01	50		8322
ENV	ISTRTHIREKRA	585	11	01	50		8323
ENV	NIITHIREKRA	586	11	01	50		8324
ENV	VTSNGNSA	161	8	01	20		8325
ENV	DSSNSTGNY	218	9	01	20		8326
ENV	STNGTETF	537	8	01	17		8327
ENV	STNGTETFR	537	9	01	17		8328
ENV	NDTENNTETFR	537	10	01	17		8329
ENV	NTETNKTETFR	537	10	01	17		8330
ENV	NTTGNTTETFR	537	10	01	17		8331

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	NDTENNTIEIR	517	11	01	17		8332
ENV	NTETNKITEIF	517	11	01	17		8333
ENV	NTTGNITEIF	537	11	01	17		8334
ENV	NGSENGTETIF	537	10	02	33		8335
ENV	NGSENGTETIF	537	11	02	33		8336
ENV	GSENGTETIF	538	9	02	18		8337
ENV	GSENGTETIF	538	10	02	18		8338
ENV	TIGAMFLGF	599	9	03	27		8339
ENV	NDITLPCR	477	9	03	20		8340
ENV	NDITLPCR	477	11	03	20		8341
ENV	MLGAMFLGF	599	9	04	36		8342
ENV	RGWEALKY	895	8	06	19		8343
ENV	KGLRLWEGIL	891	11	08	27		8344
ENV	LOWEGLKY	895	8	09	29		8345
ENV	RLGWEGILKY	894	9	09	29		8346
ENV	GLRLGWEGILK	892	11	09	29		8347
ENV	LCRRGWEGALK	883	10	09	15		8348
ENV	LLGRRGWEGAL	882	11	09	15		8349
ENV	ENGDIRQA	372	9	09	15		8350
ENV	LILGLVICS	21	11	09	15		8351
ENV	TGEIGDIRQA	370	11	09	15		8352
ENV	RLGWEGILK	894	8	10	32		8353
ENV	GLRLGWEGILK	892	10	10	32		8354
ENV	LCRRGWEGIA	883	8	10	16		8355
ENV	LLGRRGWEGIA	882	9	10	16		8356
ENV	DHCDIRQAII	372	10	10	16		8357
ENV	ELLGRRGWEGIA	881	10	10	16		8358
ENV	TGDHIGDIRQA	370	11	10	16		8359
ENV	GLVICS	28	8	10	16		8360
ENV	RVGQAMYA	498	8	10	16		8361
ENV	PLGVAPTR	571	8	10	16		8362
ENV	LGVAPTRA	572	8	10	16		8363
ENV	DTTNWLWY	769	8	10	16		8364
ENV	RDILIAA	869	8	10	16		8365
ENV	DFILIAAR	870	8	10	16		8366
ENV	DTIAIYA	923	8	10	16		8367
ENV	LGLVICS	27	9	10	16		8368
ENV	STITQACPK	243	9	10	16		8369
ENV	IOPGQTIFYA	358	9	10	16		8370
ENV	FDITNWLWY	768	9	10	16		8371
ENV	RDILIAAR	869	9	10	16		8372
ENV	NSAVSLINA	916	9	10	16		8373
ENV	ILGLVICS	26	10	10	16		8374
ENV	LLGLMICS	26	10	10	16		8375
ENV	PIIYCTPAGF	260	10	10	16		8376
ENV	FAIKCNDDK	269	10	10	16		8377
ENV	RIOPGQTIFYA	357	10	10	16		8378
ENV	MLQLTWGHIK	651	10	10	16		8379
ENV	RVLAVERYLR	665	10	10	16		8380
ENV	WFDITNWLW	767	10	10	16		8381

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0301	SEQ ID NO.
ENV	EGIEEGGER	828	10	10	16		R382
ENV	PIUYCTPAGFA	260	11	10	16		R383
ENV	GFAILKCNDRK	268	11	10	16		R384
ENV	FAILKCNDRKF	269	11	10	16		R385
ENV	GDIGDIRQAI	371	11	10	16		R386
ENV	NYPWSSWSN	693	11	10	16		R387
ENV	WMWEIREIDN	723	11	10	16		R388
ENV	NSAVSLNAT	916	11	10	16		R389
ENV	IAIAVAECTDR	925	11	10	16		R390
ENV	RGWEALKY	886	8	11	18		R391
ENV	GIGAVFLGF	598	9	11	18		R392
ENV	KLWVTVY	44	8	11	17		R393
ENV	AVGIGAVF	595	8	11	17		R394
ENV	RAYGIGAVF	594	8	11	17		R395
ENV	AVGIGAVFLGF	595	11	11	17		R396
ENV	TITQACTK	244	8	11	17		R397
ENV	YCTPAGFA	263	8	11	17		R398
ENV	RIGHQOTF	357	8	11	17		R399
ENV	IGPGQTFY	358	8	11	17		R400
ENV	LFLGFLGA	603	8	11	17		R401
ENV	LAVIRYL	667	8	11	17		R402
ENV	NLCFSYII	859	8	11	17		R403
ENV	SAVSLNA	917	8	11	17		R404
ENV	VSLNATA	919	8	11	17		R405
ENV	LGLMLCSA	27	9	11	17		R406
ENV	RIGPGQTFY	357	9	11	17		R407
ENV	ITTHSFNCR	431	9	11	17		R408
ENV	NITLPCHK	482	9	11	17		R409
ENV	ALFLGFLGA	602	9	11	17		R410
ENV	LFLGFLGA	603	9	11	17		R411
ENV	VLAVERYLR	666	9	11	17		R412
ENV	ISNWLWYIK	770	9	11	17		R413
ENV	NLCFSYIIR	859	9	11	17		R414
ENV	AVSLNATA	918	9	11	17		R415
ENV	GDIGDIRQA	371	10	11	17		R416
ENV	EITTHSFNCR	430	10	11	17		R417
ENV	VGIGAVFLGF	596	10	11	17		R418
ENV	GALFLGFLGA	601	10	11	17		R419
ENV	ALFLGFLGA	602	10	11	17		R420
ENV	SAVSLNATA	917	10	11	17		R421
ENV	VSLNATAIA	919	10	11	17		R422
ENV	YATGDIGDIR	368	11	11	17		R423
ENV	GALFLGFLGA	601	11	11	17		R424
ENV	ISNWLWYIKF	770	11	11	17		R425
ENV	DLNLCFSYII	856	11	11	17		R426
ENV	NLCFSYIIRL	859	11	11	17		R427
ENV	AVSLNATAIA	918	11	11	17		R428
ENV	PTRRQGLERA	951	11	11	17		R429
ENV	TODIGDIR	370	9	12	19		R430
ENV	DIIGDIRQA	372	9	12	19		R431

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Coverage (%)	$\Delta^*0.101$	SEQ ID NO.
ENV	EAQIILLK	646	8	12	19		8432
ENV	GMLMCSA	28	8	12	19		8433
ENV	ILKCNDDK	271	8	12	19		8434
ENV	TTISFNCR	432	8	12	19		8435
ENV	ICAVFLGF	600	8	12	19		8436
ENV	MTWMEWER	721	8	12	19		8437
ENV	GGERDRDR	834	8	12	19		8438
ENV	AILKCNDDK	270	9	12	19		8439
ENV	ILKCNDDKFF	271	9	12	19		8440
ENV	LAEEVVIR	312	9	12	19		8441
ENV	AMELGLGA	602	9	12	19	0.0002	8442
ENV	NMTWMEWER	720	9	12	19		8443
ENV	GIEEGGER	829	9	12	19		8444
ENV	EGGERDRDR	833	9	12	19		8445
ENV	RSIRLVNGF	841	9	12	19		8446
ENV	WGOELKNSA	910	9	12	19		8447
ENV	WSQELKNSA	910	9	12	19		8448
ENV	KTLFCASDA	60	10	12	19		8449
ENV	AILKCNDDKFF	270	10	12	19		8450
ENV	SLAEFEVVIR	311	10	12	19		8451
ENV	ATGDIIGDIR	369	10	12	19		8452
ENV	IINMWQEVOK	492	10	12	19		8453
ENV	GAMFLGLGA	601	10	12	19		8454
ENV	AMFLGLGAA	602	10	12	19		8455
ENV	AIEAQHLLK	644	10	12	19		8456
ENV	QIDLALDKWA	753	10	12	19		8457
ENV	SIRLVSGFLA	842	10	12	19		8458
ENV	LLQYWSQELK	906	10	12	19		8459
ENV	AILHIIPRRIR	946	10	12	19		8460
ENV	PTIRIOGLER	951	10	12	19		8461
ENV	KTLFCASDA	60	11	12	19		8462
ENV	TTISFNCRGE	310	11	12	19		8463
ENV	QINMWQEVG	491	11	12	19		8464
ENV	IINMWQEVOK	492	11	12	19		8465
ENV	ITKWLWYKIF	601	11	12	19		8466
ENV	GIEEGGERDR	770	11	12	19		8467
ENV	RSIRLVSGFLA	829	11	12	19		8468
ENV	NLLQYWSQEL	841	11	12	19		8469
ENV	RAILHIIPRRIR	905	11	12	19		8470
ENV	NTSVITQA	945	11	12	19		8471
ENV	SVEINCTR	241	8	13	20		8472
ENV	GDIIGDIR	340	8	13	20		8473
ENV	MFLGLGA	371	8	13	20		8474
ENV	KLTWVGK	603	8	13	20		8475
ENV	SIRLVNGF	653	8	13	20		8476
ENV	SIRLVSGF	842	8	13	20		8477
ENV	RLVNGFLA	842	8	13	20		8478
ENV	RAILHIIPR	844	8	13	20		8479
ENV		945	8	13	20		8480
ENV					-20		8481

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
ENV	AILIIPRR	946	8	13	20		R482
ENV	KAKRRVVQR	579	9	13	20	0.0002	R483
ENV	MPLGLGAA	603	9	13	20		R484
ENV	RSRLYSGF	841	9	13	20		R485
ENV	RAILIIIPRR	945	9	13	20		R486
ENV	ILIIIPRR	947	9	13	20		R487
ENV	SGGDEIVMII	425	10	13	20		R488
ENV	LLKLTWGIK	651	10	13	20		R489
ENV	NTSVTQACPK	241	11	13	20		R490
ENV	CTNVSTVQCT	285	11	13	20		R491
ENV	SSGDLLEITTH	424	11	13	20		R492
ENV	SSGDPPEIVMII	424	11	13	20		R493
ENV	VMISENCGGE	432	11	13	20		R494
ENV	PTKAKRRVQ	576	11	13	20		R495
ENV	KAKRRVVQRE	579	11	13	20		R496
ENV	ILLKLTWGI	650	11	13	20		R497
ENV	VGLGLRIIF	784	11	13	20		R498
ENV	SLLNATAIAVA	920	11	13	20		R499
ENV	TGEIGDIR	370	9	14	23		R500
ENV	NTSAITQA	241	8	14	22		R501
ENV	AITQACPK	244	8	14	22		R502
ENV	GDPEIVMII	427	8	14	22		R503
ENV	QDLLALDK	753	8	14	22		R504
ENV	NATAIAVA	923	8	14	22		R505
ENV	SAITQACPK	243	9	14	22	0.0002	R506
ENV	FAILKCNDR	269	9	14	22		R507
ENV	GDPEIVMII	426	9	14	22		R508
ENV	TITLPCRIK	482	9	14	22		R509
ENV	SLLNATAIA	920	9	14	22		R510
ENV	NCNTSAITQA	239	10	14	22		R511
ENV	TSATQACPK	242	10	14	22		R512
ENV	TSVITQACPK	242	10	14	22		R513
ENV	GFAILKCNDR	268	10	14	22		R514
ENV	GDPEIVMIISF	427	10	14	22		R515
ENV	IFAVLSIVNR	793	10	14	22		R516
ENV	LLNATAIAVA	921	10	14	22		R517
ENV	NTSAITQACPK	241	11	14	22		R518
ENV	VITQACPKVSF	244	11	14	22		R519
ENV	AGFAILKCNDR	267	11	14	22		R520
ENV	GGDPPEIVMIISF	426	11	14	22		R521
ENV	ITNWLWYIKIF	770	11	14	22		R522
ENV	IFAVLSIVNR	792	11	14	22		R523
ENV	KIEPQVAPTK	568	11	14	22		R524
ENV	FDPIIHY	255	11	15	23		R525
ENV	PAGYAILK	266	8	15	23		R526
ENV	NMWQEVGK	494	8	15	23		R527
ENV	LLNATAIA	921	8	15	23		R528
ENV	NMWQEVOKA	494	9	15	23		R529
ENV	DLLALDKWA	754	9	15	23		R530
ENV	ITNWLWYIK	770	9	15	23		R531

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GLIGRIIF	786	9	15	23		8532
ENV	DLRLNLCF	855	9	15	23		8533
ENV	SGGLEITTH	425	10	15	23		8534
ENV	IFRPGGDMR	545	10	15	23		8535
ENV	GGLIGRIIF	785	10	15	23		8536
ENV	GLIGRIIFA	786	10	15	23		8537
ENV	WDDLRLNLCF	854	10	15	23		8538
ENV	NMWQEVGKA	494	11	15	23		8539
ENV	EIFRPGGDMR	544	11	15	23		8540
ENV	GGLIGRIIFA	785	11	15	23		8541
ENV	DDLRLNLCFSY	855	11	15	23		8542
ENV	SFNCRGFF	437	8	16	25		8543
ENV	LIGRIIF	787	8	16	25		8544
ENV	VSGFLALA	846	8	16	25		8545
ENV	IISFNCRGFF	434	9	16	25		8546
ENV	SFNCRGFF	437	9	16	25		8547
ENV	ITKWLWYIK	770	9	16	25		8548
ENV	LIGRIIFA	787	9	16	25		8549
ENV	LVSGLALA	845	9	16	25		8550
ENV	IISFNCRGFF	434	10	16	25		8551
ENV	SFNCRGFF	437	10	16	25		8552
ENV	RLVSGFLALA	844	10	16	25		8553
ENV	DLRLNLCFSY	856	10	16	25		8554
ENV	TTIISFNCGGE	432	11	16	25		8555
ENV	IISFNCRGFF	434	11	16	25		8556
ENV	RLNCNTSA	236	9	17	27		8557
ENV	KAYDTEVII	72	8	17	27		8558
ENV	LINCNTSA	237	8	17	27		8559
ENV	VITOACPK	244	8	17	27		8560
ENV	RVVQREKR	587	8	17	27	0.0003	8561
ENV	VVQREKRA	588	8	17	27		8562
ENV	IGLRIIFA	788	8	17	27		8563
ENV	DLRLNLCF	856	8	17	27		8564
ENV	SVITOACPK	243	9	17	27		8565
ENV	VAPTAKRR	574	9	17	27		8566
ENV	RVVQREKRA	587	9	17	27	0.0002	8567
ENV	DAKAYDTEVII	70	10	17	27		8568
ENV	YDTEVINVWA	74	10	17	27		8569
ENV	GVAPTAKARR	573	10	17	27		8570
ENV	VFAVLSIVNR	793	10	17	27		8571
ENV	SDAKAYDTEV	69	11	17	27		8572
ENV	DTEVINVWAT	75	11	17	27		8573
ENV	NCTRPNNTNR	344	11	17	27		8574
ENV	LGVAPTAKRR	572	11	17	27		8575
ENV	IVFAVLSIVNR	792	11	17	27		8576
ENV	PIHYCTPA	260	8	18	28		8577
ENV	EYCKAMYA	498	8	18	28		8578
ENV	DTEVINVWA	75	9	18	28		8579
ENV	VLAVERYLK	666	9	18	28		8580
ENV	ELLELDKWA	754	9	18	28		8581

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	KIRPLGVA	568	8	23	37		8632
ENV	LGVAPTKA	572	8	23	36		8633
ENV	TVQCTIGIR	290	9	23	36	0.0018	8634
ENV	PLGVARTKA	571	9	23	36		8635
ENV	STVQCTIGIR	289	10	23	36		8636
ENV	VVKIEPLGVA	566	10	23	36		8637
ENV	QSNLLRAIEA	638	10	23	36		8638
ENV	ATTLFCASD	59	11	23	36		8639
ENV	VSTVQCTIGIR	288	11	23	36		8640
ENV	KVKIEPLGVA	565	11	23	36		8641
ENV	ATTLFCA	59	8	24	38		8642
ENV	EATTLFCA	58	9	24	38		8643
ENV	TTLFCASDA	60	10	24	38		8644
ENV	TRPFGGDMR	545	10	24	38		8645
ENV	ALAWDDL	851	8	25	39		8646
ENV	LALAWDDL	850	9	25	39		8647
ENV	IVQQQNNLLR	634	10	25	39		8648
ENV	FLALAWDDL	849	10	25	39		8649
ENV	GIVQQQNNLLR	633	11	25	39		8650
ENV	IVQQQNNLLR	634	11	25	39		8651
ENV	GHLALAWDDL	848	11	25	39	0.0024	8652
ENV	ITLPCRIK	483	8	26	41		8653
ENV	PLGVAPTK	571	8	26	41		8654
ENV	LAVERYLK	667	8	26	41		8655
ENV	IVQQQNNLLR	634	10	26	41		8656
ENV	GIVQQQNNLLR	633	11	26	41		8657
ENV	IVQQQNNLLR	634	11	26	41		8658
ENV	LDKWASLWN	758	11	26	41		8659
ENV	IIGDIRQAI	377	9	27	44		8660
ENV	ESQNQQEK	743	8	27	42		8661
ENV	PHLYCAPAGF	260	10	27	42		8662
ENV	PHLYCAPAGFA	260	11	27	42		8663
ENV	VGLGLRIVF	784	11	27	42		8664
ENV	IIGDIRQAI	378	8	28	44		8665
ENV	YCAPAGFA	263	8	28	44		8666
ENV	TVQCTIGIK	290	9	28	44	0.0021	8667
ENV	CTRPNNNTR	345	9	28	44		8668
ENV	ASITLTQA	619	9	28	44		8669
ENV	VSEFPIPIY	253	10	28	44		8670
ENV	STVQCTIGIK	289	10	28	44		8671
ENV	AASITLTQA	618	10	28	44		8672
ENV	ASITLTQAAR	619	10	28	44		8673
ENV	KVSEFPIPIY	252	11	28	44		8674
ENV	YCAPAGFAILK	263	11	28	44		8675
ENV	VSTVQCTIGIK	288	11	28	44		8676
ENV	GAASITLTQA	617	11	28	44		8677
ENV	AASITLTQAAR	618	11	28	44		8678
ENV	LIGLRIVF	787	8	29	45		8679
ENV	VSEFPIPIH	253	9	29	45		8680
ENV	GLIGLRIVF	786	9	29	45		8681

Table XVI
IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	FSYIHLRDF	863	9	18	28		8582
ENV	PIHIYCTPA	258	10	18	28		8583
ENV	RVLAVERYLK	665	10	18	28		8584
ENV	LFSYIHLRDF	862	10	18	28		8585
ENV	CLFSYIHLRDF	861	11	18	28		8586
ENV	NCRGIEFY	419	8	19	30		8587
ENV	GVAPTAKK	573	8	19	30		8588
ENV	VAPTAKKR	574	8	19	30		8589
ENV	VFLGFLGA	603	8	19	30		8590
ENV	LLALDKWA	755	8	19	30		8591
ENV	LGVAPTKAK	572	9	19	30		8592
ENV	GVAPTAKR	573	9	19	30		8593
ENV	AVFLGFLGA	602	9	19	30		8594
ENV	VFLGFLGAA	603	9	19	30		8595
ENV	SGKLICTTA	685	9	19	30		8596
ENV	PLGVAPTAKK	571	10	19	30		8597
ENV	LGVAPTKAKR	572	10	19	30		8598
ENV	GAFLGFLGA	601	10	19	30		8599
ENV	AVFLGFLGAA	602	10	19	30		8600
ENV	CSGKLICTTA	684	10	19	30		8601
ENV	SSNITGLLLTR	516	11	19	30		8602
ENV	PLGVAPTAKK	571	11	19	30		8603
ENV	GAFLGFLGA	601	11	19	30		8604
ENV	GCSGKLICTTA	683	11	19	30		8605
ENV	ATLKCNDK	270	8	20	31		8606
ENV	RLVSGFLA	844	8	20	31		8607
ENV	ETFRPGGGDM	544	11	20	31		8608
ENV	LIE:SONQKEK	740	11	20	31		8609
ENV	GDLIETII	427	8	21	33		8610
ENV	YCNTSGLF	446	8	21	33		8611
ENV	LLELDKWA	755	8	21	33		8612
ENV	GODLEITTH	426	9	21	33		8613
ENV	DLEITTHSF	428	9	21	33		8614
ENV	LIGLRVFA	787	9	21	33		8615
ENV	GDLIETHISF	427	10	21	33		8616
ENV	FYCNISGLF	444	10	21	33		8617
ENV	GLIGLRVFA	786	10	21	33		8618
ENV	SFEMPIIYCA	254	11	21	33		8619
ENV	GGDLIETHISF	426	11	21	33		8620
ENV	EPFYCNISGLF	443	11	21	33		8621
ENV	GGIGLRVFA	785	11	21	33		8622
ENV	TAIAVAEGTDR	925	11	21	33		8623
ENV	IGLRVFA	788	8	22	34		8624
ENV	RIVELLGR	878	8	22	34		8625
ENV	IVELLGRR	879	8	22	34		8626
ENV	RIVELLGRR	878	9	22	34		8627
ENV	NCTRPNNNTR	344	10	22	34		8628
ENV	CTRPNNTNRK	345	10	22	34		8629
ENV	PVWKEATTL	54	11	22	34		8630
ENV	TTTLFCASDA	60	11	22	34	0.0550	8631

Table XVI
ILV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Site ID NO.
ENV	ITOACPKVSF	245	10	29	45		R682
ENV	KVSFEPIIIL	252	10	29	45		R683
ENV	CAPAGFAILK	264	10	29	45		R684
ENV	GGILGLRIVF	785	10	29	45		R685
ENV	RSLEYKYKVV	558	11	29	45		R686
ENV	IIGDIRQA	377	8	30	49		R687
ENV	WASLWNWF	761	8	30	47		R688
ENV	AVLSIVNR	795	8	31	48		R689
ENV	AVALEGDIR	928	8	31	48		R690
ENV	VTEFNFMWK	102	9	31	48		R691
ENV	SFEPIIILY	254	9	31	48		R692
ENV	FAVLSIVNR	794	9	31	48		R693
ENV	SLCLESYIR	859	9	31	48		R694
ENV	IYVAECTDR	927	9	31	48		R695
ENV	NVTENFMW	101	10	31	48	0.0004	R696
ENV	AVLSIVNRVR	795	10	31	48		R697
ENV	RSCLFSYIIR	858	10	31	48		R698
ENV	AIYVAECTDR	926	10	31	48		R699
ENV	FAVLSIVNRVR	794	11	31	48		R700
ENV	DIILRSICLFSY	855	11	31	48		R701
ENV	SLCLESYIIRLR	859	11	31	48		R702
ENV	ELYKYKVVK	560	9	32	51		R703
ENV	RVVEREKRA	587	8	32	50		R704
ENV	VVEREKRA	588	8	32	50		R705
ENV	SITLTVOA	620	8	32	50		R706
ENV	ITLTVOAIR	621	8	32	50		R707
ENV	SLCLESYIIR	859	8	32	50		R708
ENV	RVVEREKRA	587	9	32	50		R709
ENV	SITLTVOAR	620	9	32	50		R710
ENV	RSCLFSYIIR	858	9	32	50		R711
ENV	DLRSICLFSYIIR	856	11	32	50		R712
ENV	SFEPIIIL	254	8	33	52		R713
ENV	RVLAVERY	665	8	33	52	0.0009	R714
ENV	QARVLAVER	663	9	33	52		R715
ENV	DIILRSICLF	855	9	33	52		R716
ENV	QARVLAVERY	663	10	33	52		R717
ENV	WDILRSICLF	854	10	33	52		R718
ENV	QLQARVLAVE	661	11	34	52		R719
ENV	IMVGGILGLR	781	11	34	54		R720
ENV	GVVFWKEA	52	8	34	53		R721
ENV	GVVFWKEA	51	9	34	53		R722
ENV	RIROGLERA	953	9	34	53		R723
ENV	LLQLITWGIK	631	10	34	53	0.0055	R724
ENV	ILLQLITWGI	650	11	34	53		R725
ENV	LSINRVROQY	797	11	34	53		R726
ENV	NLWVTVYY	44	8	35	56		R727
ENV	NCGGEFF	439	8	35	55		R728
ENV	RSCLFSY	858	8	35	55		R729
ENV	EVINRWATH	77	9	35	55		R730
ENV	SPNCGGEFF	437	9	35	55		R731

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
ENV	NITGLLLTR	519	9	35	55	0.0004	8732
ENV	EVINWATIA	77	10	35	55		8733
ENV	ISFNCGGEFF	434	10	35	55		8734
ENV	SFNCGGEFF	437	10	35	55		8735
ENV	DLASCLFSY	856	10	35	55		8736
ENV	ISFNCGGEFF	434	11	35	55		8737
ENV	SFNCGGIEF	437	8	36	56		8738
ENV	ISFNCGGIEF	434	9	36	56		8739
ENV	PIPIHYCAPA	258	10	36	56		8740
ENV	GGGDMRDNW	549	10	36	56		8741
ENV	MVGGGLIGLR	782	10	36	56		8742
ENV	SIVNRVROGY	798	10	36	56	0.0008	8743
ENV	PGGDMRDN	548	11	36	56		8744
ENV	PIPIHYCAPA	260	8	37	58		8745
ENV	ITGLLLTR	520	8	37	58		8746
ENV	DMRDNWRSEL	552	11	37	58		8747
ENV	PAGFAILK	266	8	38	59		8748
ENV	LSIVNRVR	797	8	38	59		8749
ENV	DLRSCLLF	856	8	38	59		8750
ENV	VLSIVNRVR	796	9	38	59		8751
ENV	IVNRVROGY	799	9	38	59		8752
ENV	ISLWDQSLK	121	10	38	59	0.0410	8753
ENV	DIISLWDQSLK	120	11	38	59		8754
ENV	GDMRDNWR	551	8	39	61		8755
ENV	GGDMRDNWR	550	9	39	61		8756
ENV	QACTPKVSF	248	8	40	63		8757
ENV	PIPIHYCA	258	8	40	63		8758
ENV	RDNRSELY	554	9	40	63	0.0003	8759
ENV	RDNRSELYK	554	10	40	63	0.0008	8760
ENV	TLFCASDAKA	64	11	40	63		8761
ENV	RDNRSELYK	554	11	40	63		8762
ENV	GIKQARVLA	658	11	41	63		8763
ENV	QLQARVLA	661	8	41	64		8764
ENV	TVYVGVPVWK	48	10	41	64	3.0000	8765
ENV	TVYVGVPVW	47	11	41	64	0.0000	8766
ENV	CASDAKAY	67	8	42	66		8767
ENV	LCLFSYIIR	860	8	42	66		8768
ENV	FCASDAKAY	76	9	42	66		8769
ENV	IVGGLIGLR	783	9	42	66		8770
ENV	CLFSYIHLR	861	9	42	66		8771
ENV	LFCASDAKAY	65	10	42	66	0.0004	8772
ENV	GAAGSTMGA	610	10	42	66		8773
ENV	LCLFSYIHLR	860	10	42	66		8774
ENV	LGAAGSTMGA	609	11	42	66		8775
ENV	VGGLIGLR	784	8	43	67		8776
ENV	QLTVWGK	653	8	44	69		8777
ENV	LFSYIHLR	862	8	44	69		8778
ENV	RIRQLER	953	8	44	69		8779
ENV	TLFCASDAK	61	11	44	69		8780
ENV	AAGSTMGA	611	9	45	70		8781

Table XVI
IIIY Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	TLFCASDAKA	64	10	46	72		R782
ENV	SLWDOSLK	123	8	47	75		R783
ENV	ISLWDOSLK	122	9	47	73	0.0048	R784
ENV	WDOSLPCVK	123	10	47	73		R785
ENV	RVROGYSPLSF	802	11	47	73		R786
ENV	QSLKPCVK	127	8	48	75		R787
ENV	FLGFLGAA	604	8	48	75		R788
ENV	QGYSPLSF	805	8	48	75		R789
ENV	TVWGIKQLQA	655	11	48	75		R790
ENV	GKQLQAR	658	8	49	77	0.0004	R791
ENV	WGKQLQAR	657	9	49	77		R792
ENV	TVWGIKQLQA	655	10	49	77		R793
ENV	LTWGIKQLQ	654	11	49	77		R794
ENV	FCASDAKA	66	8	50	78		R795
ENV	AGSTMGA	612	8	50	78		R796
ENV	WLWYIKIF	773	8	50	78		R797
ENV	LFCASDAKA	65	9	50	78		R798
ENV	LGIWGCSCG	679	9	50	78	0.0097	R799
ENV	TLFCASDAK	61	10	50	78		R800
ENV	LLGIWGCSCG	678	10	50	78	0.0920	R801
ENV	NLLRAIEAQQII	640	11	50	78	0.1200	R802
ENV	QLLGIWGCSCG	677	11	50	78		R803
ENV	VSTVQCTII	288	8	51	80		R804
ENV	NLLRAIEA	640	8	51	80		R805
ENV	RAIEAQQII	643	8	51	80		R806
ENV	WGKQLQA	657	8	51	80		R807
ENV	NVSTVQCTII	287	9	51	80		R808
ENV	LLRAIEAQQII	641	10	51	80		R809
ENV	GIWGCSCG	680	8	52	81		R810
ENV	TLFCASDA	61	9	52	81		R811
ENV	TLFCASDAK	64	9	52	81	0.0930	R812
ENV	RSELYKYK	64	8	54	84		R813
ENV	LLNGSLA	558	8	54	84		R814
ENV	QLLNGSLA	305	8	55	86		R815
ENV	GAGSTMGA	610	9	55	86		R816
ENV	LGAAGSTMGA	609	10	55	86		R817
ENV	STQLLNGSLA	303	10	55	86		R818
ENV	FLGAGSTMGA	608	11	55	86		R819
ENV	LFCASDAK	65	11	55	86		R820
ENV	AAGSTMGA	611	8	57	89		R821
GAG	EDTSARQA	133	8	58	91		R822
GAG	AAAIMMQK	405	8	01	33		R823
GAG	SATIMMQK	405	8	01	25		R824
GAG	TAPPIESF	508	8	01	25		R825
GAG	KDKDKELY	535	8	01	33		R826
GAG	ETIDKELY	537	8	01	25		R827
GAG	NSATIMMQK	404	9	01	25		R828
GAG	PTAPPIESF	507	9	01	33		R829
GAG	TAPPIESFR	508	9	01	33		R830
							R831

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		8832
GAG	NGRQANFLGK	461	10	01	25		8833
GAG	PTAPPESFR	507	10	01	33		8834
GAG	TAPPESFR	508	10	01	33		8835
GAG	TIDKDLVLA	538	10	01	25		8836
GAG	AAAIMQKSN	405	11	01	25		8837
GAG	SATIMMQGN	405	11	01	25		8838
GAG	NGKQANFLGK	461	11	01	25		8839
GAG	PTAPPESFR	507	11	01	33		8840
GAG	KDKKELYPL	535	11	01	25		8841
GAG	ETIDKDLVLA	537	11	01	25		8842
GAG	PAADIKK	123	8	01	50		8843
GAG	ASAOQDLK	392	8	01	50		8844
GAG	ATAQDLK	392	8	01	50		8845
GAG	PAFTAPPA	492	9	01	50		8846
GAG	AADKGVSNY	130	10	01	50		8847
GAG	SAQQDLKGGY	393	10	01	50		8848
GAG	TAQQDLKGGY	393	10	01	50		8849
GAG	GTRPGNYVQK	480	10	01	50		8850
GAG	GTRPGNYVQK	480	10	01	50		8851
GAG	ITSLPKQEQK	526	10	01	50		8852
GAG	PAADIKKDS	123	11	01	50		8853
GAG	GANSIPVGDHY	276	11	01	50		8854
GAG	ASAOQDLKGG	392	11	01	50		8855
GAG	ATAQDLKGG	392	11	01	50		8856
GAG	ETSLPKQEQK	525	11	01	50		8857
GAG	YTAVEMQR	405	8	02	50		8858
GAG	TAPPESF	508	8	02	67		8859
GAG	PTAPPESF	507	9	02	67		8860
GAG	PTAPPESFR	508	9	02	67		8861
GAG	PTAPPESFR	507	10	02	67		8862
GAG	PTAPPESFR	508	10	02	67		8863
GAG	PTAPPESFR	507	11	02	67		8864
GAG	EGRQANFLGK	462	10	02	100		8865
GAG	AADKGVSNY	129	11	02	18		8866
GAG	AADKGVSNY	129	10	04	36		8867
GAG	AAIMMQK	400	8	04	19		8868
GAG	AAIMMQKSNF	406	10	06	15		8869
GAG	AAIMMQKSNF	406	11	06	15		8870
GAG	KTVKCFNCGK	421	10	08	16		8871
GAG	NIMMQGNF	407	9	10	17		8872
GAG	GARASILR	2	8	10	16		8873
GAG	PGNFPQSR	483	8	10	16		8874
GAG	MGARASILR	1	9	10	16		8875
GAG	KIWISSKGR	472	9	10	16		8876
GAG	TGNSSQVSON	139	11	10	16		8877
GAG	NFLGKIWFSSK	468	11	10	16		8878
GAG	NFLQNRPEPTA	485	11	10	16		8879
GAG	PVAPQMR	243	8	10	16		8880
							8881

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
GAG	MMOKSNFK	409	8	10	16		8882
GAG	MMORGNEK	409	8	10	16		8883
GAG	KLDKWEKIR	12	9	10	16		8884
GAG	GGKKKYKLR	24	9	10	16	0.0001	8885
GAG	RDTKEALDK	97	9	10	16		8886
GAG	ALSPRTLNA	167	9	10	16		8887
GAG	IMMOKSNFK	408	9	10	16		8888
GAG	LGKIWPSSK	470	9	10	16		8889
GAG	FGKKKKYKLR	23	10	10	16		8890
GAG	GGKKKYKLR	24	10	10	16		8891
GAG	QALSPRTLNA	166	10	10	16		8892
GAG	AGIPAPGQMR	241	10	10	16		8893
GAG	GASLEEMTA	364	10	10	16		8894
GAG	FLGKIWPSSK	469	10	10	16		8895
GAG	FLQNHPTA	486	10	10	16		8896
GAG	TAPPAESGF	496	10	10	16		8897
GAG	KLDKWEKIRL	12	11	10	16		8898
GAG	FGKKKYKLR	23	11	10	16		8899
GAG	LGKIWPSSKGR	470	11	10	16		8900
GAG	PTAPPAESGF	495	11	10	16		8901
GAG	ATIMMQRGNF	406	10	11	28		8902
GAG	ATIMMQRGNF	406	11	11	28		8903
GAG	PSKQEPIDK	528	11	11	18		8904
GAG	SSKGRPGNF	476	9	11	18		8905
GAG	TTSTLQEQIA	260	10	11	17		8906
GAG	DVKDTKEA	95	8	11	17		8907
GAG	HPVGDY	279	8	11	17		8908
GAG	SLEEMMTA	366	8	11	17		8909
GAG	MSQVTNSA	391	8	11	17		8910
GAG	IMMOKSNF	408	8	11	17		8911
GAG	IDVKDTKEA	94	9	11	17		8912
GAG	ASLEEMMTA	365	9	11	17		8913
GAG	AMSQVTNSA	390	9	11	17		8914
GAG	TKCFNCGK	422	9	11	17		8915
GAG	TVKCFNCGK	422	9	11	17		8916
GAG	EAMSQVTNSA	389	10	11	17		8917
GAG	PSSKGRPGNF	475	10	11	17		8918
GAG	GTSTLQEQIA	259	11	11	17		8919
GAG	TIMMQRGNF	407	10	12	21		8920
GAG	QTGSEELR	71	8	12	19		8921
GAG	KSKKKAQQA	112	10	12	19		8922
GAG	KSKKKAQQA	112	11	12	19		8923
GAG	PGKKKYK	23	8	12	19		8924
GAG	TYCVIQK	86	8	12	19		8925
GAG	DTKEALEK	98	8	12	19		8926
GAG	MLNIVGGII	208	8	12	19		8927
GAG	NIVGGIIQA	210	8	12	19		8928
GAG	IVGGIIQA	211	8	12	19		8929
GAG	STLQEQIA	262	8	12	19		8930
GAG	PTSILDIR	303	8	12	19		8931

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0301	SIQ ID NO.
GAG	LTSLSLF	549	8	12	19		8932
GAG	GSEELRSY	73	9	12	19		8933
GAG	ATLYCVIHK	85	9	12	19		8934
GAG	KDYEALKE	97	9	12	19		8935
GAG	MMNLVGGII	207	9	12	19		8936
GAG	NIVGGIIQAA	210	9	12	19		8937
GAG	TSTLQEQIA	261	9	12	19		8938
GAG	PLTSLKSLF	548	9	12	19		8939
GAG	PLTSLRSY	548	9	12	19		8940
GAG	TGSEELRSY	72	10	12	19		8941
GAG	VATLYCVIHK	84	10	12	19		8942
GAG	NAOCQMVHQ	158	10	12	19		8943
GAG	NMMLNIVGGII	206	10	12	19		8944
GAG	MLNIVGGIIQA	208	10	12	19		8945
GAG	YSPISLDIR	301	10	12	19		8946
GAG	RAHQASQEVK	329	10	12	19		8947
GAG	RLKPGKKKY	20	11	12	19		8948
GAG	TVATLYCVIHK	83	11	12	19		8949
GAG	MMNLVGGIIQ	207	11	12	19		8950
GAG	MLNIVGGIIQA	208	11	12	19		8951
GAG	TSILDIRQGP	304	11	12	19		8952
GAG	TIMMORGNF	407	9	13	22		8953
GAG	PGNLFQNR	483	8	13	21		8954
GAG	IARNCRAPR	434	9	13	21		8955
GAG	KIWPNSNKR	472	9	13	21		8956
GAG	NCKEGHIAH	427	10	13	21		8957
GAG	IARNCRAPRK	434	10	13	21		8958
GAG	IARNCRAPRKK	434	11	13	21		8959
GAG	NFLGRIWTSNK	468	11	13	21		8960
GAG	KGRPGNLFQ	478	11	13	21		8961
GAG	KLKIIWVA	31	8	13	20		8962
GAG	RIEVKDTK	93	8	13	20		8963
GAG	IARNCRKA	433	8	13	20		8964
GAG	LTSLSLF	549	8	13	20		8965
GAG	IVKCFNCGK	422	9	13	20		8966
GAG	CGKEGHIAH	428	9	13	20		8967
GAG	EGHIAHNCR	431	9	13	20		8968
GAG	LGRKIWPSNK	470	9	13	20		8969
GAG	KLKIIWVASR	31	10	13	20		8970
GAG	RIEVKDTKEA	93	10	13	20		8971
GAG	TLRALGPGA	356	10	13	20		8972
GAG	EGHIAHNCRA	431	10	13	20		8973
GAG	HIARNCRAPR	433	10	13	20		8974
GAG	FLGKIWPSNK	469	10	13	20		8975
GAG	EVKDTKEALD	95	11	13	20		8976
GAG	FSPEVPMETA	185	11	13	20		8977
GAG	ALEWDRVIIPV	230	11	13	20		8978
GAG	KTILRALGPGA	355	11	13	20		8979
GAG	HIARNCRAPRK	433	11	13	20		8980
GAG	LGKIWPSNKG	470	11	13	20		8981

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
GAG	NSSQVSQNY	144	9	14	31		8982
GAG	KSKKKAQQA	112	9	14	22		8983
GAG	NCCKEGIIAK	427	10	14	22		8984
GAG	IAKNCRAPRKK	434	11	14	22		8985
GAG	EYIMFTA	188	8	14	22		8986
GAG	RGINFRNQIK	412	9	14	22		8987
GAG	CGKEGIIAK	428	9	14	22		8988
GAG	EGIIAKNCR	431	9	14	22		8989
GAG	EGIIAKNCRA	431	10	14	22		8990
GAG	PSNKGRGNF	475	10	14	22		8991
GAG	TAIPESFRF	496	10	14	22		8992
GAG	TVATLYCVIIQ	83	11	14	22		8993
GAG	IVQNAQGMV	155	11	14	22		8994
GAG	PTAPIESFRF	495	11	14	22		8995
GAG	SSQVSQNY	145	8	15	31		8996
GAG	VSONYHVQNA	149	11	15	26		8997
GAG	RSLYNTVATL	78	11	15	24		8998
GAG	TLVCVHQR	86	8	15	23		8999
GAG	FTALSEGA	193	8	15	23		9000
GAG	AAEWDRVII	230	8	15	23		9001
GAG	WDRVHPIVII	233	8	15	23		9002
GAG	RGNFRNQR	412	8	15	23		9003
GAG	TAIPESF	496	8	15	23		9004
GAG	LASLSLF	549	8	15	23		9005
GAG	VLSGGKLLDA	7	9	15	23		9006
GAG	LFNTVATLY	80	9	15	23		9007
GAG	ATLYCVHQR	85	9	15	23	0.0150	9008
GAG	MTALSEGA	192	9	15	23		9009
GAG	EAIEWDRVII	229	9	15	23		9010
GAG	WDRVHPIVII	233	9	15	23		9011
GAG	PTAPIESF	495	9	15	23		9012
GAG	TAIPESFR	496	9	15	23		9013
GAG	PLASLSLF	548	9	15	23		9014
GAG	VLSGGKLLDA	6	10	15	23		9015
GAG	SGGKLDAWEK	9	10	15	23		9016
GAG	ELRSLYNTVA	76	10	15	23		9017
GAG	SLFNTVATLY	79	10	15	23		9018
GAG	VATLYCVHQR	84	10	15	23		9019
GAG	KIEEQNKSK	105	10	15	23		9020
GAG	PMFTALSEGA	191	10	15	23		9021
GAG	RAEQATQDVK	329	10	15	23		9022
GAG	PTAPIESFR	495	10	15	23		9023
GAG	ASVLSGGKLLD	5	11	15	23		9024
GAG	LSGGKLDAWE	8	11	15	23		9025
GAG	PGLETSECCR	50	11	15	23		9026
GAG	KIEEQNKSKK	105	11	15	23		9027
GAG	RLIPVIAAGPIA	235	11	15	23		9028
GAG	MMORGNGFRN	409	11	15	23		9029
GAG	IAKNCRAPRK	434	10	16	25		9030
GAG	LSGGKLDA	8	8	16	25		9031

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
GAG	LDWWEKIR	13	8	16	25		9032
GAG	NAOQGMVII	158	8	16	25		9033
GAG	PVSILDIK	303	8	16	25		9034
GAG	ILKALGPA	357	8	16	25		9035
GAG	KLDWWEKIR	12	9	16	25		9036
GAG	GGKKYRLK	24	9	16	25		9037
GAG	TILKALGPA	356	9	16	25		9038
GAG	ILKALGPA	357	9	16	25		9039
GAG	VLAEMSQA	386	9	16	25	0.0003	9040
GAG	LDWWEKIR	13	10	16	25		9041
GAG	PGKKYRLK	23	10	16	25		9042
GAG	GGKKYRLKII	24	10	16	25		9043
GAG	GLLETSEGR	51	10	16	25		9044
GAG	YSPVSILDIK	301	10	16	25		9045
GAG	KILKALGPA	355	10	16	25		9046
GAG	TILKALGPA	356	10	16	25		9047
GAG	AATLEEMMTA	364	10	16	25		9048
GAG	RVLAEAMSQA	385	10	16	25		9049
GAG	GGKLDWWEKI	10	11	16	25		9050
GAG	KLDWWEKIRL	12	11	16	25		9051
GAG	PGKKYRLK	23	11	16	25		9052
GAG	VSILDIKQPK	304	11	16	25		9053
GAG	KILKALGPA	355	11	16	25		9054
GAG	PAATLEEMMT	363	11	16	25		9055
GAG	IIAKNCRAPRK	433	11	16	25		9056
GAG	LAEMSQA	387	8	17	27		9057
GAG	RLKILVVA	31	8	17	27		9058
GAG	LSPTLNA	168	8	17	27		9059
GAG	PIPGQMR	243	8	17	27		9060
GAG	GGKLDWWEK	10	9	17	27		9061
GAG	DAWWEKIRL	14	9	17	27		9062
GAG	LLETSEGR	52	9	17	27		9063
GAG	RLKILVWASR	31	10	17	27		9064
GAG	LDKIEEQNK	103	10	17	27		9065
GAG	AGPIPGQMR	241	10	17	27		9066
GAG	ALDKIEEQNK	102	11	17	27		9067
GAG	LSPTLNAWV	168	11	17	27		9068
GAG	IIAGPIPGQMR	240	11	17	27		9069
GAG	PIPGQMR	243	11	17	27		9070
GAG	PGATLEEMMT	363	11	17	27		9071
GAG	RSLYNTVA	78	8	18	29		9072
GAG	IAKNCRAPR	434	9	18	29	0.0009	9073
GAG	LDKWEKIR	13	8	18	28		9074
GAG	PVGDYKR	281	8	18	28		9075
GAG	PDCKTILR	352	8	18	28		9076
GAG	DCCKTILRA	353	8	18	28		9077
GAG	IIAKNCRA	433	8	18	28		9078
GAG	PDCKTILRA	352	9	18	28		9079
GAG	ILRALGPA	357	9	18	28		9080
GAG	LDKWEKIRL	13	10	18	28		9081

Table XVI
 111V ΔQ3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
GAG	SILDIKQGP	305	10	18	28		9082
GAG	IIIAKNCRAPR	433	10	18	28		9083
GAG	IIAGPIAPQPM	240	11	18	28		9084
GAG	NANPCKTLR	349	11	18	28		9085
GAG	LARNCRAPRK	434	11	19	30		9086
GAG	PVLIAGPA	238	8	19	30		9087
GAG	PIAPQMR	243	8	19	30		9088
GAG	LDIKQGP	307	8	19	30		9089
GAG	ILDIKQGP	306	9	19	30		9090
GAG	PSIAKARVLA	380	9	19	30		9091
GAG	AGPIAPQMR	241	10	19	30		9092
GAG	IAPQMR	244	10	19	30		9093
GAG	DIKQPKPEFF	308	10	19	30		9094
GAG	RLRTGGKKKY	20	11	19	30		9095
GAG	IVWASRELER	35	11	19	30		9096
GAG	PIAPQMR	243	11	19	30		9097
GAG	LDIKQPKPEFF	307	11	19	30		9098
GAG	DIKQPKPEFF	308	11	19	30		9099
GAG	GGPSIAKARVLA	378	11	19	30		9100
GAG	PSIAKARVLA	380	11	19	30		9101
GAG	LARNCRAPRK	434	9	20	32		9102
GAG	LARNCRAPRK	434	10	20	32		9103
GAG	PGKKKKYR	23	8	20	31		9104
GAG	TAPPAESF	496	8	20	31		9105
GAG	IMMQKGNFR	408	9	20	31		9106
GAG	PTAPPAESF	495	9	20	31		9107
GAG	IVWASRELER	35	10	20	31	0.0099	9108
GAG	IIIAKNCRAPR	433	10	20	31		9109
GAG	IIIAKNCRAPR	34	11	20	31		9110
GAG	IIIAKNCRAPR	433	11	20	31		9111
GAG	IIIAKNCRA	433	8	21	33		9112
GAG	EGHILARNCR	431	9	21	33		9113
GAG	NLQGMVLIQA	158	10	21	33		9114
GAG	EGHILARNCR	431	10	21	33		9115
GAG	QSRPEPTAPPA	488	11	21	33		9116
GAG	KIWPSTIKGR	472	9	22	35		9117
GAG	EVKDTKEA	95	8	22	34	0.0770	9118
GAG	ETINEEAA	224	8	22	34		9119
GAG	DTLLVQNA	343	8	22	34		9120
GAG	GGPSIAKAR	378	8	22	34		9121
GAG	TDLLVQNA	342	9	22	34		9122
GAG	VGGHSHKAR	377	9	22	34		9123
GAG	SLYNTVATLY	79	10	22	34		9124
GAG	MLKETINEEA	221	10	22	34		9125
GAG	MTDILLVQNA	341	10	22	34		9126
GAG	VGGPSIAKAR	376	10	22	34		9127
GAG	QMLKETINEEA	220	11	22	34		9128
GAG	MLKETINEEA	221	11	22	34		9129
GAG	WMTDILLVQ	340	11	22	34		9130
GAG	QGVGGPSIKA	375	11	22	34		9131

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
GAG	LGKIWPISIKG	470	11	22	34		9132
GAG	NFLGKIWPISIK	468	11	23	37		9133
GAG	KIEERQNK	105	8	23	36		9134
GAG	QVGVPISII	373	8	23	36		9135
GAG	GVGVPISIK	376	8	23	36		9136
GAG	VGGPSIIKA	377	8	23	36		9137
GAG	MMQRGNFR	409	8	23	36		9138
GAG	QGVGVPISIK	375	9	23	36		9139
GAG	GVGVPISIIKA	376	9	23	36		9140
GAG	LGKIWPISIK	470	9	23	36		9141
GAG	ACQGVGGPSII	373	10	23	36		9142
GAG	QVGVPISIIKA	375	10	23	36		9143
GAG	FLGKIWPISIK	469	10	23	36	0.0200	9144
GAG	PSIIKGRPGNF	475	10	23	36		9145
GAG	TACQGVGGPS	372	11	23	36		9146
GAG	ACQGVGGPSII	373	11	23	36		9147
GAG	NCQKEGILAR	427	10	24	38		9148
GAG	KVIEEKAF	178	8	24	38		9149
GAG	CKQEGILAR	428	9	24	38		9150
GAG	WVKVIEKAF	176	10	24	38		9151
GAG	YSIYSILDIR	301	10	24	38		9152
GAG	NFLGKIWPISII	468	10	25	40		9153
GAG	PVSILDIR	303	8	25	39		9154
GAG	LGKIWPISII	470	8	25	39		9155
GAG	KDTKEALDK	97	9	25	39		9156
GAG	WVKVIEKA	176	9	25	39		9157
GAG	FLGKIWPISII	469	9	25	39		9158
GAG	LVWASRELER	35	11	25	39		9159
GAG	NAWVKVIEEK	174	11	25	39		9160
GAG	VSILDIRQUPK	304	11	25	39		9161
GAG	LVWASRELER	35	10	26	41		9162
GAG	ILVWASRELE	34	11	26	41		9163
GAG	CFNCKQEGHIA	425	11	26	41		9164
GAG	NCQKEGIIA	427	9	27	43		9165
GAG	NCQKEGIIA	427	9	27	43		9166
GAG	RFKTLRA	323	8	27	42		9167
GAG	IMMQGNF	408	8	27	42		9168
GAG	CKQEGIIA	428	8	27	42		9169
GAG	CKQEGIIA	428	8	27	42		9170
GAG	MVIQAIISPR	163	9	27	42	0.1800	9171
GAG	VDRFFKTLR	321	9	27	42		9172
GAG	QMVIIQAIISPR	162	10	27	42	0.0260	9173
GAG	YVDRFFKTLR	320	10	27	42		9174
GAG	VDRFFKTLR	321	10	27	42		9175
GAG	FFKTLRAEQ	324	10	27	42		9176
GAG	RAEQATQEVK	329	10	27	42		9177
GAG	NAWVKVIEEK	174	11	27	42		9178
GAG	YVDRFFKTLR	320	11	27	42		9179
GAG	RFKTLRAEQ	323	11	27	42		9180
GAG	RFYKTLRAEQ	323	11	27	42		9181

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
GAG	NANPCKTILK	349	11	27	42		9182
GAG	CFCNGREGIL	425	11	27	42		9183
GAG	KGRIGNFLOS	478	11	28	44		9184
GAG	NFQSRPEPTA	483	11	28	44		9185
GAG	KVVEEKAF	178	8	28	44		9186
GAG	RFYKTLKA	323	8	28	44		9187
GAG	PDCKTILK	352	8	28	44		9188
GAG	DKCKTILKA	353	8	28	44		9189
GAG	WVKVVEEKA	176	9	28	44		9190
GAG	VDRFYKTLR	321	9	28	44		9191
GAG	PDCKTILKA	352	9	28	44		9192
GAG	WVKVVEEKAF	176	10	28	44		9193
GAG	PFQDVVDREY	316	10	28	44		9194
GAG	YVDRFYKTLR	320	10	28	44	0.00033	9195
GAG	VDRFYKTLRA	321	10	28	44		9196
GAG	GATLEEMMTA	364	10	28	44		9197
GAG	FQSRPEPTA	486	10	28	44		9198
GAG	PFQDVVDREY	316	11	28	44	0.00015	9199
GAG	YVDRFYKTLR	320	11	28	44		9200
GAG	GARASVLSGG	2	11	29	46		9201
GAG	ASVLSGGK	5	8	29	45		9202
GAG	NLQGMVHI	158	8	29	45		9203
GAG	WVKVVEEK	176	8	29	45		9204
GAG	WDRLIIPVII	233	8	29	45		9205
GAG	RDYVDRFY	318	8	29	45		9206
GAG	RASVLSGGK	4	9	29	45		9207
GAG	ASPRTLNA	167	9	29	45	0.0050	9208
GAG	WDRLIIPVIA	233	9	29	45		9209
GAG	RDYVDRFYK	318	9	29	45	0.0007	9210
GAG	QASPRTLNA	166	10	29	45		9211
GAG	NAWVKVVEEK	174	10	29	45		9212
GAG	IVQNLOGQMV	155	11	29	45		9213
GAG	AAEWDRLIIPV	230	11	29	45		9214
GAG	PGNFQSR	483	8	30	48		9215
GAG	NAWVKVVEEK	174	10	30	47	0.0004	9216
GAG	KIRLRPGGKKK	18	11	30	47		9217
GAG	WVKVVEEK	176	8	31	47	0.00033	9218
GAG	MLKDTINEEA	221	10	32	50		9219
GAG	QMLKDTINEEA	220	11	32	50		9220
GAG	MLKDTINEEA	221	11	32	50		9221
GAG	DTINEEA	223	8	33	52		9222
GAG	DTINEEA	224	8	33	52		9223
GAG	KDTINEEA	223	9	33	52		9224
GAG	RDYVDRFFK	318	9	33	52		9225
GAG	PFQDVVDREY	316	11	33	52		9226
GAG	RLRPGGKKK	20	9	34	53		9227
GAG	RLRPGGKKKY	20	10	34	53		9228
GAG	PIPVGEIYKR	279	10	34	53		9229
GAG	PIPVGEIY	279	8	35	55	0.00033	9230
GAG	RDYVDRFF	318	8	35	55		9231

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	N _o of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SFQ ID NO.
GAG	PIPVGEIYK	279	9	35	55	0.0002	9232
GAG	PGIHKARVLA	380	9	35	55		9233
GAG	IFRDYVDRFF	316	10	35	55		9234
GAG	WMTETLLVQN	340	11	35	55		9235
GAG	GGPGHKARVL	378	11	35	55		9236
GAG	PGIHKARVLAIE	380	11	35	55		9237
GAG	DTKEALDK	98	8	36	56	0.0003	9238
GAG	ISPTLNA	168	8	36	56		9239
GAG	QGVGGPGII	375	8	36	56		9240
GAG	QSRPEPTA	488	8	36	56		9241
GAG	QGVGGPGHK	375	9	36	56	0.0004	9242
GAG	MTETLLVQNA	341	10	36	56		9243
GAG	ACQGVGGPGH	373	10	36	56		9244
GAG	QGVGGPGHKA	373	10	36	56		9245
GAG	ISPTLNAWV	168	11	36	56		9246
GAG	TACQGVGGPG	372	11	36	56	0.0001	9247
GAG	ACQGVGGPGH	373	11	36	56		9248
GAG	QGVGGPGHKA	375	11	36	56		9249
GAG	QGVGGPGHKA	160	8	37	58		9250
GAG	ETLLVQNA	343	8	37	58		9251
GAG	GVGGPGHK	376	8	37	58	0.0012	9252
GAG	GVGGPGHKA	377	8	37	58		9253
GAG	GGPGHKAR	378	8	37	58		9254
GAG	GVGGPGHKA	376	9	37	58		9255
GAG	GVGGPGHKAR	377	9	37	58		9256
GAG	AAEWDIRLII	376	10	37	58	0.0013	9257
GAG	AAEWDIRLII	220	8	39	61		9258
GAG	PVGEIYKR	229	9	39	61		9259
GAG	TVATLYCVII	281	8	40	63	0.0003	9260
GAG	NTVATLYCVII	83	9	40	63		9261
GAG	SILDIRQGP	82	10	40	63		9262
GAG	FSPEVIMFSA	305	10	40	63	0.3100	9263
GAG	DIRQGPKEPF	185	11	40	63		9264
GAG	DIRQGPKEPF	308	10	41	64		9265
GAG	DIRQGPKEPF	307	11	41	64		9266
GAG	VATLYCVII	308	11	41	64		9267
GAG	LDIRQGP	84	8	42	66		9268
GAG	LDIRQGP	307	8	42	66		9269
GAG	NTMLNTVGGH	306	9	42	66	0.0420	9270
GAG	TMLNTVGGH	207	10	42	66		9271
GAG	TMLNTVGGH	207	9	43	67		9272
GAG	KGCWKCKG	444	8	43	67		9273
GAG	KIRLRPGK	18	9	44	69		9274
GAG	ASRELERFA	38	9	44	69		9275
GAG	KIRLRPGKK	18	10	44	69		9276
GAG	WASRELERFA	37	10	44	69	1.9000	9277
GAG	QMRPRGSDIA	248	11	44	69		9278
GAG	KGCWKCKCKG	444	11	44	69		9279
GAG	FSALSEGA	193	8	45	70		9280
GAG							9281

Table XVI
 HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy [%]	A*0301	SI:Q ID NO.
GAG	PGOMREPR	246	8	45	70		9282
GAG	MESALSEGA	192	9	45	70		9283
GAG	CGKEGHIQMK	449	9	45	70		9284
GAG	PMFSALSEGA	191	10	45	70		9285
GAG	KCKEGEHIQMK	448	10	45	70		9286
GAG	ASRELERF	38	8	46	72		9287
GAG	EVPMFSA	188	8	46	72		9288
GAG	TLFEMMTA	366	8	46	72		9289
GAG	WASRELERF	37	9	46	72		9290
GAG	ATLEEMMTA	365	9	46	72	0.0003	9291
GAG	MLNTVGGII	208	8	47	73		9292
GAG	MLTVGGIIQA	210	8	47	73		9293
GAG	TVGGIIQAA	211	8	47	73		9294
GAG	NTVGGIIQAA	210	9	47	73		9295
GAG	MLNTVGGIIQA	208	10	47	73		9296
GAG	MLNTVGGIIQA	208	11	47	73	0.0005	9297
GAG	WASRELER	37	8	48	75		9298
GAG	GCWKCKEGEII	445	10	48	75		9299
GAG	RLRPGGKK	20	8	49	77		9300
GAG	QMKDCTER	455	8	49	77		9301
GAG	QMKDCTERQA	455	10	49	77		9302
GAG	EGIIQMKDCTE	452	11	49	77		9303
GAG	AFSPEVPMF	184	10	50	78		9304
GAG	KAFSPEVPMF	183	11	50	78	0.0007	9305
GAG	RAPRKCCWK	439	10	51	80		9306
GAG	KDCTERQA	457	8	52	83		9307
GAG	KDCTERQANF	457	10	52	83		9308
GAG	CTERQANFLG	459	11	52	83		9309
GAG	CTERQANF	458	9	52	81		9310
GAG	NCRAPRK	437	8	53	84		9311
GAG	TINEEAIEWD	225	11	53	83		9312
GAG	KTLRAEQA	326	8	54	84		9313
GAG	FSPEVPMF	185	9	54	84		9314
GAG	CTERQANF	459	8	55	87		9315
GAG	WILLGLNK	289	8	57	89		9316
GAG	KARVLAEA	383	8	57	89		9317
GAG	CFNCGKEGII	425	9	57	89	0.0003	9318
GAG	ILGLNKIVR	290	10	57	89		9319
GAG	KCFNCGKEGII	424	10	57	89		9320
GAG	WILLGLNKIVR	289	11	57	89		9321
GAG	ILGLNKIVRMY	291	11	57	89		9322
GAG	ILGLNKIVR	291	9	58	91	0.0008	9323
GAG	LGLNKIVRMY	292	10	58	91	0.0004	9324
GAG	LLVQNANPDC	345	11	58	91		9325
GAG	LGLNKIVR	292	8	59	92		9326
GAG	LVQNANPDC	346	10	59	92	0.0002	9327
GAG	GLNKIVRMY	293	9	60	94	0.0100	9328
GAG	QAAMQMLK	216	8	61	95		9329
GAG	GGHQAMQM	213	11	61	95		9330
GAG	RTLNAWVK	171	8	63	98	0.0410	9331

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ 0.0001	SEQ ID NO.
GAG	QGPKEPR	311	8	63	98		9332
GAG	PFDRYVDR	316	8	63	98		9333
GAG	QGIKEPRDY	311	9	63	98		9334
GAG	QAIPEAAAGVG	34	10	63	98	0.0004	9335
NEF	RAQAEPA	32	11	01	33		9336
NEF	RAQAEPA	32	8	01	17		9337
NEF	RAQAEPA	32	9	01	17		9338
NEF	QTEPAAGVG	32	11	01	17		9339
NEF	RAEPAADGVG	32	11	01	17		9340
NEF	RTEPAAGVG	32	11	01	17		9341
NEF	QAEPAAGVG	33	11	01	17		9342
NEF	QAFTAAGVG	33	11	01	17		9343
NEF	AADGVGAVSR	42	10	09	15		9344
NEF	SSVGVWTA	8	8	09	15		9345
NEF	VGWPAIRER	11	9	10	17		9346
NEF	AAEGVGAA	42	8	10	16		9347
NEF	FDSRLAFII	310	8	10	16		9348
NEF	FDSRLAFIII	310	9	10	16		9349
NEF	DSRLAFIII	311	8	10	16		9350
NEF	AVSQDLDK	48	8	10	16		9351
NEF	PLRIMTFK	102	8	10	16		9352
NEF	KGAFLSF	109	8	10	16		9353
NEF	GAFDLSFF	110	8	10	16		9354
NEF	GAVSQDLDK	47	9	10	16		9355
NEF	QVPLRPMTF	100	9	10	16		9356
NEF	KGAFLSFF	109	9	10	16		9357
NEF	GLEGLYSK	125	9	10	16		9358
NEF	MARELIPEY	321	9	10	16		9359
NEF	VGAVSQDLDK	46	10	10	16		9360
NEF	QVPLRPMTEK	100	10	10	16		9361
NEF	GAFDLSFLK	110	10	10	16		9362
NEF	GGLEGLYSK	124	10	10	16		9363
NEF	CFKLVVDPR	226	10	10	16		9364
NEF	IMARELIPEY	320	10	10	16		9365
NEF	MARELIPEY	321	10	10	16		9366
NEF	GVGAVSQDLK	45	11	10	16		9367
NEF	KGAFLSFLK	109	11	10	16		9368
NEF	KGLEGLYSK	122	11	10	16		9369
NEF	WCFKLVVDPR	225	11	10	16		9370
NEF	IMARELIPEY	320	11	10	16		9371
NEF	MARELIPEY	321	11	10	16		9372
NEF	AVSRDLEK	48	11	10	16		9373
NEF	VSRDLEKH	49	8	11	17		9374
NEF	KLVVDPR	228	8	11	17		9375
NEF	GAVSRDLEK	47	9	11	17	0.0002	9376
NEF	AVSRDLEKH	48	9	11	17		9377
NEF	VGAVSRDLEK	46	10	11	17		9378
NEF	GAVSRDLEKH	47	10	11	17		9379
NEF	VSRDLEKHGA	49	10	11	17		9380
NEF	NSLLIPICOH	255	10	11	17		9381

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SHQ ID NO.
NEF	GVGAVSRDLE	45	11	11	17		9382
NEF	VGAVSRDLEK	46	11	11	17		9383
NEF	AVSRDLEKIIG	48	11	11	17		9384
NEF	AATNADCA	70	8	12	22		9385
NEF	ATNADCAWLE	71	11	12	22		9386
NEF	EGENNCLLII	251	9	12	19		9387
NEF	PMYTGAF	105	8	12	19		9388
NEF	YTIQGVGR	207	8	12	19		9389
NEF	TAATNADCA	69	9	12	19		9390
NEF	DILDLWVYII	185	9	12	19		9391
NEF	NTAATNADCA	68	10	12	19		9392
NEF	QDILDLWVYII	184	10	12	19		9393
NEF	ITSSNTAATNA	64	11	12	19		9394
NEF	PLRPMYTKGA	102	11	12	19		9395
NEF	PGIRYPLTF	211	9	13	21		9396
NEF	PGIRYPLTF	211	9	13	21		9397
NEF	KGNNCLLIH	251	9	13	21		9398
NEF	WYIITQGF	191	8	13	20		9399
NEF	GRYPLTF	213	8	13	20		9400
NEF	GTRPLTF	213	8	13	20		9401
NEF	SSNTAATNA	66	9	13	20		9402
NEF	WYIITQGF	191	9	13	20		9403
NEF	YTIQGVGR	207	9	13	20		9404
NEF	TSSNTAATNA	65	10	13	20		9405
NEF	VDLSIFLKEK	112	10	13	20		9406
NEF	DLWVYITQGF	188	10	13	20		9407
NEF	AVDLSIFLKEK	111	11	13	20		9408
NEF	LDLWVYITQGF	187	11	13	20		9409
NEF	DLWVYITQGF	188	11	13	20		9410
NEF	PGPGIRYPLTF	209	11	13	20		9411
NEF	PGPGTRFPLTF	209	11	13	20		9412
NEF	VDLSIFLK	112	8	14	22		9413
NEF	DGLIYSKK	172	8	14	22		9414
NEF	ELIPEFYK	324	8	14	22		9415
NEF	ATSSNTAA	63	9	14	22	0.0003	9416
NEF	AVDLSIFLK	111	9	14	22	0.0740	9417
NEF	LDGLIYSKK	171	9	14	22		9418
NEF	DGLIYSKKR	172	9	14	22		9419
NEF	SLIIPICQII	236	9	14	22		9420
NEF	GAITSSNTAA	62	10	14	22		9421
NEF	GLDGLIYSKK	125	10	14	22		9422
NEF	LDGLIYSKKR	171	10	14	22		9423
NEF	IIGAITSSNTAA	61	11	14	22		9424
NEF	GGLDGLIYSKK	124	11	14	22		9425
NEF	GLDGLIYSKKR	125	11	14	22		9426
NEF	PAADGVGA	41	8	15	23		9427
NEF	ITSSNTAA	64	8	15	23		9428
NEF	CLLIIPMSQII	256	9	15	23		9429
NEF	NCLLIIPMSQII	255	10	15	23		9430
NEF	EAQEEVEVGF	82	10	16	25		9431

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	RDLEKIIQA	51	8	16	25		9432
NEF	LDGLIYSK	171	8	16	25		9433
NEF	GLDGLIYSK	125	9	16	25		9434
NEF	GGIDGLIYSK	124	10	16	25		9435
NEF	KGGLDGLIYSK	122	11	16	25		9436
NEF	RFPLTFGWCF	216	10	17	27		9437
NEF	RFPLTFGWCF	216	11	17	27		9438
NEF	ADCAWLEA	74	8	17	27		9439
NEF	FFPDWQNY	199	8	17	27		9440
NEF	LLHMSQH	257	8	17	27		9441
NEF	NADCAWLEA	73	9	17	27		9442
NEF	GFPPDWQNY	198	9	17	27		9443
NEF	YTFPGIRY	207	9	17	27		9444
NEF	FDLSFLKEK	112	10	17	27		9445
NEF	QGFPPDWQNY	196	10	17	27		9446
NEF	AFDLSFLKEK	111	11	17	27		9447
NEF	FDSFLK	112	8	18	28		9448
NEF	LLHPCQH	257	8	18	28		9449
NEF	AFDLSFLK	111	9	18	28		9450
NEF	KGLEGLY	124	8	19	30		9451
NEF	KGLEGLY	122	9	19	30		9452
NEF	DLDLWVY	185	8	20	31		9453
NEF	YTFPGIR	207	8	20	31		9454
NEF	QDLDLWVY	184	9	20	31		9455
NEF	PLRPMTYKAA	102	10	20	31		9456
NEF	QVPLRPMTYK	100	11	20	31		9457
NEF	PAAEVGGA	41	8	21	33		9458
NEF	GGIDGLIY	124	8	21	33		9459
NEF	WVYIITQGY	191	8	21	33		9460
NEF	YTFPGIR	207	8	21	33		9461
NEF	PLRPMTYKA	102	9	21	33		9462
NEF	KGGLDGLIY	122	9	21	33		9463
NEF	WVYIITQGY	191	9	21	33		9464
NEF	DLWVYIITQGY	188	10	21	33		9465
NEF	DLWVYIITQGY	187	11	21	33		9466
NEF	DLWVYIITQGY	188	11	21	33		9467
NEF	LSFLKEK	114	8	22	34		9468
NEF	ELIPEYK	324	8	22	34		9469
NEF	DLSFLKEK	113	9	22	34		9470
NEF	ELDLWVYII	185	9	22	34		9471
NEF	GLIYSKKR	173	8	23	36		9472
NEF	PLRPMTYKGA	102	10	25	39		9473
NEF	AITSNTA	63	8	27	42		9474
NEF	LSHFLKEK	114	8	27	42		9475
NEF	GAITSNTA	62	9	27	42		9476
NEF	DLSHFLKEK	113	9	27	42		9477
NEF	IIGAITSSNTA	61	10	27	42		9478
NEF	FILDWVY	185	8	33	52		9479
NEF	ILDLWVYII	186	8	34	53		9480
NEF	YFPDWQNY	199	8	36	56		9481

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
NEF	QGYFDWQNY	196	10	36	56	0.0004	9482
NEF	LTFGWCFK	221	8	39	61		9483
NEF	PLTFGWCFK	219	9	39	61		9484
NEF	PLTFGWCF	219	8	43	67		9485
NEF	QVLRPMTY	100	9	46	72		9486
NEF	QVLRPMTYK	100	10	46	72		9487
NEF	IVRIQVILR	95	9	48	75	0.6100	9488
NEF	GFVRIQVPLR	93	11	48	75		9489
NEF	PLRPMTYK	102	8	49	77		9490
POL	STNSPTSR	32	8	01	33	0.0010	9491
POL	RANSISR	35	8	01	33		9492
POL	NSNSPTSR	31	9	01	33		9493
POL	PTSRELOVR	36	9	01	33		9494
POL	QTRANSISR	33	10	01	33		9495
POL	QTRANSPTTR	35	10	01	33		9496
POL	NSPTSRELOVR	34	11	01	33		9497
POL	RANSPTTR	37	8	01	33		9498
POL	PTSRELOVR	39	9	01	50		9499
POL	PSRANSPTSR	24	10	01	50		9500
POL	NSPTSRELOVR	37	11	01	50		9501
POL	NSPTSRELOV	39	11	01	50		9502
POL	ADROGVSF	71	9	01	20		9503
POL	DDROGVVSF	71	10	01	20		9504
POL	GADROGVVSF	70	10	01	20		9505
POL	GDDROGVVSF	71	11	01	20		9506
POL	ADROGVVSF	71	11	01	20		9507
POL	AGADROGVVSF	69	11	01	17		9508
POL	AGDDROGVVS	69	11	01	17		9509
POL	GTLNFPQITF	79	11	01	17		9510
POL	NLAFFQGEA	5	9	10	16		9511
POL	NLAFFQGEAR	5	10	10	16		9512
POL	KTGKYAKMRT	542	11	10	16		9513
POL	ILIECGII	149	8	10	16		9514
POL	LIEICGIIK	150	8	10	16		9515
POL	YAKMRTAI	546	8	10	16		9516
POL	LIEICGIIKA	150	9	10	16		9517
POL	RSALTNDVK	550	9	10	16		9518
POL	AFQGEAREF	7	10	10	16		9519
POL	LIEALLDTGA	106	10	10	16		9520
POL	TGKYAKMRTA	543	10	10	16		9521
POL	ETWETWTD	588	10	10	16		9522
POL	ETWETWTE	588	10	10	16		9523
POL	ETWWTYDQ	591	10	10	16		9524
POL	VSLDTITNOK	659	10	10	16		9525
POL	LAFQGEAREF	6	11	10	16		9526
POL	QLIEALLDTGA	105	11	10	16		9527
POL	MLTQLGCTLN	176	11	10	16		9528
POL	TGKYAKMRTA	543	11	10	16		9529
POL	VVSLDTITNQ	658	11	10	16		9530
							9531

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
POL	QTELOKQIHK	961	11	10	16		9532
POL	QTRANSPTRR	21	10	11	18		9533
POL	LDGIDKAQEDII	754	11	11	17		9534
POL	IGGFIKVK	137	8	11	17		9535
POL	RIGPENPY	238	8	11	17		9536
POL	VIPLTEEA	481	8	11	17		9537
POL	TAITNDVK	551	8	11	17		9538
POL	QLTEVQVK	559	8	11	17		9539
POL	IDKAQEDII	757	8	11	17		9540
POL	WAGIQQEF	884	8	11	17		9541
POL	VVPRKVK	1012	8	11	17		9542
POL	KIKDYGK	1019	8	11	17		9543
POL	GIGGFIKVK	136	9	11	17		9544
POL	EVPLTEEA	480	9	11	17		9545
POL	SLDITTNQK	660	9	11	17		9546
POL	GIDKAQEDII	756	9	11	17		9547
POL	KVVRKVK	1011	9	11	17		9548
POL	GGIGGFIKVK	135	10	11	17		9549
POL	ISRIGPENPY	236	10	11	17		9550
POL	STNNEITGIR	323	10	11	17		9551
POL	ESWTNDIQK	439	10	11	17		9552
POL	ETNQKTELI	663	10	11	17		9553
POL	DGIDKAQEDII	755	10	11	17		9554
POL	GSNFTSTTVK	870	10	11	17		9555
POL	GIQIEGIPY	886	10	11	17		9556
POL	SDIQIKLELOK	958	10	11	17		9557
POL	IKDYGKQMA	1020	10	11	17		9558
POL	IGGIGGFIKVK	134	11	11	17		9559
POL	KISRIGPENPY	235	11	11	17		9560
POL	PSTNNEITGIR	322	11	11	17		9561
POL	STNNEITGIRY	323	11	11	17		9562
POL	LTEVPLTEEA	478	11	11	17		9563
POL	VVSLTETTNQ	658	11	11	17		9564
POL	ETNQKTELI	663	11	11	17		9565
POL	NGSNFTSTTV	869	11	11	17		9566
POL	GSNFTSTTVK	870	11	11	17		9567
POL	ACWVAGIQQE	881	11	11	17		9568
POL	AGIQQEGIPY	885	11	11	17		9569
POL	IDIASDIQTK	953	11	11	17		9570
POL	VDIATIDIQTK	953	11	11	17		9571
POL	ASDIQTKELQK	957	11	11	17		9572
POL	NSEIKVVPK	1007	11	11	17		9573
POL	KIKDYGKQMA	1019	11	11	17		9574
POL	NLSLEAGA	60	8	12	20		9575
POL	QTRANSPTSR	21	10	12	19		9576
POL	IKIQNFR	969	8	12	19		9577
POL	QIVPGIKVK	458	9	12	19		9578
POL	QDQWYQIY	526	9	12	19		9579
POL	IKIQNFRVY	969	10	12	19		9580
POL	ASQIVPGIKVK	456	11	12	19		9581

Table XVI
 IIIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
POL	IKIQNFRVYY	969	11	12	19		9582
POL	LAIPQGEA	6	8	12	19		9583
POL	LAIPQGEA	6	8	12	19		9584
POL	AFQGEAR	7	8	12	19		9585
POL	KTELQAIY	668	8	12	19		9586
POL	ELQAIYLA	670	8	12	19		9587
POL	QIKIQNF	968	8	12	19		9588
POL	KDYGKQMA	1022	8	12	19		9589
POL	LAIPQGEAR	6	9	12	19		9590
POL	ENLPQKWK	122	9	12	19		9591
POL	TTNQTLELI	664	9	12	19		9592
POL	QIKIQNFR	968	9	12	19		9593
POL	VIQDNSEIK	1003	9	12	19		9594
POL	NSEIKVVPR	1007	9	12	19		9595
POL	VLEENLPQK	119	10	12	19		9596
POL	TTNQTLELIA	664	10	12	19		9597
POL	KTELQAIYLA	668	10	12	19		9598
POL	VVIQDNSEIK	1002	10	12	19		9599
POL	NSHIKVVPR	1007	10	12	19		9600
POL	TVLEENLPQK	118	11	12	19		9601
POL	ENLPQKWKPK	122	11	12	19		9602
POL	ELRQILLRWG	393	11	12	19		9603
POL	QGQDQWYQI	524	11	12	19		9604
POL	RMKGAIITNDV	548	11	12	19		9605
POL	QIKIQNFRVY	968	11	12	19		9606
POL	AVVIQDNSEIK	1000	11	12	19		9607
POL	QDNSEIKVVPR	1005	11	12	19		9608
POL	ELQKQIK	964	8	13	21		9609
POL	EFSEQTRA	16	9	13	21		9610
POL	KTGKYARMR	542	9	13	21		9611
POL	NLKTGKYARM	540	11	13	21		9612
POL	KTGKYARMRG	542	11	13	21		9613
POL	EDINLPQK	121	8	13	20		9614
POL	IVPLTEEA	481	8	13	20		9615
POL	TKGYARMR	543	8	13	20		9616
POL	YARMRGAI	546	8	13	20		9617
POL	IGQVREQA	914	8	13	20		9618
POL	QVREQALH	916	8	13	20		9619
POL	DINLPQKWK	122	9	13	20		9620
POL	LIEICGKKA	150	9	13	20		9621
POL	DIVPLTEEA	480	9	13	20		9622
POL	IKQVREQA	913	9	13	20		9623
POL	VLEINLPQK	119	10	13	20		9624
POL	EDINLPQKWK	121	10	13	20		9625
POL	ILIEICGKKA	149	10	13	20		9626
POL	RAKIELREH	388	10	13	20		9627
POL	TVQPIVLPQK	429	10	13	20		9628
POL	TDIVPLTEEA	479	10	13	20		9629
POL	TKGYARMRG	543	10	13	20		9630
POL	AGRWPVKTHI	857	10	13	20	0.1640	9631

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	KIIGVRIEQA	912	10	13	20		9632
POL	IGQVRFQAEH	914	10	13	20		9633
POL	QVREQAELIK	916	10	13	20		9634
POL	EIKVVRKKA	1009	10	13	20		9635
POL	TLWRPLVTV	91	11	13	20		9636
POL	LVTKIGQGLK	97	11	13	20		9637
POL	TVLEDINLPGK	118	11	13	20		9638
POL	DINLPGKWKP	122	11	13	20		9639
POL	QILIECGKKA	148	11	13	20		9640
POL	KIELREILLK	390	11	13	20		9641
POL	WTQPIVLPEK	428	11	13	20	0.0011	9642
POL	LTDIVPLTEEA	478	11	13	20		9643
POL	TGKYARMRGA	543	11	13	20		9644
POL	LAGRWVPVKT	856	11	13	20		9645
POL	IGQVRFQAEH	913	11	13	20		9646
POL	DSRDPLWKGIP	981	11	13	20		9647
POL	EIKVVRKKA	1009	11	13	20		9648
POL	EFSEIOTR	16	8	14	22		9649
POL	QIYPGKVR	458	9	14	22		9650
POL	ASQIYPIKVR	456	11	14	22		9651
POL	IATSESVIWK	567	11	14	22		9652
POL	ILIEICGK	149	8	14	22		9653
POL	LIIEICGK	150	8	14	22		9654
POL	NFTSTTVK	872	8	14	22		9655
POL	FTSTTVKA	873	8	14	22		9656
POL	TSTTVKAA	874	8	14	22		9657
POL	IASDIQTK	956	8	14	22		9658
POL	DSRDPLWK	981	8	14	22		9659
POL	QILIEICGK	148	9	14	22		9660
POL	ILIEICGK	149	9	14	22		9661
POL	NFTSTTVKA	872	9	14	22		9662
POL	FTSTTVKAA	873	9	14	22	0.0003	9663
POL	IASDIQTK	955	9	14	22		9664
POL	DSRDPLWK	980	9	14	22		9665
POL	RDPLWKGP	983	9	14	22		9666
POL	QILIEICGK	148	10	14	22		9667
POL	RTKIELRQII	388	10	14	22		9668
POL	PGIKVRQLCK	461	10	14	22		9669
POL	TIITDNGSNF	864	10	14	22		9670
POL	NFTSTTVKAA	872	10	14	22		9671
POL	TTVKAACWW	876	10	14	22	0.0006	9672
POL	AGERIVDIIA	948	10	14	22		9673
POL	DIASDIQTK	954	10	14	22		9674
POL	RDPLWKGP	983	10	14	22		9675
POL	FSFQITLWQR	85	11	14	22		9676
POL	YDQILIEICGK	146	11	14	22		9677
POL	ELREILLKWG	393	11	14	22		9678
POL	KTPKFKLPIQK	577	11	14	22		9679
POL	GIDKAEQEEH	756	11	14	22		9680
POL	STTVKAACW	875	11	14	22		9681

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
POL	SAGERIVDIIA	947	11	14	22		9682
POL	QTRANSPTR	21	9	15	24		9683
POL	LVEICTEMEX	221	10	15	24	0.0002	9684
POL	FFIEDLAF	1	8	15	23		9685
POL	FSSEQTRA	17	8	15	23		9686
POL	ELRQIILLR	393	8	15	23		9687
POL	QCQDQWTY	524	8	15	23		9688
POL	KTELQAIHI	668	8	15	23		9689
POL	AGIRKVLV	746	8	15	23		9690
POL	PIOKETWEA	584	9	15	23		9691
POL	SAGIRKVLV	745	9	15	23		9692
POL	EIKVVRKR	1009	9	15	23		9693
POL	LTQLGCTLNF	177	10	15	23		9694
POL	KTELQAIHIA	668	10	15	23		9695
POL	LGIIQAPDIR	695	10	15	23		9696
POL	VDKLVSAGIR	740	10	15	23		9697
POL	VSAGIRKVLV	744	10	15	23		9698
POL	IDKAQEEIER	757	10	15	23		9699
POL	ALVEICTEMEX	220	11	15	23		9700
POL	KIELRQIILLR	390	11	15	23		9701
POL	ALGIIQAPDIR	694	11	15	23		9702
POL	LYNQHIEQLK	709	11	15	23		9703
POL	QVDKLVSAGIR	739	11	15	23		9704
POL	VDKLVSAGIRK	740	11	15	23		9705
POL	LVSAGIRKVLV	743	11	15	23		9706
POL	IDKAQEEIERV	757	11	15	23		9707
POL	KAQEEIER	759	8	16	25		9708
POL	NLAFQGEA	5	9	16	25		9709
POL	KAQEEIERV	759	9	16	25		9710
POL	NLAFQQGEAR	5	10	16	25		9711
POL	KAQEEIERV11	759	10	16	25		9712
POL	LAFQQGEA	6	8	16	25		9713
POL	AFQQGEAR	7	8	16	25		9714
POL	RANSPTIR	36	8	16	25		9715
POL	QLGCTLNF	179	8	16	25		9716
POL	SAITNDVX	351	8	16	25		9717
POL	ELQAIHIA	670	8	16	25		9718
POL	IIQAQDIR	697	8	16	25		9719
POL	QVDKLVS	719	8	16	25		9720
POL	KLSAGIR	742	8	16	25		9721
POL	LVSAGIRK	743	8	16	25		9722
POL	EIKVVRKR	1009	8	16	25	0.0091	9723
POL	LAFQQGEAR	6	9	16	25		9724
POL	GIIQAQDIR	696	9	16	25		9725
POL	KLSAGIRK	742	9	16	25		9726
POL	QLEKEPIVGA	620	10	16	25	0.1300	9727
POL	RANSPTIR	26	8	17	27		9728
POL	KIELRQII	390	8	17	27		9729
POL	ELREHLLK	393	8	17	27		9730
POL	WCKTPKFK	575	8	17	27		9731

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	TIKIGGQLK	99	9	17	27	0.27100	9732
POL	VTIKIGGQIK	98	10	17	27	0.0370	9733
POL	TVQPIQLPEK	429	10	17	27		9734
POL	VWGKTTPKFK	573	10	17	27		9735
POL	TLWQRPVYI	91	11	17	27		9736
POL	TIKIGGQLKEA	99	11	17	27		9737
POL	MLTIQIGCTLNF	176	11	17	27		9738
POL	WTVPQIQLPEK	428	11	17	27		9739
POL	IVWGGTTPKFK	572	11	17	27		9740
POL	ETTNQKTELQ	663	11	17	27		9741
POL	KDFRKYTAF	311	9	18	29		9742
POL	YFSVPLDKDF	304	10	18	29		9743
POL	YFSVPLDKDFR	304	11	18	29		9744
POL	NLKTGKYAKM	540	11	18	29		9745
POL	SVPLDKDF	306	8	18	28		9746
POL	PDIVYQY	365	8	18	28		9747
POL	FVPLDKDF	305	9	18	28		9748
POL	SVPLDKDFR	306	9	18	28		9749
POL	FVPLDKDFR	305	10	18	28		9750
POL	SVPLDKDFRK	306	10	18	28		9751
POL	AGIKVKQLCK	461	10	18	28		9752
POL	FVPLDKDFRK	305	11	18	28		9753
POL	SVPLDKDFRK	306	11	18	28		9754
POL	LDKDFRKYTA	309	11	18	28		9755
POL	YAGIKVKQLCK	460	11	18	28		9756
POL	LVSQHIEQLIK	709	11	18	28		9757
POL	PLDKDFRK	308	8	19	30		9758
POL	KDFRKYTA	311	8	19	30		9759
POL	PLDKDFRKY	308	9	19	30		9760
POL	KTGKYAKMR	542	9	19	30		9761
POL	PLDKDFRKYT	308	11	19	30		9762
POL	LDKDFRKY	309	8	19	30		9763
POL	KIEELREH	390	8	19	30		9764
POL	TGKYAKMR	543	8	19	30		9765
POL	GAITNDVK	551	8	19	30		9766
POL	LTDITNQK	661	8	19	30		9767
POL	PLWKGPAK	985	8	19	30		9768
POL	GIKVRQLCK	462	9	19	30		9769
POL	RGAITNDVK	550	9	19	30		9770
POL	LDKDFRKYTA	309	10	19	30		9771
POL	KVRQLCKLLR	464	10	19	30		9772
POL	ATESIVWGR	568	10	19	30	0.0007	9773
POL	VSQHIEQLIK	710	10	19	30		9774
POL	MAGDDCVASR	1028	10	19	30		9775
POL	VSQHIEQLIKK	710	11	19	30		9776
POL	QIKKEKVVLA	716	11	19	30		9777
POL	QMAGDDCVAS	1027	11	19	30		9778
POL	QIVAGIKVK	458	9	20	32	0.0750	9779
POL	KVYLAWVPA	722	9	20	32	0.0280	9780
POL	KVYLAWVPAII	722	10	20	32		9781

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	KAACWWAGIK	879	10	20	32	0.0300	9782
POL	ASQVAGIKVK	456	11	20	32		9783
POL	KVYLAWVPAIL	722	11	20	32	8.6000	9784
POL	KFKLHIQK	580	8	20	31		9785
POL	GDGCVASR	1030	8	20	31		9786
POL	AGDDCVASR	1029	9	20	31		9787
POL	VSLTETINOK	659	10	20	31		9788
POL	LIKKEKVYLA	717	10	20	31		9789
POL	LLKLAGRWPV	853	11	20	31		9790
POL	YFSVPLDK	304	8	21	33		9791
POL	KVHITDNGSNF	863	11	21	33		9792
POL	ACWWAGIK	881	8	21	33		9793
POL	WAGIKQEF	884	8	21	33		9794
POL	SLTETINOK	660	9	21	33		9795
POL	AAACWWAGIK	880	9	21	33	0.0130	9796
POL	DAYFSVPLDK	302	10	21	33		9797
POL	DLEIGQIRTK	381	10	21	33		9798
POL	QLCKLLRGTK	467	10	21	33		9799
POL	SDFNLPPIVA	776	10	21	33		9800
POL	LLTQIGCTLNF	176	11	21	33		9801
POL	IFAIKKKIDSTK	249	11	21	33		9802
POL	GDAYSVPFLD	301	11	21	33		9803
POL	SDLEIGQIRTK	380	11	21	33		9804
POL	QLCKLLRGTK	467	11	21	33		9805
POL	ASDFNLPPIVA	775	11	21	33		9806
POL	SDFNLPPIVAK	776	11	21	33		9807
POL	ACWWAGIKQEF	881	11	21	33		9808
POL	AGIKQEFQIPY	885	11	21	33		9809
POL	EDFRKYTA	311	8	22	35		9810
POL	EDFRKYTAF	311	9	22	35		9811
POL	EIGQIRTK	383	8	22	34		9812
POL	RTKIELR	388	8	22	34		9813
POL	YLAWVPAIL	724	8	22	34		9814
POL	LAWVPAILK	725	8	22	34	0.0770	9815
POL	YLAWVPAILK	724	9	22	34		9816
POL	NFPIQTLWQR	86	10	22	34	0.0150	9817
POL	MTKILEPFRK	353	10	22	34		9818
POL	KVILVAVIVA	821	10	22	34		9819
POL	AGRWPVKVHI	857	10	22	34		9820
POL	GKQEFQIPY	886	10	22	34	0.0002	9821
POL	SMTKILEPFRK	352	11	22	34		9822
POL	KTPKFRLLHIQK	577	11	22	34		9823
POL	LAGRWPKVI	856	11	22	34		9824
POL	KVLSWVPA	722	9	23	37		9825
POL	KVLSWVPAIL	722	10	23	37		9826
POL	KVLSWVPAIL	722	11	23	37		9827
POL	KILEPFRK	355	8	23	36		9828
POL	ECKVILVA	821	8	23	36		9829
POL	KVILVAVII	823	8	23	36		9830
POL	KIGQLKEA	101	9	23	36		9831

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
POL	DFNLPIVA	777	9	23	36		9832
POL	VILVAVIVA	824	9	23	36		9833
POL	TVKAACWVA	877	9	23	36		9834
POL	SFQITLWQR	86	10	23	36		9835
POL	DFNLPIVAK	777	10	23	36		9836
POL	IILEGKVLVA	819	10	23	36		9837
POL	EGKVLVAVII	821	10	23	36		9838
POL	LLKVGFTTPD	398	11	23	36		9839
POL	LLRWGFTTPD	398	11	23	36		9840
POL	IDHATIDITK	953	11	23	36		9841
POL	KLLRGITKA	470	8	24	38		9842
POL	NTPIFAIK	246	8	24	38		9843
POL	GDCCVAGR	1030	8	24	38		9844
POL	NTPIFAIKK	246	9	24	38		9845
POL	LCKLLRGITK	468	9	24	38	0.0004	9846
POL	AGDDCVAGR	1029	9	24	38		9847
POL	NTPIFAIKKK	246	10	24	38		9848
POL	LCKLLRGITKA	468	10	24	38		9849
POL	VIHTDGSNF	864	10	24	38		9850
POL	MAGDDCVAGR	1028	10	24	38		9851
POL	QLCKLLRGAK	467	11	24	38		9852
POL	QGQGWYTI	524	11	24	38		9853
POL	QLGKAGVTD	643	11	24	38		9854
POL	TAYFLKLAG	849	11	24	38		9855
POL	QMAGDDCVAG	1027	11	24	38		9856
POL	KLLRGAKA	470	8	25	40	0.0004	9857
POL	QGQWYTIY	526	9	25	40		9858
POL	IGGQLKEA	102	8	25	39		9859
POL	PIFAIKK	248	8	25	39		9860
POL	QGQGWY	534	8	25	39		9861
POL	FLKLAGR	852	8	25	39		9862
POL	QLCKLLRGA	467	9	25	39		9863
POL	IVAKEIVA	782	9	25	39		9864
POL	YFLKLAGR	851	9	25	39		9865
POL	QLCKLLRGAK	467	10	25	39		9866
POL	LCKLLRGAKA	468	10	25	39		9867
POL	LKGAGVYVDR	644	10	25	39		9868
POL	IDKAQEEIEK	757	10	25	39		9869
POL	SDFNLPPVA	776	10	25	39		9870
POL	PSKIDIAEIQK	513	11	25	39		9871
POL	DTINQKTELQ	663	11	25	39		9872
POL	GIDKAQEEIEK	756	11	25	39		9873
POL	IDKAQEEIEKY	757	11	25	39		9874
POL	ASDFNLPPVA	775	11	25	39		9875
POL	SDFNLPPVAK	776	11	25	39		9876
POL	RAKIEELR	388	8	26	41		9877
POL	LCKLLRGA	468	8	26	41		9878
POL	KFRLIQK	580	8	26	41		9879
POL	NLPPIVAK	779	8	26	41		9880
POL	IVAKEIVA	783	8	26	41		9881

Table XVI
 HIV A13 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Cross-reactivity (%)	A*0301	SEQ ID NO.
POL	LCKLRGAK	468	9	26	41		9882
POL	LTEAVQKIA	560	9	26	41		9883
POL	SSGIRKVLV	745	9	26	41		9884
POL	DFNLPIVVA	777	9	26	41		9885
POL	QLTEAVQKIA	559	10	26	41		9886
POL	VSSGIRKVLV	744	10	26	41		9887
POL	DFNLPIVVA	777	10	26	41		9888
POL	GSNFTSAAVK	870	10	26	41		9889
POL	LVSSGIRKVLV	743	11	26	41		9890
POL	TQGETAYFL	845	11	26	41		9891
POL	NGSNFTSAAV	869	11	26	41		9892
POL	GSNFTSAAVK	870	11	26	41		9893
POL	KAOEHEK	759	8	27	43		9894
POL	ASQIYAGIK	456	9	27	43	0.0013	9895
POL	KAOEHEK	759	9	27	43		9896
POL	KAOEHEK	759	10	27	43		9897
POL	EICTEMEK	223	8	27	42		9898
POL	EIGQIRAK	383	8	27	42		9899
POL	LVSSGIRK	743	8	27	42		9900
POL	SCIRKVLV	746	8	27	42		9901
POL	NLPIVVA	779	8	27	42		9902
POL	ETAYFLK	848	8	27	42	0.0037	9903
POL	TSAAVKAA	874	8	27	42		9904
POL	KLVSSGIRK	742	9	27	42	0.0027	9905
POL	TAYFLKLA	849	9	27	42		9906
POL	FTSAAVKAA	873	9	27	42		9907
POL	DLEIGQIRAK	381	10	27	42	0.0052	9908
POL	KLNWASQIYA	452	10	27	42		9909
POL	WASQIYAGIK	455	10	27	42		9910
POL	KVKQLCKLR	464	10	27	42		9911
POL	ETAYFLKLA	848	10	27	42		9912
POL	NFTSAAVKAA	872	10	27	42		9913
POL	EICTEMEKEGK	223	11	27	42		9914
POL	SDLEIGQIRAK	380	11	27	42		9915
POL	VDKLVSSGIRK	740	11	27	42		9916
POL	ASQIYPGIK	456	9	28	44		9917
POL	KDLIAEQK	515	9	28	44		9918
POL	NLKTQRYAK	540	9	28	44		9919
POL	DLIAEQK	516	8	28	44		9920
POL	IVGAETFY	625	8	28	44		9921
POL	IVGAETFY	626	8	28	44		9922
POL	GSNFTSAA	870	8	28	44		9923
POL	NFTSAAVK	872	8	28	44		9924
POL	FTSAAVKA	873	8	28	44	0.0012	9925
POL	CTEMEKEGK	225	9	28	44		9926
POL	DLEIGQIRAK	381	9	28	44		9927
POL	GKVKOLCK	462	9	28	44		9928
POL	IVGAETFY	625	9	28	44		9929
POL	QLIKKEKVV	716	9	28	44		9930
POL	PVVAKEIVA	782	9	28	44		9931

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NGSNTSAA	869	9	28	44		9932
POL	NFTSAAYKA	872	9	28	44		9933
POL	ICTEMEKEGK	224	10	28	44		9934
POL	SDLEIGQIRA	380	10	28	44		9935
POL	WASQIYPIK	455	10	28	44		9936
POL	AAVKAACW	876	10	28	44		9937
POL	GSDEIGQIRA	379	11	28	44		9938
POL	VGAEIFYVDG	627	11	28	44		9939
POL	TDGNSNFTA	867	11	28	44		9940
POL	SAAVKAACW	875	11	28	44		9941
POL	NLKTGKYAR	540	9	29	46	0.0008	9942
POL	KLVSSGIR	742	8	29	45		9943
POL	VIWGTTPKFR	573	10	29	45		9944
POL	VDKLVSIGIR	740	10	29	45		9945
POL	PLTFAELELA	483	11	29	45		9946
POL	IVIWGTTPKFR	572	11	29	45		9947
POL	QVIDKLVSIGIR	739	11	29	45		9948
POL	WGKTPIKFR	575	8	30	47		9949
POL	LITETNQK	661	8	30	47		9950
POL	ILVAVIIVA	824	9	30	47		9951
POL	AANRETGLGK	637	10	30	47	0.0007	9952
POL	IEQLIKKEK	713	10	30	47	0.0004	9953
POL	KILVAVIIVA	823	10	30	47		9954
POL	GAANRETGLG	636	11	30	47		9955
POL	AANRETGLGK	637	11	30	47		9956
POL	QIEQLIKKEK	712	11	30	47		9957
POL	ILKLGRWIV	853	11	30	47		9958
POL	VVAREIVA	783	8	31	48		9959
POL	EGKIILVA	821	8	31	48		9960
POL	KILVAVII	823	8	31	48		9961
POL	ETAYFILK	848	8	31	48		9962
POL	YFILKLGR	851	9	31	48		9963
POL	ILEGKIILVA	819	10	31	48		9964
POL	EGKIILVAVII	821	10	31	48		9965
POL	ETAYFILKLA	848	10	31	48		9966
POL	PSINNETPGIR	322	11	31	48		9967
POL	TGQETAYFILK	845	11	31	48		9968
POL	TAYFILKLGR	849	11	31	48		9969
POL	FILKLGR	852	8	32	50		9970
POL	NDVKQLTEA	555	9	32	50		9971
POL	TAYFILKLA	849	9	32	50		9972
POL	AVKAACWVA	877	9	32	50		9973
POL	SINNETPGIR	323	10	32	50		9974
POL	SINNETPGIRY	323	11	32	50		9975
POL	SSMTKILEPFR	351	11	32	50		9976
POL	IITNDVKQLTE	553	11	32	50		9977
POL	IISNWRAMAS	768	11	32	50		9978
POL	QTKELQKQITK	961	11	32	50		9979
POL	DVKQLTEA	556	8	33	52	0.0050	9980
POL	NGSNFTA	869	8	33	52		9981

Table XVI
 IIIY A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	EMIECKKISK	229	10	33	52	0.0004	9982
POL	SSMTKLEIFF	351	10	33	52	0.0004	9983
POL	TONGSNFTSA	867	10	33	52		9984
POL	QSSMTKLEIFF	350	11	33	52		9985
POL	DYKQLTEAVQ	536	11	33	52	0.0048	9986
POL	HTDNGSNFTS	866	11	33	52		9987
POL	YDPSKDIA	511	9	34	53		9988
POL	DIATDIQTK	934	10	34	53	0.0056	9989
POL	QLKEALLDTG	105	11	34	53		9990
POL	ELQKQITK	964	8	35	56		9991
POL	LIKKEKVV	717	8	35	55		9992
POL	QITKIONF	968	8	35	55		9993
POL	DSRDPIWK	981	8	35	55		9994
POL	ETRLKAGY	641	9	35	55		9995
POL	IATDIQTK	935	9	35	55	0.0250	9996
POL	QITKIONFR	968	9	35	55	0.0021	9997
POL	RJSDIHWK	980	9	35	55		9998
POL	TDIQTKELOK	958	10	35	55	0.0007	9999
POL	RDPIWKGP	983	10	35	55		10000
POL	ATDIQTKELQK	937	11	35	55	0.0051	10001
POL	QITKIONFRVY	968	11	35	55		10002
POL	DSRDPIWKGP	981	11	35	55		10003
POL	SDIKVVPKKA	1008	11	35	55		10004
POL	ITKIONFR	969	8	36	57		10005
POL	ITKIONFRVY	969	10	36	57	0.0016	10006
POL	ITKIONFRVY	969	11	36	57		10007
POL	IATDIQTK	936	8	36	56		10008
POL	PIWKGP	985	8	36	56		10009
POL	NLPKWKPK	124	9	36	56		10010
POL	AIQSSMTK	347	9	36	56	1.0000	10011
POL	PAIQSSMTK	346	10	36	56	0.0740	10012
POL	LTEAELELA	484	10	36	56		10013
POL	VFAIKKDDSTK	249	11	36	56		10014
POL	NTPVFAIK	246	8	37	58	0.0003	10015
POL	PVFAIKKK	248	8	37	58	0.0003	10016
POL	QLTEAVOX	559	8	37	58		10017
POL	QIEQLIK	712	8	37	58		10018
POL	IEQLIKK	713	8	37	58		10019
POL	YLSWVPAH	724	8	37	58		10020
POL	LSWVPAIK	725	8	37	58		10021
POL	NTPVFAIK	246	9	37	58	0.0330	10022
POL	QIEQLIKK	712	9	37	58	0.0091	10023
POL	YLSWVPAIK	724	9	37	58		10024
POL	RDPIWKGP	983	9	37	58		10025
POL	VIQNSDIK	1003	9	37	58	0.0009	10026
POL	NTPVFAIKK	246	10	37	58	0.0006	10027
POL	VVIQNSDIK	1002	10	37	58	0.0005	10028
POL	AVVIQNSDIK	1000	11	37	58		10029
POL	IFQSSMTK	348	8	38	59	0.0055	10030
POL	ILKEPVIIGVY	498	11	38	59		10031

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
POL	LDGIDKAQEII	754	11	39	62		10032
POL	IISNWRAMA	768	8	39	61		10033
POL	AGYVTDGR	647	9	39	61		10034
POL	YVTDGRGK	649	9	39	61	0.0011	10035
POL	KAGVTDGR	646	10	39	61		10036
POL	LGIIQAQPDK	695	10	39	61	0.0007	10037
POL	DGIDKAQEII	755	10	39	61		10038
POL	DIKVVPRRKA	1009	10	39	61		10039
POL	PVIGVYYDPS	505	11	39	61		10040
POL	AGVYTDGRQ	647	11	39	61		10041
POL	ALGIQAQPDK	694	11	39	61		10042
POL	DIKVVPRRKAK	1009	11	39	61		10043
POL	VTDRGRQK	650	8	40	63	0.0090	10044
POL	IIQAQPDK	697	8	40	63		10045
POL	GIQAQPDK	696	9	40	63	0.0009	10046
POL	GIDKAQEII	756	9	40	63		10047
POL	NSDIKVVPR	1007	9	40	63		10048
POL	ILKEPVIGVY	498	10	40	63		10049
POL	NSDIKVVPRR	1007	10	40	63	0.0007	10050
POL	ELKEPVIGVY	497	11	40	63		10051
POL	WTYQIYQEPF	529	11	40	63	0.9200	10052
POL	OIYQIYQEPF	532	11	40	63	0.2800	10053
POL	SAGERIHHIA	947	11	40	63		10054
POL	QDNSDIKVVPR	1005	11	40	63		10055
POL	NSDIKVVPRR	1007	11	40	63		10056
POL	ESIVWVGKTPK	570	11	41	65		10057
POL	FFRENIAF	1	8	41	64		10058
POL	QIGCTLNF	179	8	41	64		10059
POL	OIYQEPK	532	8	41	64	0.0010	10060
POL	IDKAQEII	757	8	41	64		10061
POL	KAKIRDY	1017	8	41	64		10062
POL	LTQIGCTLNF	177	10	41	64	0.0001	10063
POL	AGERIIDIA	948	10	41	64		10064
POL	KAKIRIDYK	1017	10	41	64	0.0048	10065
POL	KISKIGPENPY	235	11	41	64		10066
POL	SIVWVGKTPKF	571	11	41	64		10067
POL	DFRKYTAF	312	8	42	66		10068
POL	KAGYVTD	646	8	42	66		10069
POL	ISKIGPENPY	236	10	42	66		10070
POL	SMTKILEPFR	352	10	42	66	0.0004	10071
POL	WTYQIYQEPF	529	10	42	66		10072
POL	SIVWVGKTPK	571	10	42	66		10073
POL	TTNQKTELQA	664	10	42	66	0.0004	10074
POL	IVIQYMDLLY	367	11	42	66		10075
POL	VVPRRKAKIR	1012	11	42	66		10076
POL	GVYVDPK	508	8	43	67		10077
POL	SCDKCOLK	791	8	43	67		10078
POL	SMTKILEPFR	352	9	43	67	0.0004	10079
POL	MTKILEPFR	353	9	43	67	0.0008	10080
POL	HGVYVDPK	507	9	43	67	0.0004	10081

Table XVI
H1V Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
POL	ASCDKCOLK	790	9	43	67	0.0027	10082
POL	DSWTVDIQK	439	10	43	67	0.0007	10083
POL	TFYVIGAAHR	631	10	43	67	0.0003	10084
POL	VASCDKCOLK	789	10	43	67	0.0004	10085
POL	KIIGQVRDQA	912	10	43	67		10086
POL	KDSWTVDIQ	438	11	43	67		10087
POL	ETFYVDGAAN	630	11	43	67		10088
POL	IVASCDKCOLK	788	11	43	67	0.0970	10089
POL	SCDKQLKGE	791	11	43	67		10090
POL	MTKLEPF	353	8	44	69		10091
POL	IGQVRDQA	914	8	44	69		10092
POL	SDIKVVPK	1008	8	44	69		10093
POL	MAGDDCYA	1028	8	44	69		10094
POL	IIGQVRDQA	913	9	44	69		10095
POL	SDIKVVPK	1008	9	44	69	0.0012	10096
POL	QNAQDGLCA	1027	9	44	69	0.0013	10097
POL	VDGAANRETK	634	10	44	69		10098
POL	IGQVRDQAEH	914	10	44	69		10099
POL	QVRDQAEHLK	916	10	44	69	0.0089	10100
POL	SDIKVVPK	1008	10	44	69	0.0004	10101
POL	IFKNLKTGKY	537	11	44	69		10102
POL	GAETFYVDGA	628	11	44	69		10103
POL	YVDGAANRETK	633	11	44	69		10104
POL	IIGQVRDQAEH	913	11	45	71		10105
POL	VAKELVASCOK	784	11	45	70		10106
POL	GAANRETK	636	8	45	70		10107
POL	EIVASCDK	787	8	45	70		10108
POL	DGAANRETK	635	9	45	70	0.0004	10109
POL	PFKNLKTGKY	537	10	45	70		10110
POL	RDQAEHLKTA	918	10	45	70		10111
POL	PLVKLWYQLE	613	11	45	70		10112
POL	EILKEPVII	497	8	46	72		10113
POL	KLWYQLEK	616	8	46	72		10114
POL	RDQAEHLK	918	8	46	72		10115
POL	PFKNLKTGK	537	9	46	72		10116
POL	DIQTKELQK	959	9	46	72	0.0009	10117
POL	LVKLWYQLEK	614	10	46	72	0.0560	10118
POL	KVKQWPLTEE	207	11	46	72	0.0750	10119
POL	VIWGTTPKF	573	9	47	73		10120
POL	VIWGTTPKF	572	10	47	73		10121
POL	VIWGTTPK	573	8	48	75		10122
POL	QVRDQAEH	916	8	48	75		10123
POL	DIKVVPRK	1009	8	48	75		10124
POL	VIWGTTPK	572	9	48	75	0.0850	10125
POL	DIKVVPRK	1009	9	48	75	0.0002	10126
POL	GAETFYVDGA	628	10	48	75		10127
POL	KVFLDGDIGK	750	10	48	75		10128
POL	CDKQLKGEA	792	10	48	75	0.3600	10129
POL	KCOLKGEAMII	794	10	48	75		10130
POL	VVESNMKELK	902	10	48	75		10131

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ ID NO.
POL	KVFLDGIDKA	750	11	48	75		10132
POL	GVVESMNKEL	901	11	48	75		10133
POL	VVESMNKELK	902	11	48	75		10134
POL	GVVESMNK	901	8	49	77		10135
POL	RDYQKQMA	1022	8	49	77		10136
POL	QGVVESMNK	900	9	49	77		10137
POL	KLKPGMDGPK	107	10	49	77	0.3900	10138
POL	IRDYQKQMA	1020	10	49	77		10139
POL	OSQGVVESMN	808	11	49	77		10140
POL	KIRDYQKQMA	1019	11	49	77		10141
POL	ESIVWGGK	570	8	50	79		10142
POL	YVDGAANR	633	8	50	78	0.0003	10143
POL	LAGRVPVK	856	8	50	78		10144
POL	KIRDYQK	1019	8	50	78		10145
POL	KLGRVPVK	855	9	50	78	2.7000	10146
POL	GMDGPKVK	201	8	51	80	0.0007	10147
POL	KIGPENPY	238	8	51	80		10148
POL	FTTPDKKII	403	8	51	80		10149
POL	TFYVDGAA	631	8	51	80		10150
POL	ITDNGSNF	866	8	51	80		10151
POL	PGMDGPKVK	200	9	51	80	0.0004	10152
POL	GFTTPDKKII	402	9	51	80		10153
POL	ETFYVDGAA	630	9	51	80	0.0380	10154
POL	VLFLDGIDK	751	9	51	80	0.0007	10155
POL	VYQYMDDL	368	10	51	80		10156
POL	WGFTTPDKKII	401	10	51	80		10157
POL	FTTPDKKIIHQK	403	10	51	80	0.0002	10158
POL	VLFLDGIDKA	751	10	51	80	0.0004	10159
POL	KSIVTVLDVGD	293	11	51	80		10160
POL	GFTTPDKKIIQ	402	11	51	80		10161
POL	QATWIPEWEF	599	10	52	83	0.0004	10162
POL	PAGLKKKK	286	8	52	81		10163
POL	SDLEIGQII	380	8	52	81		10164
POL	DLEIGQIR	381	8	52	81		10165
POL	WGFTTPDK	401	8	52	81		10166
POL	GFTTPDKK	402	8	52	81		10167
POL	KCOLKGIA	794	8	52	81		10168
POL	VASGYIEA	831	8	52	81		10169
POL	KIQNFRVY	971	8	52	81		10170
POL	KVPRRKA	1011	8	52	81	0.0027	10171
POL	VVPRRKA	1012	8	52	81		10172
POL	ETGIRYQY	377	9	52	81		10173
POL	GSDLEIGQII	379	9	52	81		10174
POL	SDLEIGQIR	380	9	52	81	0.0003	10175
POL	WGFTTPDKK	401	9	52	81	0.0004	10176
POL	ATWIPEWEF	600	9	52	81		10177
POL	IVASGYIEA	830	9	52	81	0.0003	10178
POL	KIQNFRVY	971	9	52	81	0.1200	10179
POL	KVPRRKA	1011	9	52	81	0.0290	10180
POL	VGSDLEIGQII	378	10	52	81		10181

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	GSDLEIGQHR	379	10	52	81		10182
POL	KIONFVYVR	971	10	52	81	0.0320	10183
POL	NFRVYVRSR	974	10	52	81		10184
POL	IGGIGGFKVR	134	11	52	81		10185
POL	VGPTPNIGR	164	11	52	81		10186
POL	YVGSDEIGQHI	377	11	52	81		10187
POL	VGSDEIGQHR	378	11	52	81		10188
POL	AVIVASGYIEA	828	11	52	81		10189
POL	SGYIEAEVIPA	833	11	52	81		10190
POL	GIPIFAGLKKK	282	11	53	84		10191
POL	IGGFKVR	137	8	53	83		10192
POL	GPIKVRQY	139	8	53	83		10193
POL	PIETVVK	190	8	53	83		10194
POL	ETVPVKLK	192	8	53	83		10195
POL	ELELAENR	489	8	53	83	0.0049	10196
POL	QLKGEAMII	796	8	53	83		10197
POL	ESMKNELK	904	8	53	83		10198
POL	SMNKLK	905	8	53	83		10199
POL	GIGGFKVR	136	9	53	83	0.0008	10200
POL	GIGKVRQY	138	9	53	83	0.0004	10201
POL	YIEAEVIPA	835	9	53	83	0.0003	10202
POL	ESMKNELK	904	9	53	83		10203
POL	GIGGFKVR	135	10	53	83	0.0004	10204
POL	IGGFKVRQY	137	10	53	83	0.0004	10205
POL	ISPIETVVK	188	10	53	83	0.0003	10206
POL	PIETVPVKLK	190	10	53	83	0.0002	10207
POL	EAELEAENR	487	10	53	83		10208
POL	LVAVIIVASGY	826	10	53	83		10209
POL	GIGGFKVRQY	136	11	53	83		10210
POL	PISPIETVVK	187	11	53	83		10211
POL	ILVAVIIVASGY	825	11	53	83		10212
POL	FVNTPIVK	608	9	54	86	0.0120	10213
POL	GIPIFAGLKK	282	10	54	86	0.0110	10214
POL	LGIPFAGLKK	281	11	54	86		10215
POL	ILVAVIIVA	825	8	54	84		10216
POL	PTTVNIQR	166	9	54	84	0.0008	10217
POL	PLTEEKKA	212	9	54	84		10218
POL	LAENREIK	492	9	54	84	0.0002	10219
POL	EVQLGRIIPA	278	10	54	84		10220
POL	ELAENREIK	491	10	54	84		10221
POL	EFVNTPIVK	607	10	54	84	0.0002	10222
POL	PLTEEKIK	212	8	55	86		10223
POL	ETFYVIDGA	610	8	55	86		10224
POL	FLDGDIA	752	8	55	86		10225
POL	FLDGDIA	753	8	55	86		10226
POL	FLDGDIA	752	9	55	86		10227
POL	QLGRIIPA	280	8	56	89		10228
POL	GIPIFAGLKK	282	9	56	89	0.2300	10229
POL	KGGGGYSA	940	9	56	89		10230
POL	LGIPFAGLKK	281	10	56	89	0.0370	10231

Table XVI
 HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
POL	QLGIPAPGLK	280	11	56	89		10232
POL	LTEEKIKIA	213	8	56	88		10233
POL	VTLDVGDAY	295	10	56	88	0.0001	10234
POL	ELKKIIGQVR	909	10	56	88		10235
POL	DFWEVQLGIPII	275	11	56	88		10236
POL	SVTLVDVGDA	294	11	56	88		10237
POL	VTLDVGDAY	295	11	56	88		10238
POL	PAETGQETAY	842	11	56	88		10239
POL	KTAVQMAVFI	925	11	56	88		10240
POL	TGQETAYF	845	8	57	89		10241
POL	AIKKKDKTK	251	9	57	89	0.0017	10242
POL	ELNKRTOQF	268	9	57	89		10243
POL	VTLDVGDAY	295	9	57	89		10244
POL	TVLDVGDAY	296	9	57	89		10245
POL	ITPDKKHQK	404	9	57	89	0.0002	10246
POL	ETQKETAYF	844	9	57	89	0.0002	10247
POL	ILKTAVOMA	923	9	57	89	0.0003	10248
POL	KTAVQMAVF	925	9	57	89	0.0003	10249
POL	FAIKKDKSTK	250	10	57	89	0.0004	10250
POL	SVTLVDVGDA	294	10	57	89		10251
POL	TVLDVGDAYF	296	10	57	89		10252
POL	NTPLVVKLWY	610	10	57	89	0.0004	10253
POL	AIKKKDKSTKW	251	11	57	89	0.0002	10254
POL	ILKTAVOMAV	923	11	57	89		10255
POL	MAYFIHFKR	930	11	57	89		10256
POL	GGIGGYSAGER	941	11	57	89		10257
POL	NILTKGYA	540	8	58	92		10258
POL	VLFGWKGSP	337	11	58	92		10259
POL	KDSTKWRK	255	8	58	91		10260
POL	EVQLGPII	278	8	58	91		10261
POL	TVLDVGDAY	296	8	58	91		10262
POL	YALGIQA	693	8	58	91		10263
POL	GGNEQVDK	735	8	58	91		10264
POL	FIHFKRK	933	8	58	91		10265
POL	GGYSAGER	944	8	58	91		10266
POL	RVYVRSR	976	8	58	91		10267
POL	IGNEQVDK	734	9	58	91	0.0004	10268
POL	PAETGQETA	842	9	58	91		10269
POL	VFIHFKRK	932	9	58	91	0.0004	10270
POL	IGGYSAGER	943	9	58	91	0.0004	10271
POL	STKWRKLVDF	257	10	58	91	0.0003	10272
POL	GIGGNEQVDK	733	10	58	91	0.0005	10273
POL	PAETGQETAY	842	10	58	91		10274
POL	AVFIHFKRK	931	10	58	91	0.6600	10275
POL	GIGGYSAGER	942	10	58	91	0.0003	10276
POL	DSTKWRKLVDF	256	11	58	91		10277
POL	STKWRKLVDF	257	11	58	91		10278
POL	DSQYALGIQA	690	11	58	91		10279
POL	KGIGGNEQVDK	732	11	58	91		10280
POL	VIPAEQGQETA	840	11	58	91		10281

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HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QGWKGSQA	340	8	59	92		10282
POL	AVIVASGY	828	8	59	92		10283
POL	ETQGETAY	844	8	59	92		10284
POL	QAEILKTA	920	8	59	92		10285
POL	GGIGGYS	941	8	59	92		10286
POL	GIWOLDCTII	811	9	59	92		10287
POL	VAVIVASGY	827	9	59	92	0.0004	10288
POL	KGPAPKLLWK	988	9	59	92	0.0021	10289
POL	QGWKGSQAIF	340	10	59	92	0.0004	10290
POL	EVNIVTDSQY	684	10	59	92		10291
POL	PGIWOLDCTII	810	10	59	92		10292
POL	TAVQMAVFIH	926	10	59	92	0.0004	10293
POL	VGKLNWASQI	450	11	59	92		10294
POL	EVNIVTDSQYA	684	11	59	92		10295
POL	NFRKKGGIGGY	936	11	59	92		10296
POL	PAKILLWKGGG	990	11	59	92		10297
POL	QLDXTILLEGK	814	10	60	95	0.0010	10298
POL	DFRELNKR	285	8	60	94		10299
POL	VLDVGDAY	297	8	60	94		10300
POL	MAVFIHNF	930	8	60	94		10301
POL	VDFRELNKR	264	9	60	94		10302
POL	VLDVGDAYF	297	9	60	94		10303
POL	MGYELIPDK	419	9	60	94	0.0640	10304
POL	KLWASQIY	452	9	60	94	0.1200	10305
POL	AVQMAVFIH	927	9	60	94		10306
POL	QMAVFIHNF	929	9	60	94	0.0010	10307
POL	MAVFIHNF	930	9	60	94	0.0170	10308
POL	KLLWKGEA	992	9	60	94	0.0003	10309
POL	LVDFRELNKR	263	10	60	94		10310
POL	WMGYELIPDK	418	10	60	94		10311
POL	QMAVFIHNF	929	10	60	94	0.0005	10312
POL	MAVFIHNF	930	10	60	94	0.6100	10313
POL	KLVDRELNKR	262	11	60	94	0.0068	10314
POL	PKKKIQKEIPF	406	11	60	94		10315
POL	AVQMAVFIH	927	11	60	94		10316
POL	QMAVFIHNF	929	11	60	94		10317
POL	EALDTGA	108	8	61	95		10318
POL	LDVGDAYF	298	8	61	95		10319
POL	LVGKLNWA	449	8	61	95		10320
POL	IVTDSQYA	687	8	61	95		10321
POL	TAVQMAVF	926	8	61	95		10322
POL	NDIQKLVGK	444	9	61	95	0.0003	10323
POL	KLVGKLNWA	448	9	61	95		10324
POL	NIVTDSQYA	686	9	61	95		10325
POL	LDCTILLEGK	815	9	61	95		10326
POL	TVNDIQKLVGK	442	11	61	95	0.0400	10327
POL	MIGGIQGF	133	8	62	97		10328
POL	VDFRELNKR	264	8	62	97		10329
POL	WTVNDIQK	441	8	62	97	0.0003	10330
POL	DIQKLVGK	445	8	62	97		10331

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HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*OJ01	SEQ ID NO.
POL	NIVTDSOY	686	8	62	97		10332
POL	DTIILEGK	816	8	62	97		10333
POL	AVFIINEK	931	8	62	97	0.0280	10334
POL	VFIINFKR	932	8	62	97		10335
POL	LLWKGEQA	993	8	62	97	0.0004	10336
POL	KMIGGIGGF	132	9	62	97	0.0110	10337
POL	LVDRELNK	263	9	62	97	0.1700	10338
POL	AVFIINFKR	931	9	62	97	0.0099	10339
POL	MIGGIGGFIK	133	10	62	97	0.5100	10340
POL	KLVDFRELNK	262	10	62	97	2.1000	10341
POL	KMIGGIGGFIK	132	11	62	97	0.0003	10342
POL	NVLPQGWK	336	8	63	100	0.0004	10343
POL	IGGIGGFIK	134	9	63	98		10344
POL	GGIGGFIK	135	8	64	100		10345
POL	FLWMGYELII	416	9	64	100		10346
POL	PFLWMGYELII	415	10	64	100		10347
REV	GTRQTRKNR	37	9	01	50		10348
REV	TTRQARRNR	37	9	01	50		10349
REV	GTRQTRKNR	37	10	01	50		10350
REV	TTRQARRNR	37	10	01	50		10351
REV	GTRQTRKNR	37	11	01	50		10352
REV	TTRQARRNR	37	11	01	50		10353
REV	GTRQTRKNR	37	11	01	50		10354
REV	TTRQARRNR	37	11	01	19		10355
REV	GTETGVGR	103	8	06	19		10356
REV	QGTETGVGR	102	9	06	16		10357
REV	LLKTVRLIK	12	9	10	17		10358
REV	GDSDELLK	6	9	11	17		10359
REV	PLQIPIIER	76	9	11	17		10360
REV	SGDSDELLK	5	10	11	17		10361
REV	RSQDSDELLK	4	11	11	17		10362
REV	PVPLQPIIER	74	11	11	19		10363
REV	RAQRQIR	50	8	12	19		10364
REV	DSDELLK	7	8	12	19		10365
REV	ILSTCLGR	63	8	12	19		10366
REV	ILSTCLGR	62	9	12	20		10367
REV	AVRIKILY	17	9	13	20		10368
REV	PSPECTROA	31	9	13	20		10369
REV	QLPPLERLII	78	9	13	20		10370
REV	PSPECTROAR	31	10	13	20		10371
REV	PSPECTROAR	31	11	13	20		10372
REV	PLQIPIELII	76	11	13	22		10373
REV	GTRQARRNR	36	11	14	24		10374
REV	RAQRQIHI	50	8	15	23		10375
REV	GTRQARRNR	36	9	15	23		10376
REV	GTRQARRNR	36	10	15	25		10377
REV	OARKNRNR	40	9	16	25		10378
REV	OARKNRNR	40	11	16	27		10379
REV	OARKNRNR	40	8	17	28		10380
REV	QARKNRNR	40	11	17	41		10381
REV	IKILYQSNPY	20	11	18	26		10382
REV	KILYQSNPY	22	9	26	42		10383
REV	ILYQSNPY	23	8	27			10384

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HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
REV	EGTRQARR	35	8	27	42		10382
REV	EGTRQARRNR	35	10	27	42		10383
REV	EGTRQARRNR	35	11	27	42		10384
REV	GTROARRNR	36	9	34	53		10385
REV	GTROARRNR	36	10	34	53		10386
REV	GTROARRNR	36	11	34	53		10387
REV	PVQLQPLER	74	11	34	53		10388
REV	PLQLPLER	76	9	35	55		10389
REV	QARRNRNR	40	11	37	58		10390
REV	QARRNRNR	40	8	38	59		10391
REV	QARRNRNR	40	9	38	59		10392
TAT	PGGYPRK	104	8	01	50		10393
TAT	AGPGGYPR	102	9	01	50		10394
TAT	TGPGGQPCII	102	9	01	50		10395
TAT	ETGPGQPCII	101	10	01	50		10396
TAT	KAGPGGYPRK	101	10	01	50		10397
TAT	AGPGGYPRK	102	10	01	50		10398
TAT	KAGPGGYPR	101	11	01	50		10399
TAT	GGYPRKKGSC	105	11	01	50		10400
TAT	PGSQRTA	17	8	10	16		10401
TAT	ACTNCCYCK	24	8	10	16		10402
TAT	TACTNCCYCK	23	9	10	16		10403
TAT	YCKKCCFII	29	8	11	17		10404
TAT	YCKKCCYII	29	8	11	17		10405
TAT	CFIICQVCF	34	8	11	17		10406
TAT	VDPRLEPWK	4	9	11	17		10407
TAT	ACNNCCYCKK	24	9	11	17		10408
TAT	CCFIICQVCF	33	9	11	17		10409
TAT	PVDPRLEPWK	3	10	11	17	0.0005	10410
TAT	VDPRLEPWKII	4	10	11	17		10411
TAT	TACNNCCYCKK	23	10	11	17		10412
TAT	PVDPRLEPWK	3	11	11	17		10413
TAT	RGDPTGPKES	84	11	11	17		10414
TAT	GDPTGPKESK	85	11	11	17		10415
TAT	ESKKKVIKSK	93	9	12	19		10416
TAT	GDPTGPKESK	85	10	12	19		10417
TAT	PTGPKESKKK	88	10	12	19		10418
TAT	TGPKESKKK	89	9	13	20		10419
TAT	FLNKGGLGISY	41	10	14	22		10420
TAT	PVDPRLEPWNI	3	11	14	22		10421
TAT	CFLNKGGLGISY	40	11	14	22		10422
TAT	RGDPTGPK	84	8	16	25		10423
TAT	VDPRLEPWNI	4	10	16	25		10424
TAT	ACNNCCYCK	24	8	17	27		10425
TAT	TACNNCCYCK	23	9	17	27		10426
TAT	PTGPKESKK	88	9	18	28		10427
TAT	TGPKESKK	89	8	19	30		10428
TAT	PTGPKESK	88	8	20	31		10429
TAT	YGRKKRRQR	50	11	22	34		10430
TAT	PGSQPKTA	17	8	26	41		10431

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
TAT	YGRKKRQR	50	10	38	59		10432
TAT	ISYGRKKRQR	48	11	39	61		10433
TAT	YGRKKRQR	50	9	41	64		10434
TAT	GISYGRKKRR	47	10	45	70	0.0003	10435
TAT	LGISYGRKKRR	46	11	45	70		10436
TAT	ISYGRKKRR	48	9	46	72	0.0008	10437
TAT	GLGISYGRKKRR	45	11	54	86		10438
TAT	GLGISYGR	45	8	55	87		10439
TAT	GLGISYGRK	45	9	55	87	0.0340	10440
TAT	GLGISYGRKK	45	10	55	87		10441
TAT	KGLGISYGR	44	9	55	86	0.0006	10442
TAT	KGLGISYGRK	44	10	55	86	0.0100	10443
TAT	KGLGISYGRKK	44	11	55	86		10444
TAT	GISYGRKKR	47	9	57	89	0.0008	10445
TAT	LGISYGRKKR	46	10	57	89		10446
TAT	LGISYGRK	46	8	58	91		10447
TAT	GISYGRKK	47	8	58	91		10448
TAT	ISYGRKKR	47	8	58	91		10449
TAT	LGISYGRKK	46	9	58	91		10450
TAT	LIVWQVDR	8	8	10	16	0.0004	10451
VIF	RMRLNTWK	15	8	10	16		10452
VIF	LKPKKIK	158	8	10	16		10453
VIF	KGWFFRIIHIY	36	9	10	16		10454
VIF	ALIKPKKIK	157	9	10	16		10455
VIF	VDRMRINTWK	11	10	10	16		10456
VIF	GVSEWRLLR	87	10	10	16		10457
VIF	QVDRMRINTW	12	11	10	16		10458
VIF	RLVITTYWGL	65	11	10	16		10459
VIF	QTGERDWHLG	75	11	10	16		10460
VIF	GVSEWRLLR	87	11	10	16		10461
VIF	IDPDLADQLIH	103	11	10	16		10462
VIF	LVEDRWNKIQ	178	11	10	16		10463
VIF	YSTQIDPDLA	99	10	11	17		10464
VIF	YSTQIDPDLA	99	10	11	17		10465
VIF	SEWRLLR	89	8	11	17		10466
VIF	TALIKPKK	156	8	11	17		10467
VIF	LVEDRWNK	178	8	11	17		10468
VIF	VSIEWRLRR	88	9	11	17		10469
VIF	SEWRLLRY	89	9	11	17		10470
VIF	STQVDPGLA	100	9	11	17		10471
VIF	SLQYLALKA	149	9	11	17		10472
VIF	LTALIKPKK	155	9	11	17		10473
VIF	KLVEDRWNK	177	9	11	17		10474
VIF	VSIEWRLRRY	88	10	11	17		10475
VIF	GLADQLIHMH	106	10	11	17		10476
VIF	IVSPRCEYQA	133	10	11	17		10477
VIF	GSLOYLALKA	148	10	11	17		10478
VIF	ALTALIKPKK	154	10	11	17		10479
VIF	PGLADQLIHMH	105	11	11	17		10480
VIF	GLADQLIHMH	106	11	11	17		10481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0301	SEQ ID NO.
VIF	VGSLOYLALK	147	11	11	17		10482
VIF	LALTALIKPKK	153	11	11	17		10483
VIF	WFRUIIYESR	38	11	12	19		10484
VIF	KOWFYRIIII	36	8	12	19		10485
VIF	WGLQTGER	72	8	12	19		10486
VIF	QTGERDWII	75	8	12	19		10487
VIF	SDSAIRKA	121	8	12	19		10488
VIF	SLOYLALA	149	8	12	19		10489
VIF	IVWQVDIRMK	9	9	12	19		10490
VIF	STQIDPDLA	100	9	12	19		10491
VIF	FSDSAIRKA	120	9	12	19		10492
VIF	FSISAIRNA	120	9	12	19		10493
VIF	GSLOYLALA	148	9	12	19		10494
VIF	SLOYLALA	149	9	12	19		10495
VIF	KIRTWNSLVK	17	10	12	19		10496
VIF	LVKIIIMYVSK	24	10	12	19		10497
VIF	GLQTGERDWII	73	10	12	19		10498
VIF	TGERDWILGII	77	10	12	19		10499
VIF	IIGVSEWILR	86	10	12	19		10500
VIF	CFSDSAIRKA	119	10	12	19		10501
VIF	CFSESIRNA	119	10	12	19		10502
VIF	VGSLOYLALA	147	10	12	19		10503
VIF	GSLOYLALA	148	10	12	19		10504
VIF	IVWQVDRMKI	9	11	12	19		10505
VIF	KIRTWNSLVK	17	11	12	19		10506
VIF	SLVKIIIMYVS	23	11	12	19		10507
VIF	LVKIIIMYVSK	24	11	12	19		10508
VIF	WGLQTGERD	72	11	12	19		10509
VIF	DCFSESAIRKA	118	11	12	19		10510
VIF	ICFSESAIRNA	118	11	12	19		10511
VIF	KVGSLOYLAL	146	11	12	19		10512
VIF	VGSLOYLALA	147	11	12	19		10513
VIF	WFRUIIYESR	38	10	13	21		10514
VIF	QVDRMKIR	12	8	13	20		10515
VIF	IIMYVSKKA	28	8	13	20		10516
VIF	IHIPGDKAR	56	8	13	20		10517
VIF	ADQLIIMH	108	8	13	20		10518
VIF	CFSDSAIR	119	8	13	20		10519
VIF	FSDSAIRK	120	8	13	20		10520
VIF	SLOYLALK	149	8	13	20		10521
VIF	LTALIKPK	155	8	13	20		10522
VIF	LADQLIIMH	107	9	13	20		10523
VIF	ADQLIIMH	108	9	13	20		10524
VIF	CFSDSAIRK	119	9	13	20		10525
VIF	FSDSAIRKA	120	9	13	20		10526
VIF	GSLOYLALK	148	9	13	20		10527
VIF	ALTALIKPK	154	9	13	20		10528
VIF	SVKLTEDR	174	9	13	20		10529
VIF	EVHPLGDAR	54	10	13	20		10530
VIF	LADQLIIMH	107	10	13	20		10531

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	ADQLIIMIFY	108	10	13	20		10532
VIF	DFSESARK	118	10	13	20		10533
VIF	CFSESARKA	119	10	13	20		10534
VIF	VGSLYLALK	147	10	13	20		10535
VIF	LALTALIKP	153	10	13	20		10536
VIF	PSVKKLTEDR	173	10	13	20		10537
VIF	LADQLIIMIFY	107	11	13	20		10538
VIF	QLIILYFDCF	110	11	13	20		10539
VIF	DFCFESARK	117	11	13	20		10540
VIF	YLALTALIKP	152	11	13	20		10541
VIF	QLIILYF	110	8	14	22		10542
VIF	QLIIMIFY	110	8	14	22		10543
VIF	FSESAIRK	120	8	14	22		10544
VIF	IVSPICEY	133	8	14	22		10545
VIF	GVSEWRRLR	87	9	14	22		10546
VIF	ADQLIILY	108	9	14	22		10547
VIF	CFSESARK	119	9	14	22		10548
VIF	VDRMRRTWK	13	10	14	22		10549
VIF	LADQLIILY	107	10	14	22		10550
VIF	ADQLIILYF	108	10	14	22		10551
VIF	RDYQAGINK	137	10	14	22		10552
VIF	QVDRMRRTWK	12	11	14	22		10553
VIF	RRTWNSLVK	17	11	14	22		10554
VIF	LADQLIILYF	107	11	14	22		10555
VIF	QLIIMIFYDCF	110	11	14	22		10556
VIF	RMRTWK	15	8	15	23		10557
VIF	RTWKS LVK	19	8	15	23		10558
VIF	VSIEWRLR	88	8	15	23		10559
VIF	ADQLIILY	108	8	15	23		10560
VIF	IIMIFYDCF	113	8	15	23		10561
VIF	RTWKS LVKII	19	9	15	23		10562
VIF	QGVSEWRK	86	9	15	23		10563
VIF	LADQLIILY	107	9	15	23		10564
VIF	ARKALGII	124	9	15	23		10565
VIF	CDYQAGINK	138	9	15	23		10566
VIF	RRTWKS LVK	17	10	15	23		10567
VIF	RRTWNSLVK	17	10	15	23		10568
VIF	RTWKS LVKIII	19	10	15	23		10569
VIF	IIMIFYDCF	111	10	15	23		10570
VIF	SAIRKALGII	123	10	15	23		10571
VIF	RRTWKS LVK	17	11	15	23		10572
VIF	LQQGVSEWR	84	11	15	23		10573
VIF	VDPGLADQLIII	103	11	15	23		10574
VIF	ITTYWGLH	68	8	16	25		10575
VIF	GVSEWRK	87	8	16	25		10576
VIF	ILYYFDCF	113	8	16	25		10577
VIF	RCDYQAGII	137	8	16	25		10578
VIF	LALTALIK	153	8	16	25		10579
VIF	VITTYWGLII	67	9	16	25		10580
VIF	YLALTALIK	152	9	16	25		10581

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	KTKGIRGSII	188	9	16	25	0.0004	10582
VIF	LVITTYWGLII	66	10	16	25		10583
VIF	LHILYEDCF	111	10	16	25		10584
VIF	EDRWNPQKT	180	11	17	27		10585
VIF	KSLVKIIMY	22	9	18	28		10586
VIF	EDRWNPQKT	180	11	18	28		10587
VIF	RCEYQAGIINK	137	10	19	30		10588
VIF	HIPLGEAR	56	8	20	31		10589
VIF	EVHIPLGEAR	54	10	20	31		10590
VIF	IITGERDWH	75	8	21	33		10591
VIF	DLADQLII	106	8	21	33		10592
VIF	PLADQLII	105	9	21	33		10593
VIF	VSPRCEYQA	134	9	21	33		10594
VIF	GLITGERDWH	73	10	21	33		10595
VIF	WGLITGERD	72	11	21	33		10596
VIF	VSPRCEYQAG	134	11	21	33		10597
VIF	LTEDRWNPQ	178	11	21	33		10598
VIF	GSITMNGII	194	8	22	34	0.0390	10599
VIF	RGSHIMNGII	193	9	22	34		10600
VIF	TTYWGLITGE	69	11	22	34		10601
VIF	IILGHGVSEW	83	11	22	34		10602
VIF	SSEVIHPLGDA	52	11	23	36		10603
VIF	NSLVKIIIMY	22	9	24	38		10604
VIF	EVHIPLGDA	54	9	24	38		10605
VIF	QGVSEWR	86	8	25	39		10606
VIF	EVHIPLGEA	54	9	25	39		10607
VIF	LQGVSEWR	84	10	25	39		10608
VIF	SSEVIHPLGEA	52	11	25	39		10609
VIF	IILGGVSEW	83	11	25	39		10610
VIF	RCEYQAGII	137	8	26	41		10611
VIF	RTWNSLVKII	19	9	26	41		10612
VIF	RTWNSLVKIII	19	10	26	41		10613
VIF	RTWNSLVK	19	8	27	42		10614
VIF	HGVSEWR	86	8	27	42		10615
VIF	GLADQLII	106	8	27	42		10616
VIF	PGLADQLII	105	9	27	42		10617
VIF	LGHGVSEWR	84	10	27	42		10618
VIF	YFDCFSAIR	116	11	27	42		10619
VIF	WGLITGER	72	8	28	44		10620
VIF	YFDCFSIA	116	9	28	44		10621
VIF	DCFSIAIR	118	9	28	44		10622
VIF	DCFSIAIR	117	10	28	44		10623
VIF	DCFSIA	117	8	29	45		10624
VIF	CFSESAIR	119	8	29	45	0.0130	10625
VIF	KLTERDWNK	177	9	29	45		10626
VIF	VGSLOYLALT	147	11	30	47		10627
VIF	LTEDRWNK	178	8	31	48	0.0003	10628
VIF	SLOYLATA	149	9	31	48		10629
VIF	GSLOYLATA	148	10	31	48		10630
VIF	IYWQVDRMRI	9	11	33	52		10631

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SEQ ID NO.
VIF	QVDRMRIR	12	8	34	53		10632
VIF	EDRWKIPQK	180	9	39	61		10633
VIF	VMIVWQVDR	7	11	41	64		10634
VIF	QVMIVWQVDR	6	10	43	67		10635
VIF	MIVWQVDRM	8	10	43	67	0.0062	10636
VIF	AGINKVGSLSQ	142	11	43	67		10637
VIF	SLVKIHIMY	23	8	44	69		10638
VIF	VMIVWQVDR	7	9	44	69	0.0034	10639
VIF	MIVWQVDR	8	8	46	72		10640
VIF	IVWQVDRMR	9	9	47	73	0.0008	10641
VIF	KVGSLOYLA	146	9	52	81	0.0036	10642
VIF	VGSLOYLA	147	8	58	91		10643
VPR	#LPRRRGR	85	8	01	50		10644
VPR	NIRRRVR	85	8	01	50		10645
VPR	#LPRRRGRNG	85	11	01	50		10646
VPR	WALLELELK	18	10	09	15		10647
VPR	QLLFVIFR	66	8	10	16		10648
VPR	ISIRIGIR	79	8	10	16		10649
VPR	RIGTRQR	81	8	10	16		10650
VPR	IGTRQR	82	8	10	16		10651
VPR	ALLELELK	19	9	10	16		10652
VPR	RIGTRQR	81	9	10	16		10653
VPR	ISIRIGTRQR	79	10	10	16		10654
VPR	ISIRIGTRQR	79	11	10	16		10655
VPR	WLIIGLQY	38	8	11	17		10656
VPR	IFRIGCRH	71	8	11	17		10657
VPR	ISIRIGTR	79	8	11	17		10658
VPR	FIIFRIGCR	69	9	11	17		10659
VPR	FIIFRIGCR	68	10	11	17		10660
VPR	FIIFRIGCRH	69	10	11	17		10661
VPR	FVIFRIGCQH	69	10	11	17		10662
VPR	IFRIGCRHSR	71	10	11	17		10663
VPR	LLFIIFRIGCR	67	11	11	17		10664
VPR	LFVIFRIGCRH	68	11	11	17		10665
VPR	LFVIFRIGCQH	68	11	11	17		10666
VPR	RIGCRHSR	74	8	12	19		10667
VPR	LQHIYNTY	42	9	13	20		10668
VPR	LQYIYETY	42	9	13	20		10669
VPR	IFPKIWLH	33	8	14	22		10670
VPR	KSEAVRIHPR	27	10	14	22		10671
VPR	AVRIHPRWL	30	11	14	22		10672
VPR	KSEAVRHF	27	8	15	23		10673
VPR	ELKSEAVRIIF	25	10	15	23		10674
VPR	ELKSEAVR	25	8	16	25		10675
VPR	ETYGDTWA	48	8	16	25		10676
VPR	DTWAGVEA	52	8	16	25		10677
VPR	AGVEAIR	55	8	16	25		10678
VPR	LLELKSEA	22	9	16	25		10679
VPR	ELKSEAVRIH	25	9	16	25		10680
VPR	GDTWAGVEA	51	9	16	25		10681

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.101$	SI:Q ID NO.
VPR	WAGVEAIR	54	9	16	25		10682
VPR	ELLEELKNEA	21	10	16	25		10683
VPR	ELLEELKSEA	21	10	16	25		10684
VPR	YGDWAGVEA	50	10	16	25		10685
VPR	LLLELKSEAVR	22	11	16	25		10686
VPR	DTWAGVEAIR	52	11	16	25		10687
VPR	ELKNEAVR	25	8	17	27		10688
VPR	ELLEELKNEA	22	9	17	27		10689
VPR	ELKNEAVRH	25	9	17	27		10690
VPR	LGQIYYET	42	9	17	27		10691
VPR	ELKNEAVRIIF	25	10	17	27		10692
VPR	ELLEELKNEAVR	22	11	17	27		10693
VPR	EGVEAIR	55	8	18	28		10694
VPR	DTWEGVEAIR	52	11	18	28		10695
VPR	RARNQASR	93	8	19	30		10696
VPR	WLIIGLQHI	38	8	20	31		10697
VPR	IIGLQHIY	40	8	20	31		10698
VPR	WLIIGLQHIY	38	10	20	31		10699
VPR	DTWEGVEA	52	8	23	36		10700
VPR	GDTWEGVEA	51	9	23	36		10701
VPR	YGDWEGVEA	50	10	23	36		10702
VPR	LFHFRIGCQII	68	11	29	45		10703
VPR	FIHFRIGCQII	69	10	30	47		10704
VPR	FIHFRWLII	33	8	31	49		10705
VPR	AVRIHPRPWL	30	13	31	48		10706
VPR	RIQQQLFHIF	62	11	34	53	0.0130	10707
VPR	RIQQQLFHIF	63	11	35	55		10708
VPR	RIQQQLFHIF	63	11	35	55		10709
VPR	RIQQQLFHIF	62	10	36	56		10710
VPR	RIQQQLFHIF	63	9	37	58		10711
VPR	EDQGIHQREPY	6	10	37	58		10712
VPR	AIIRLQQLLF	59	11	38	59		10713
VPR	QAPEDQGFQR	3	10	39	62		10714
VPR	IRILQQLLF	60	10	41	64		10715
VPR	WTLELEELK	18	10	42	69		10716
VPR	QGIHQREPY	8	8	43	68		10717
VPR	QLLFHIFR	66	8	44	69		10718
VPR	IFRIGCQII	71	8	44	69		10719
VPR	TLELEELK	19	9	44	69		10720
VPR	IFRIGCQISR	71	10	44	69		10721
VPR	RIQQQLLF	62	8	45	70		10722
VPR	RIGCQISR	74	8	47	73		10723
VPR	EAVRIHPR	29	8	59	92		10724
VPU	IDYRLGVGA	9	9	01	33		10725
VPU	VDYRIVIVA	9	9	01	33		10726
VPU	VDYRLGVGA	9	9	01	33		10727
VPU	KVDYRIVIVA	7	10	01	33		10728
VPU	KDYRLGVGA	7	10	01	33		10729
VPU	RIDYRLGVGA	7	10	01	33		10730
VPU	VDYRIVIVA	9	10	01	33		10731

Table XVI
HIV Δ03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Antim Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPV	KVDYRIVVAF	7	11	01	33		10732
VPV	LVQRKQDR	43	8	01	50		10731
VPV	GVEMGHIA	91	8	01	50		10734
VPV	VTLSSSK	94	8	01	50		10735
VPV	LVQRKQDR	43	9	01	50		10736
VPV	LVTLLSSK	91	9	01	50		10737
VPV	RIKEIRDSDY	64	11	01	50		10738
VPV	RIREIRDSDY	64	11	01	50		10739
VPV	LAVALVVA	13	9	09	15		10740
VPV	WTIVFIEYR	34	9	10	16		10741
VPV	TIVFIEYR	35	8	10	16		10742
VPV	IDRLIDRIR	54	9	10	16		10743
VPV	RLIDRIR	56	9	10	16		10744
VPV	KIDRLIDRIR	52	10	10	16		10745
VPV	VVWTIVFIEYR	31	11	10	16		10746
VPV	ESIGDQEELSA	77	11	10	16		10747
VPV	EGDQEELSA	77	9	11	17		10748
VPV	WTIVFIEY	34	8	12	19		10749
VPV	AIVALVVA	14	8	12	19		10750
VPV	IVFIEYRK	36	8	12	19		10751
VPV	IDRIRERA	59	8	12	19		10752
VPV	LIDRIRERA	58	9	12	19		10753
VPV	VVWTIVFIEY	31	10	12	19		10754
VPV	IVVWTIVFIEY	30	11	12	19		10755
VPV	GDQEELSA	78	8	14	22		10756
VPV	LIDRIRER	58	8	14	22		10757
VPV	AIVVWTIVF	29	9	14	22		10758
VPV	IVVWTIVF	30	8	15	23		10759
VPV	KIDRLIDR	52	8	15	23		10760
VPV	ILRQRKIDR	46	9	15	23		10761
VPV	KILRQRKIDR	45	10	15	23	0.0039	10762

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1001	SEQ ID NO.
ENV	IGPGQTFY	361	8	01	25		10763
ENV	IGSGOAFY	361	8	01	25		10764
ENV	GTAGNSR	375	8	01	33		10765
ENV	NNTSPKR	375	8	01	33		10766
ENV	ADNLWTVY	42	9	01	33		10767
ENV	GIGPGQTFY	360	9	01	33		10768
ENV	SIGSGOAFY	360	9	01	33		10769
ENV	ADNLWTVY	42	10	01	33		10770
ENV	EGKNEINDY	217	10	01	33		10771
ENV	NTSPKSRVAY	376	10	01	33		10772
ENV	TAGNSRRAAY	376	10	01	33		10773
ENV	GTAGNSRRAA	375	11	01	33		10774
ENV	NNTSPKSRVA	375	11	01	33		10775
ENV	KLREKQFENK	405	11	01	25		10776
ENV	KNNTETNK	535	8	01	50		10777
ENV	HNHTTH	584	8	01	50		10778
ENV	VISTRTHIR	584	8	01	50		10779
ENV	HNHTPIIR	585	8	01	50		10780
ENV	STRTHIREK	586	8	01	50		10781
ENV	SNNTSPKR	374	9	01	50		10782
ENV	NANITPICR	478	9	01	50		10783
ENV	HNHTPIIR	584	9	01	50		10784
ENV	ISTRTHIREK	585	9	01	50		10785
ENV	HNHTPIREK	586	9	01	50		10786
ENV	STRTHIREK	586	9	01	50		10787
ENV	VISTRTHIREK	584	10	01	50		10788
ENV	HNHTPIREK	585	10	01	50		10789
ENV	ISTRTHIREK	585	10	01	50		10790
ENV	HNHTPIREKR	586	10	01	50		10791
ENV	ITTEGNTILOCR	478	11	01	50		10792
ENV	NANITPICR	478	11	01	50		10793
ENV	GNSTNGTETF	535	11	01	50		10794
ENV	HNHTTHIREK	584	11	01	50		10795
ENV	VISTRTHIREKR	584	11	01	50		10796
ENV	HNHTPIREKR	585	11	01	50		10797
ENV	DSSNSTGNY	218	9	01	20		10798
ENV	STNGTETFR	537	9	01	17		10799
ENV	TNSSYTNDY	458	10	01	17		10800
ENV	NDTENNTETFR	537	11	01	17		10801
ENV	NTETNKTEF	537	11	01	17		10802
ENV	NTGNTTETF	537	11	01	17		10803
ENV	NGSENGTETF	537	11	02	33		10804
ENV	GSENGTETFR	538	10	02	18		10805
ENV	NDITLPCR	477	9	03	20		10806
ENV	NDITLPCR	477	11	03	20		10807
ENV	RGWEALY	895	8	06	10		10808
ENV	KGRLGWEGKL	891	11	08	27		10809
ENV	LGWEOLY	895	8	09	29		10810
ENV	RLGWEGLY	894	9	09	29		10811
ENV	GLRLGWEGKL	892	11	09	29		10812

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
ENV	LGRRGWEALK	883	10	09	15		10813
ENV	LLGRRGWEAL	882	11	09	15		10814
ENV	RLGWIGLK	894	8	10	32		10815
ENV	GLRLGWEGLK	892	10	10	32		10816
ENV	ENLWVTYY	43	8	10	17		10817
ENV	ENLWVTYY	43	9	10	17		10818
ENV	DIIGDIRQAI	372	10	10	16		10819
ENV	NTRKSIR	350	8	10	16		10820
ENV	PLGVAPTR	571	8	10	16		10821
ENV	DTINWLWY	769	8	10	16		10822
ENV	DFLIAAR	870	8	10	16		10823
ENV	STITQACP	243	9	10	16		10824
ENV	FDITNLWY	768	9	10	16		10825
ENV	DFILIAAR	869	9	10	16		10826
ENV	FAILKCNDDK	269	10	10	16		10827
ENV	MLQLTVWGIK	651	10	10	16		10828
ENV	RVLAVERYLR	665	10	10	16		10829
ENV	WFDITNLW	767	10	10	16		10830
ENV	EGIEEGGER	828	10	10	16		10831
ENV	GFALKCNDDK	268	11	10	16		10832
ENV	GDIDIRQAI	371	11	10	16		10833
ENV	NVTWSSWSN	693	11	10	16		10834
ENV	WMEWEREDN	723	11	10	16		10835
ENV	IAIAVAEGTDR	925	11	10	16		10836
ENV	RGWEALKY	886	8	11	18		10837
ENV	KLWVTVYY	44	8	11	17		10838
ENV	WNSSWSNR	696	8	11	17		10839
ENV	TITQACTP	244	8	11	17		10840
ENV	IGPGQTFY	358	8	11	17		10841
ENV	LAVERYLR	667	8	11	17		10842
ENV	SNWLWYIK	771	8	11	17		10843
ENV	NLCFSYII	859	8	11	17		10844
ENV	RIGPGQTFY	357	9	11	17		10845
ENV	ITTHSFNCR	431	9	11	17		10846
ENV	NITLPCRIK	482	9	11	17		10847
ENV	VLAVERYLR	666	9	11	17		10848
ENV	ISNLWYIK	770	9	11	17		10849
ENV	RNLCLFSYII	858	9	11	17		10850
ENV	NLCFSYIIR	859	9	11	17		10851
ENV	EITTHSFNCR	430	10	11	17		10852
ENV	RNLCLFSYIIR	858	10	11	17		10853
ENV	YATGDIGDIR	368	11	11	17		10854
ENV	DLRNLCLFSYII	856	11	11	17		10855
ENV	NLCFSYIIRLR	859	11	11	17		10856
ENV	GNLWVTYY	43	8	12	20		10857
ENV	GNLWVTYY	43	9	12	20		10858
ENV	TGDIIGDIR	370	9	12	19		10859
ENV	EAQIILLK	646	8	12	19		10860
ENV	ILKCNDDK	271	8	12	19		10861
ENV	TTTHSFNCR	432	8	12	19		10862

Table XVII
 HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta \cdot 1101$	SEQ ID NO.
ENV	MTWMEWER	721	8	12	19		10863
ENV	GGERDRDR	834	8	12	19		10864
ENV	AILKNDKK	270	9	12	19		10865
ENV	LAEEVVIR	312	9	12	19	0.0002	10866
ENV	INMWQEVGK	493	9	12	19		10867
ENV	NMTWMEWER	720	9	12	19		10868
ENV	GIEEGGER	829	9	12	19		10869
ENV	EGGERDRDR	833	9	12	19		10870
ENV	SLAEEVVIR	311	10	12	19		10871
ENV	ATGDIGDIR	369	10	12	19		10872
ENV	IINMWQEVGK	492	10	12	19		10873
ENV	ALAQOILLK	644	10	12	19		10874
ENV	LLQYWSQELK	906	10	12	19		10875
ENV	AILIIPRRIR	946	10	12	19		10876
ENV	PIRIUOGLER	951	10	12	19		10877
ENV	KTLFCASDA	601	11	12	19		10878
ENV	GSLAEEVVIR	310	11	12	19		10879
ENV	QINMWQEVG	491	11	12	19		10880
ENV	KNEQELLELDK	750	11	12	19		10881
ENV	GIEEGGENDR	829	11	12	19		10882
ENV	NLLQYWSQEL	905	11	12	19		10883
ENV	RAILLIPRRIR	945	11	12	19		10884
ENV	SVEINCTR	340	8	13	20		10885
ENV	GDIGDIR	371	8	13	20		10886
ENV	KLTWVGIK	653	8	13	20		10887
ENV	RAILLIPR	945	8	13	20		10888
ENV	AILIIPR	946	8	13	20		10889
ENV	KAKRRVQR	579	9	13	20	0.0002	10890
ENV	RAILLIPRR	945	9	13	20		10891
ENV	ILIIIPRRIR	947	9	13	20		10892
ENV	TNVSTVQCTH	286	10	13	20		10893
ENV	SGGDEIVMII	425	10	13	20		10894
ENV	LLKLTWVGIK	651	10	13	20		10895
ENV	NTSVITQACPK	241	11	13	20		10896
ENV	CTNVSTVQCT	285	11	13	20		10897
ENV	SSGGDLIITII	424	11	13	20		10898
ENV	SSGGDEIVMII	424	11	13	20		10899
ENV	PTKAKRRVQ	576	11	13	20		10900
ENV	KAKRRVQRE	579	11	13	20		10901
ENV	ILLKLTWVGI	650	11	13	20		10902
ENV	KNEFDLLALD	370	9	14	23		10903
ENV	TOEIGDIR	370	9	14	22		10904
ENV	AITQACPK	244	8	14	22		10905
ENV	GDPEIVMI	427	8	14	22		10906
ENV	QDLLALDK	753	8	14	22		10907
ENV	SAITQACPK	243	9	14	22		10908
ENV	FAILKCNDK	269	9	14	22		10909
ENV	GGDEIVMII	426	9	14	22	0.0002	10910
ENV	TITLPCRIK	482	9	14	22		10911
ENV	TSAITQACPK	242	10	14	22		10912

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
ENV	TSVITQACP	242	10	14	22		10913
ENV	GFAILKCNDR	268	10	14	22		10914
ENV	IFAVLSINR	793	10	14	22		10915
ENV	NTSAITQACP	241	11	14	22		10916
ENV	AGFAILKCNDR	267	11	14	22		10917
ENV	IFAVLSINR	792	11	14	22		10918
ENV	KIEPLGVAPTK	568	11	15	24		10919
ENV	FDHPIIY	255	8	15	23		10920
ENV	PAGYAILK	266	8	15	23		10921
ENV	NMWQEVGK	494	8	15	23		10922
ENV	TNWLWYIK	771	8	15	23		10923
ENV	ITNWLWYIK	770	9	15	23		10924
ENV	SGDLIETII	425	10	15	23		10925
ENV	IFRGGGDMR	545	10	15	23		10926
ENV	NMWQEVGKA	494	11	15	23		10927
ENV	EIFRGGGDMR	544	11	15	23		10928
ENV	DIILNLCLFSY	855	11	15	23		10929
ENV	FNGTGPK	279	8	16	25		10930
ENV	RNLCLFSY	858	8	16	25		10931
ENV	ITKWLWYIK	770	9	16	25		10932
ENV	SHNCRGIEFFY	437	10	16	25		10933
ENV	DLRNLCLFSY	856	10	16	25		10934
ENV	IISFNGRGEFFY	434	11	16	25		10935
ENV	WNASWSNK	696	8	17	27		10936
ENV	KAYDTEVII	72	8	17	27		10937
ENV	VITQACP	244	8	17	27		10938
ENV	RVVQREKR	587	8	17	27	0.0001	10939
ENV	SVITQACP	243	9	17	27		10940
ENV	VAPTKAKRR	574	9	17	27	0.0002	10941
ENV	DAKAYDTEVII	70	10	17	27		10942
ENV	GVAPTKAKRR	573	10	17	27		10943
ENV	VFAVLSINR	793	10	17	27		10944
ENV	SDAKAYDTEV	69	11	17	27		10945
ENV	DTEVIINWAT	75	11	17	27		10946
ENV	NCTRNNTIR	344	11	17	27		10947
ENV	LGVAPIKAKR	572	11	17	27		10948
ENV	IVFAVLSINR	792	11	17	27		10949
ENV	WNSSWSNK	696	11	18	29		10950
ENV	ENVTFNFMW	100	11	18	28		10951
ENV	VLAVERYLK	666	9	18	28		10952
ENV	RVLAVERYLK	665	10	18	28		10953
ENV	NCRGEFFY	439	8	19	30		10954
ENV	GVAPTKAK	573	8	19	30		10955
ENV	VAPTKAKR	574	8	19	30		10956
ENV	FNCRGEFFY	438	9	19	30		10957
ENV	LGVAPTKAK	572	9	19	30		10958
ENV	GVAPTKAKR	573	9	19	30		10959
ENV	PLGVAPTKAK	571	10	19	30		10960
ENV	LGVAPTKAKR	572	10	19	30		10961
ENV	SSNITGLLLTR	516	11	19	30		10962

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
ENV	PLGVAPTAK	571	11	19	30		10963
ENV	AILKCNOK	270	8	20	31		10964
ENV	ETFRPGGDM	544	11	20	31		10965
ENV	LIEESQOQEK	740	11	20	31		10966
ENV	GDLEITTH	427	8	21	33		10967
ENV	GGDEBITTH	426	9	21	33		10968
ENV	TAIAVAEGTDR	925	11	21	33		10969
ENV	RIVELLGR	878	8	22	34		10970
ENV	IVELLGRR	879	8	22	34		10971
ENV	RIVELLGRR	878	9	22	34		10972
ENV	NCTRPNNNTR	344	10	22	34	0.0100	10973
ENV	CTRPNNNTRK	345	10	22	34		10974
ENV	TTTLFCASDA	60	11	22	34		10975
ENV	INCTRPNNNTR	343	11	22	34		10976
ENV	TVQCTHIGIR	290	9	22	36	0.0008	10977
ENV	STVQCTHIGIR	289	10	23	36		10978
ENV	VSTVQCTHIGIR	288	11	23	36		10979
ENV	TFRIQGGDMR	545	10	24	38		10980
ENV	ALAWDDL	851	8	25	39		10981
ENV	LALAWDDL	850	9	25	39		10982
ENV	KNVSTVQCTH	286	10	25	39		10983
ENV	IVQQNNLLR	634	10	25	39	0.0190	10984
ENV	FLALAWDDL	849	10	25	39		10985
ENV	GIVQQNNLLR	633	11	25	39		10986
ENV	GFLALAWDDL	848	11	25	39		10987
ENV	ITLPCRIK	483	8	26	41		10988
ENV	PLGVAPTAK	571	8	26	41		10989
ENV	LAVERYLK	667	8	26	41		10990
ENV	KNMVEQMH	110	9	26	41		10991
ENV	IVQQSNLLR	634	10	26	41		10992
ENV	GIVQQSNLLR	633	11	26	41		10993
ENV	IGDIRQAH	377	9	27	44		10994
ENV	ESQOQEK	743	8	27	44		10995
ENV	IGDIRQAH	378	8	28	44		10996
ENV	NNMVEQMII	111	9	28	44		10997
ENV	TVQCTHIGIK	290	9	28	44		10998
ENV	CTRPNNNTR	345	9	28	44		10999
ENV	VSEFPIHY	253	10	28	44	0.0460	11000
ENV	STVQCTHIGIK	289	10	28	44		11001
ENV	ASITLTVOAR	619	10	28	44		11002
ENV	KVSFEPHY	252	11	28	44		11003
ENV	YCAPAGFAILK	263	11	28	44		11004
ENV	VSTVQCTHIGIK	288	11	28	44		11005
ENV	AASITLTVOAR	618	11	28	44		11006
ENV	VSEFPIHI	253	9	29	45		11007
ENV	KVSFEPHY	252	10	29	45		11008
ENV	CAPAGFAILK	264	10	29	45		11009
ENV	RSELYKYKV	558	11	29	45		11010
ENV	AVLSIVNR	795	8	31	48		11011
ENV	AVAEGTDR	928	8	31	48		11012

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	VTENFNNWK	102	9	31	48		11013
ENV	SPEMPILIY	254	9	31	48		11014
ENV	FAVLSIVNR	794	9	31	48		11015
ENV	SLCLFSYIR	859	9	31	48		11016
ENV	IAVAECTDR	927	9	31	48	0.0003	11017
ENV	NVTENFNMW	101	10	31	48		11018
ENV	AVLSIVNRVR	795	10	31	48		11019
ENV	RSCLFSYIIR	858	10	31	48		11020
ENV	AIAVAECTDR	926	10	31	48		11021
ENV	FAVLSIVNRVR	794	11	31	48		11022
ENV	DRLSLCLFSY	855	11	31	48		11023
ENV	SLCLFSYIIRLR	859	11	31	48		11024
ENV	ELYKYKVK	560	9	32	51		11025
ENV	RVVEREKR	587	8	32	50		11026
ENV	ITLTVOAR	621	8	32	50		11027
ENV	SLCLFSYII	859	8	32	50		11028
ENV	SITLTVOAR	620	9	32	50		11029
ENV	RSCLFSYII	858	9	32	50		11030
ENV	DRLSLCLFSYII	856	11	32	50		11031
ENV	SPEMPILI	254	8	33	52		11032
ENV	RVLAVERY	665	8	33	52		11033
ENV	QARVLAVRY	663	9	33	52	0.0003	11034
ENV	QLQARVLAVE	661	10	33	52		11035
ENV	IMVGGIGLR	781	11	33	52		11036
ENV	LLQLTVWGI	651	10	34	54		11037
ENV	ILLQLTVWGI	650	11	34	53	0.0110	11038
ENV	LSIVNRVQGY	797	11	34	53		11039
ENV	NLWVTYY	44	8	35	53		11040
ENV	NCGGEFF	439	8	35	56		11041
ENV	RSCLFSY	858	8	35	55		11042
ENV	EVINVWATH	77	9	35	55		11043
ENV	FNCGGEFF	438	9	35	55		11044
ENV	NITGLLTR	519	9	35	55	0.0001	11045
ENV	SPNCGGEFF	437	10	35	55		11046
ENV	SNITGLLTR	517	10	35	55	0.0014	11047
ENV	DRLSLCLFSY	856	10	35	55		11048
ENV	IISFNCGGEFF	434	11	35	55		11049
ENV	GGGDMRDNW	549	10	35	55		11050
ENV	MIYGLIGLR	782	10	36	56		11051
ENV	SIVNRVQGY	798	10	36	56		11052
ENV	PGGDMRDN	548	11	36	56	0.0008	11053
ENV	ITGLLTR	520	8	37	58		11054
ENV	DMRDNRSEL	552	11	37	58		11055
ENV	PAGFAIK	266	8	38	59		11056
ENV	LSIVNRVR	797	8	38	59		11057
ENV	VLSIVNRVR	796	9	38	59		11058
ENV	IVNRVQGY	799	9	38	59		11059
ENV	ISLWDQSLK	121	10	38	59		11060
ENV	DIISLWDQSLK	120	11	38	59	0.0540	11061
							11062

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	GDMRDNR	551	8	39	61		11063
ENV	GDMRDNR	550	9	39	61		11064
ENV	RDNRSELY	554	9	40	63	0.0001	11065
ENV	RDNRSELYK	554	10	40	63	0.0028	11066
ENV	TLFCASDAKA	64	11	40	63		11067
ENV	RDNRSELYK	554	11	40	63		11068
ENV	TVYGVVVK	48	10	41	64	7.8000	11069
ENV	TVYGVVVK	47	11	41	64	4.1000	11070
ENV	CASDAKAY	67	8	42	66		11071
ENV	LCLFSYIR	860	8	42	66		11072
ENV	FCASDAKAY	66	9	42	66		11073
ENV	IVGLIGLR	783	9	42	66		11074
ENV	CLFSYIRLR	861	9	42	66		11075
ENV	LFCASDAKAY	65	10	42	66	0.0002	11076
ENV	LCLFSYIRLR	860	10	42	66		11077
ENV	VGRIGILR	784	8	43	67		11078
ENV	QLTVWGK	653	8	44	69		11079
ENV	LFSYIRLR	862	8	44	69		11080
ENV	RIRQGLR	950	8	44	69		11081
ENV	VNRVQGY	800	8	45	71		11082
ENV	SLWDQSLK	123	8	47	75		11083
ENV	ISLWDQSLK	122	9	47	73	0.0890	11084
ENV	WDQSLKPCVK	125	10	47	73		11085
ENV	QSLKPCVK	127	8	48	75		11086
ENV	TVWGIKQLQA	655	11	48	75		11087
ENV	DNWRSELY	555	8	49	77		11088
ENV	GIKQLQAR	658	8	49	77		11089
ENV	DNWRSELYK	555	9	49	77	0.0014	11090
ENV	WGKQLQAR	657	9	49	77	0.0001	11091
ENV	DNWRSELYK	555	10	49	77	0.0001	11092
ENV	DNWRSELYK	555	11	49	77		11093
ENV	LGIWGCCK	679	9	50	78	0.0023	11094
ENV	TLFCASDAK	61	10	50	78	0.2200	11095
ENV	LLGIWGCCK	678	10	50	78	0.0120	11096
ENV	LLRAIEAQH	640	11	50	78		11097
ENV	QLLGIWGCCK	677	11	50	78		11098
ENV	VSTVQCTH	288	8	51	80		11099
ENV	RAIEAQH	643	8	51	80		11100
ENV	NVSTVQCTH	287	9	51	80		11101
ENV	LLRAIEAQH	641	10	51	80		11102
ENV	GIWGCCK	680	8	52	81		11103
ENV	TLFCASDAK	64	9	52	81	0.5300	11104
ENV	RSELYK	558	8	54	84		11105
ENV	LFCASDAK	65	8	57	89		11106
GAG	AAAIMMQK	405	8	01	25		11107
GAG	SATIMMQK	405	8	01	25		11108
GAG	KDKKELY	535	8	01	25		11109
GAG	ETIDKELY	537	8	01	25		11110
GAG	NSATIMMQK	404	9	01	33		11111
GAG	TAPPESEFR	508	9	01	33		11112

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		11113
GAG	NGRQANFLGK	461	10	01	25		11114
GAG	PTAPPESPR	507	10	01	33		11115
GAG	NGKQANFLGK	461	11	01	25		11116
GAG	NGRQANFLGK	461	11	01	25		11117
GAG	PAADKEK	123	8	01	50		11118
GAG	ASAQDGLK	392	8	01	50		11119
GAG	ATAQDGLK	392	8	01	50		11120
GAG	AADKGVSONY	130	10	01	50		11121
GAG	SAQDGLGGY	393	10	01	50		11122
GAG	TAQDGLGGY	393	10	01	50		11123
GAG	GTRGNYVQK	480	10	01	50		11124
GAG	GTRGNYVQR	480	10	01	50		11125
GAG	ITSLPKQEQK	526	10	01	50		11126
GAG	PAADKEKDS	123	11	01	50		11127
GAG	GANSIPVGDY	276	11	01	50		11128
GAG	PNQHPVGDY	276	11	01	50		11129
GAG	ASAQDGLGG	392	11	01	50		11130
GAG	ATAQDGLGG	392	11	01	50		11131
GAG	ETSLPKQEQK	525	11	01	50		11132
GAG	YTAVFMQR	405	8	02	36		11133
GAG	TAPAESFR	508	9	02	67		11134
GAG	PTAPPESFR	507	10	02	100		11135
GAG	EGRQANFLGK	462	10	02	18		11136
GAG	AADKGVSONY	129	10	02	36		11137
GAG	EADGKVSONY	129	10	04	19		11138
GAG	AAIMMOK	400	8	04	15		11139
GAG	AAIMMQSNF	406	11	06	16		11140
GAG	KTVKCFNCGK	421	10	08	16		11141
GAG	GARASILR	2	8	10	16		11142
GAG	PGNFIQSR	483	8	10	16		11143
GAG	MGARASILR	1	9	10	16		11144
GAG	KIWPSSKGR	472	9	10	16		11145
GAG	TGNSSQVSON	139	11	10	16		11146
GAG	NFLGKIWPSSK	468	11	10	16		11147
GAG	PVAPQMR	243	8	10	16		11148
GAG	MMQKSNFK	409	8	10	16		11149
GAG	MMQKSNFK	409	8	10	16		11150
GAG	KLDKWEKIR	12	9	10	16		11151
GAG	GGKKKYKLK	24	9	10	16	0.0001	11152
GAG	RDIXEALDK	97	9	10	16		11153
GAG	IMMQKSNFK	408	9	10	16		11154
GAG	LKGIWPSSK	470	9	10	16		11155
GAG	PGKKKYKLK	23	10	10	16		11156
GAG	GGKKKYKLKH	24	10	10	16		11157
GAG	AGPVAPQMR	241	10	10	16		11158
GAG	FLGKIWPSSK	469	10	10	16		11159
GAG	KLDKWEKIRL	12	11	10	16		11160
GAG	PGKKKYKLK	23	11	10	16		11161
GAG	LKGIWPSSKGR	470	11	10	16		11162

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*1001	SEQ ID NO.
GAG	ATIMQRGNF	406	11	11	28		11163
GAG	PSQKQNDK	528	10	11	18		11164
GAG	PIPVGDHY	279	8	11	17		11165
GAG	TIKCFNCGK	422	9	11	17		11166
GAG	TVKCFNCGK	422	9	11	17		11167
GAG	GNSQVSNQY	140	10	12	23		11168
GAG	YIMMQRGNFR	407	10	12	21		11169
GAG	OTGSEELR	71	8	12	19		11170
GAG	FNGCKEGIHAR	426	11	12	19		11171
GAG	PGKKKKYK	23	8	12	19		11172
GAG	TLYCVIIQK	86	8	12	19		11173
GAG	DTKEALEK	98	8	12	19		11174
GAG	MLNIVGGH	308	8	12	19		11175
GAG	PTSILDIR	303	8	12	19		11176
GAG	GSEELRSLY	73	9	12	19		11177
GAG	ATLYCVIIQK	85	9	12	19		11178
GAG	KDTKEALEK	97	9	12	19		11179
GAG	MMLNIVGGH	207	9	12	19		11180
GAG	TGSEELRSLY	72	10	12	19		11181
GAG	VATLYCVIIQK	84	10	12	19		11182
GAG	NMMLNIVGGH	206	10	12	19		11183
GAG	YSPTSILDIR	301	10	12	19		11184
GAG	RAEQASQEVK	329	10	12	19		11185
GAG	RLRPGCKKKY	20	11	12	19		11186
GAG	TVATLYCVIIQ	83	11	12	19		11187
GAG	LNMLNIVGG	205	11	12	19		11188
GAG	SNPPIPVGEIY	273	11	12	19		11189
GAG	TSILDIRQGNK	304	11	12	19		11190
GAG	PGNFLQNR	483	8	13	21		11191
GAG	IARNCRAPR	434	9	13	21		11192
GAG	KIWPNSKGR	472	9	13	21		11193
GAG	NCCKEGIHAR	427	10	13	21		11194
GAG	IARNCRAPRK	434	10	13	21		11195
GAG	IARNCRAPRK	434	11	13	21		11196
GAG	NFLGKIWTSNK	468	11	13	21		11197
GAG	KGRPGNFLQN	478	11	13	21		11198
GAG	RIEVKDTK	93	8	13	20		11199
GAG	IVKCFNCGK	422	9	13	20		11200
GAG	CKCKEGIHAR	428	9	13	20		11201
GAG	EGIHARNCR	431	9	13	20		11202
GAG	LGIWTSNK	470	9	13	20		11203
GAG	KLKIIIVWASR	31	10	13	20		11204
GAG	HIARNCRAPR	433	10	13	20		11205
GAG	FLGKIWTSNK	469	10	13	20		11206
GAG	EVDKTEALD	95	11	13	20		11207
GAG	AAEWDRIIIP	230	11	13	20		11208
GAG	HIARNCRAPRK	433	11	13	20		11209
GAG	LGIWTSNKG	470	11	13	20		11210
GAG	NSSQVSNQY	144	9	14	31		11211
GAG	NCCKEGIHAK	427	10	14	22		11212

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	FNCCKEGIIAK	426	11	14	22		11213
GAG	IAKNCIRAPKK	434	11	14	22		11214
GAG	QNAQQQMVII	157	9	14	22		11215
GAG	RGNFRNQKK	412	9	14	22		11216
GAG	CGKEGIIAK	428	9	14	22		11217
GAG	EGHIAKNCR	431	9	14	22		11218
GAG	FNVTATLYCV	81	11	14	22		11219
GAG	TVATLYCVIIQ	83	11	14	22		11220
GAG	IVQNAQQQMV	155	11	14	22		11221
GAG	SSQVSQNY	145	8	15	31		11222
GAG	RSLYNTVATL	78	11	15	24		11223
GAG	FNVTATLY	81	8	15	23		11224
GAG	TYCVIIQR	86	8	15	23		11225
GAG	AAEWDIRVII	230	8	15	23		11226
GAG	WDRVIIPIV	233	8	15	23		11227
GAG	RGNFRNQR	412	8	15	23		11228
GAG	LFNTVATLY	80	9	15	23		11229
GAG	ATLYCVIIQR	85	9	15	23		11230
GAG	EAAEWDIRVII	229	9	15	23		11231
GAG	TAIPPESEF	496	9	15	23		11232
GAG	SGGKLDWEEK	9	10	15	23		11233
GAG	SLFNTVATLY	79	10	15	23		11234
GAG	VATLYCVIIQR	84	10	15	23		11235
GAG	KIEEQNKSK	105	10	15	23		11236
GAG	RAEQATQDVK	329	10	15	23		11237
GAG	PTAPPESEF	495	10	15	23		11238
GAG	LSGGKLDWEE	8	11	15	23		11239
GAG	PGLLETSEGR	50	11	15	23		11240
GAG	KIEEQNKSKK	105	11	15	23		11241
GAG	MMQRGNFRN	409	11	15	23		11242
GAG	IAKNCIRAPRK	434	10	16	25		11243
GAG	LDAWEKIR	13	8	16	25		11244
GAG	NAQQQMVII	158	8	16	25		11245
GAG	PVSILDIK	303	8	16	25		11246
GAG	GNFRNQKK	413	8	16	25		11247
GAG	KLDWEEKIR	12	9	16	25		11248
GAG	GGKKKYRLK	24	9	16	25		11249
GAG	LDAWEKIRL	13	10	16	25		11250
GAG	PGKKKYRLK	23	10	16	25		11251
GAG	GGKKKYRLKII	24	10	16	25		11252
GAG	GLLETSEGR	51	10	16	25		11253
GAG	YSPVSILDIK	301	10	16	25		11254
GAG	GGKLDWEEKI	10	11	16	25		11255
GAG	KLDWEEKIRL	12	11	16	25		11256
GAG	PGKKKYRLK	23	11	16	25		11257
GAG	VSILDIKQGP	304	11	16	25		11258
GAG	HIAXNCIRAPRK	433	11	16	25		11259
GAG	PIPIGQMR	243	8	17	27		11260
GAG	GGKLDWEEK	10	9	17	27		11261
GAG	DAWEKIRL	14	9	17	27		11262

0.7100

Table XVII
 HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SIQ ID NO.
GAG	LLETSEGR	52	9	17	27		11263
GAG	RLKILYWASR	31	10	17	27		11264
GAG	LDKIEEQNK	103	10	17	27		11265
GAG	AGPIPPQMR	241	10	17	27		11266
GAG	ALDKIEEQNK	102	11	17	27		11267
GAG	LSPTLTNAV	168	11	17	27		11268
GAG	IIAGPIPPQMR	240	11	17	27		11269
GAG	PIPPQMRPR	243	11	17	27		11270
GAG	IAKNCRAPR	434	9	18	29	0.0003	11271
GAG	LDKWEKIR	13	8	18	28		11272
GAG	IVGDIYKR	281	8	18	28		11273
GAG	PDCKTILR	352	8	18	28		11274
GAG	LDKWEKRLR	13	10	18	28		11275
GAG	SILDIKQGP	305	10	18	28		11276
GAG	ANPDCKTILR	350	10	18	28		11277
GAG	IIAKNCRAPR	433	10	18	28		11278
GAG	IIAGPIPPQMR	240	11	18	28		11279
GAG	NNPIPPGELY	273	11	18	28		11280
GAG	NANPDCKTILR	349	11	18	28		11281
GAG	LARNCRAPRK	434	11	19	30		11282
GAG	PIATQMR	243	8	19	30		11283
GAG	LDIKQGP	307	8	19	30		11284
GAG	ILDIKQGP	306	9	19	30		11285
GAG	AGIATQMR	241	10	19	30		11286
GAG	IATQMRPR	244	10	19	30		11287
GAG	RLRPGKKKY	20	11	19	30		11288
GAG	PIATQMRPR	243	11	19	30		11289
GAG	DIKQGPKEFR	308	11	19	30		11290
GAG	LARNCRAPR	434	9	20	32		11291
GAG	LARNCRAPRK	434	10	20	32		11292
GAG	FGKKKKYR	23	8	20	31		11293
GAG	IMMQRNFR	408	9	20	31		11294
GAG	KNCRAPRK	436	9	20	31		11295
GAG	IVWASKELR	35	10	20	31	0.0006	11296
GAG	ILARNCRAPR	433	10	20	31		11297
GAG	IIWASRELER	34	11	20	31		11298
GAG	ILARNCRAPR	433	11	20	31		11299
GAG	EGILARNCR	431	9	21	33		11300
GAG	KIWPSTIKGR	472	9	22	35	0.0005	11301
GAG	GGPSIUKR	378	8	22	34		11302
GAG	KNCRAPRK	436	8	22	34		11303
GAG	VGGPSIUKR	377	9	22	34		11304
GAG	SLYNTVATLY	79	10	22	34		11305
GAG	GVGGPSIUKR	376	10	22	34		11306
GAG	QVGGPSIUKR	375	11	22	34		11307
GAG	LGKIWPSTIKG	470	11	22	34		11308
GAG	NFLGIWPSTIK	468	11	23	37		11309
GAG	YNTVATLY	81	8	23	36		11310
GAG	KIEEQNK	105	8	23	36		11311
GAG	QVGGPSIUKR	375	8	23	36		11312

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SFQ ID NO.
GAG	GVGGPSHK	376	8	23	36		11313
GAG	MMQRGNFR	409	8	23	36		11314
GAG	QGVGGPSHK	375	9	23	36		11315
GAG	LGKIWPSHK	470	9	23	36		11316
GAG	ACQGVGGPSH	373	10	23	36		11317
GAG	FLGIWPSHK	469	10	23	36	0.0013	11318
GAG	YNTVATLYCV	81	11	23	36		11319
GAG	TACQGVGGPS	372	11	23	36		11320
GAG	ACQGVGGPSH	373	11	23	36		11321
GAG	NCQGVGGPSH	427	10	24	38		11322
GAG	NCQGVGGPSH	427	10	24	38		11323
GAG	ENCQGVGGPSH	426	11	24	38		11324
GAG	CGQGVGGPSH	428	9	24	38		11325
GAG	YSPVSLDIR	301	10	24	38		11326
GAG	NFLGIWPSH	468	10	25	40		11327
GAG	PVSLDIR	303	8	25	39		11328
GAG	LGKIWPSH	470	8	25	39		11329
GAG	KDTKEALDK	97	9	25	39		11330
GAG	FLGIWPSH	469	9	25	39		11331
GAG	VSILDIRQGP	304	11	25	39		11332
GAG	ANFLGIWPSH	467	11	25	39		11333
GAG	LVWASRELE	35	10	26	41		11334
GAG	ILVWASRELE	34	11	26	41		11335
GAG	MVIOAISPR	163	9	27	42	0.0670	11336
GAG	VDRFKTLR	321	9	27	42		11337
GAG	QMVITQAIQSP	162	10	27	42	0.0010	11338
GAG	YVDRFKTLR	320	10	27	42		11339
GAG	RAEQATQEVK	329	10	27	42		11340
GAG	ANPDKTLK	350	10	27	42	0.0002	11341
GAG	NANPDKTLK	349	11	27	42		11342
GAG	KGRPGNELQS	478	11	28	44		11343
GAG	PDKTLK	352	8	28	44		11344
GAG	VDRFYKTLR	321	9	28	44		11345
GAG	PERDYVDRFY	316	10	28	44		11346
GAG	YVDRFYKTLR	320	10	28	44		11347
GAG	PERDYVDRFY	316	11	28	44		11348
GAG	GARASVLSGG	2	11	29	46		11349
GAG	ASVLSGGK	5	8	29	45		11350
GAG	NLQQQMVI	158	8	29	45		11351
GAG	WVKVIEEK	176	8	29	45		11352
GAG	WDRLLIPVH	233	8	29	45		11353
GAG	RDYVDRFY	318	8	29	45		11354
GAG	RASVLSGGK	4	9	29	45		11355
GAG	NLQQQMVI	157	9	29	45	0.0400	11356
GAG	RDYVDRFY	318	9	29	45		11357
GAG	NAWVKVIEEK	174	10	29	45		11358
GAG	IVQNLQQQMVI	155	11	29	45		11359
GAG	LNAWVKVIEE	173	11	29	45		11360
GAG	AAEWDRLLIPV	230	11	29	45		11361
GAG	PGNQLQR	483	8	30	48		11362
GAG	NAWVKVIEEK	174	10	30	47	0.0002	11362

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	$\$1Q$ ID NO.
GAG	KIRLPGGKKK	18	11	30	47		11363
GAG	LNAWVKVVEE	173	11	30	47		11364
GAG	WVKVVEEK	176	8	31	48	0.0001	11365
GAG	RNYVDRFFK	318	9	33	52		11366
GAG	RNCRAPRKK	436	9	33	52		11367
GAG	PERDYVDRFF	316	11	33	52		11368
GAG	RNCRAPRKK	436	8	34	53		11369
GAG	RLRPGCKKK	20	9	34	53		11370
GAG	RLRPGCKKKY	20	10	34	53		11371
GAG	PIPVGEIYKR	279	10	34	53	0.0001	11372
GAG	PIPVGEIY	279	8	35	55		11373
GAG	PIPVGEIYK	279	9	35	55	0.0012	11374
GAG	DTKEALDK	98	8	36	56	0.0001	11375
GAG	QGVGGPGII	375	8	36	56		11376
GAG	QGVGGPGIHK	375	9	36	56		11377
GAG	ACQGVGGPGII	373	10	36	56		11378
GAG	ISPRILNAWV	168	11	36	56		11379
GAG	TACQGVGGPG	372	11	36	56	0.0001	11380
GAG	ACQGVGGPGII	373	11	36	56		11381
GAG	QGVGGPGIHK	375	11	36	56		11382
GAG	GVEHGHK	376	8	37	58	0.0018	11383
GAG	GGHGHKAR	378	8	37	58		11384
GAG	VGGPGIHKAR	377	9	37	58		11385
GAG	VGGPGIHKAR	376	10	37	58	0.0001	11386
GAG	AAEWDRLLI	230	8	39	61		11387
GAG	EAIEWDRLLI	229	9	39	61		11388
GAG	PVGEIYKR	281	8	40	63	0.0001	11389
GAG	TVATLYCVII	83	9	40	63		11390
GAG	NTVATLYCVII	82	10	40	63		11391
GAG	SILDIRQGP	305	10	40	63	0.7100	11392
GAG	DIRQGPKEPR	308	11	41	64		11393
GAG	VATLYCVII	84	8	42	66		11394
GAG	LDIRQGP	307	8	42	66		11395
GAG	ILDIRQGP	306	9	42	66	0.0048	11396
GAG	NTMLNTVGGII	205	10	42	66		11397
GAG	LNTMLNTVGG	206	11	42	66		11398
GAG	TMLNTVGGII	207	9	43	67		11399
GAG	KGCWKCGK	444	8	44	69		11400
GAG	KIRLPGGK	18	9	44	69		11401
GAG	KIRLPGGKK	18	10	44	69	0.0010	11402
GAG	PGQMRPIR	246	8	45	70		11403
GAG	CGKEGIQMK	449	9	45	70		11404
GAG	KCKKEGIQMK	448	10	45	70		11405
GAG	MLNTVGGII	208	8	47	73		11406
GAG	WASRELER	37	8	48	75		11407
GAG	GCWKCKGEGH	445	10	48	75		11408
GAG	RLRPGCKK	20	8	49	77		11409
GAG	QMKDCTER	455	8	49	77		11410
GAG	EGHQMKDCTE	452	11	49	77		11411
							11412

Table XVII
 HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	RAPRKGCWK	439	10	51	80		11413
GAG	CTERQANFLG	459	11	52	83		11414
GAG	NCRAPRKK	437	8	53	84		11415
GAG	TINEEAIEWD	225	11	53	83		11416
GAG	INIEEAIEWDR	226	10	55	86		11417
GAG	FNCCKEGII	426	8	57	90		11418
GAG	WILGLNK	289	8	57	89		11419
GAG	CFNCGKEGII	425	9	57	89		11420
GAG	IILGLNKIVR	290	10	57	89	0.0006	11421
GAG	KCFNCGKEGII	424	10	57	89		11422
GAG	WILGLNKIVR	289	11	57	89		11423
GAG	ILGLNKIVRMV	291	11	57	89		11424
GAG	ILGLNKIVR	291	9	58	91	0.0001	11425
GAG	LGLNKIVRMV	292	10	58	91	0.0002	11426
GAG	LLVQANPDC	345	11	58	91		11427
GAG	LGLNKIVR	292	8	59	92		11428
GAG	LVQANPDC	346	10	59	92		11429
GAG	LNKIVRMV	294	8	60	94	0.0110	11430
GAG	GLNKIVRMV	293	9	60	94		11431
GAG	QAAMQMLK	216	8	61	95	0.0002	11432
GAG	QNANPDC	348	8	61	95		11433
GAG	GGHQAAMQM	213	11	61	95		11434
GAG	RTLNAWVK	171	8	63	98	0.0560	11435
GAG	QGPKEPER	311	8	63	98		11436
GAG	PFIDYVDR	316	8	63	98		11437
GAG	QGPKEPRDY	311	10	63	98	0.0002	11438
NEF	AADGVGAVSR	42	10	69	15		11439
NEF	ANEGENSLII	249	11	69	15		11440
NEF	VGWPAIRER	11	9	10	17		11441
NEF	FDSRLAFII	310	8	10	16		11442
NEF	FSRLAFIII	310	9	10	16		11443
NEF	AVSQDLK	311	8	10	16		11444
NEF	PLKNTTK	48	8	10	16		11445
NEF	GAVSQDLK	102	8	10	16		11446
NEF	GLEGLYSK	47	9	10	16		11447
NEF	MARELIPEY	125	9	10	16		11448
NEF	VGAVSQDLK	321	9	10	16		11449
NEF	QVPLRMTEK	46	10	10	16		11450
NEF	GAFLSFLK	100	10	10	16		11451
NEF	GGLEGLYSK	110	10	10	16		11452
NEF	CFKLVPVDR	124	10	10	16		11453
NEF	IMARELIPEY	226	10	10	16		11454
NEF	MARELIPEY	320	10	10	16		11455
NEF	MARELIPEY	321	10	10	16		11456
NEF	VGAVSQDLK	45	11	10	16		11457
NEF	KGAFDLSFLK	109	11	10	16		11458
NEF	XGLEGLYSK	122	11	10	16		11459
NEF	WCFKLVPVDP	225	11	10	16		11460
NEF	NNSLIIPICQII	254	11	10	16		11461
NEF	IMARELIPEY	320	11	10	16		11462

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	MARELIPEYY	321	11	10	16		11463
NEF	ANEENNCLL	249	11	11	18		11464
NEF	AVSRDLEK	48	8	11	17		11465
NEF	VSRDLEKII	49	8	11	17		11466
NEF	KLVPDPR	228	8	11	17		11467
NEF	GAVSRLDK	47	9	11	17		11468
NEF	AVSRDLEKII	48	9	11	17		11469
NEF	GAVSRLDK	46	10	11	17		11470
NEF	GAVSRLDKII	47	10	11	17		11471
NEF	QNYTPGQVR	205	10	11	17		11472
NEF	NSLIHPIQII	255	10	11	17		11473
NEF	GVGAVSRDLE	45	11	11	17		11474
NEF	GAVSRLDK	46	11	11	17		11475
NEF	EGENNCLLII	251	9	12	19	0.0009	11476
NEF	YTPGQVR	207	8	12	19		11477
NEF	DILDLWVYII	185	9	12	19		11478
NEF	EGENNCLLII	184	10	12	19		11479
NEF	QDILDLWVYII	251	9	13	21		11480
NEF	VDSIFLKEK	112	10	13	20		11481
NEF	AVDSIFLKEK	111	11	13	20		11482
NEF	VDSIFLKEK	112	8	14	22		11483
NEF	DGLIYSKK	172	8	14	22		11484
NEF	ELIPIEFYK	324	8	14	22		11485
NEF	AVDSIFLKEK	111	9	14	22	1.1000	11486
NEF	LDGLIYSKK	171	9	14	22		11487
NEF	DGLIYSKKR	172	9	14	22		11488
NEF	SLIIPICQII	256	9	14	22		11489
NEF	GLDGLIYSKK	125	10	14	22		11490
NEF	LDGLIYSKKR	171	10	14	22		11491
NEF	GLDGLIYSKK	124	11	14	22		11492
NEF	NNCLLIIPMSQ	125	11	14	22		11493
NEF	CLLIIPMSQII	254	9	14	22		11494
NEF	NCLLIIPMSQII	255	10	15	23		11495
NEF	QNYTPGQIRY	205	11	15	23		11496
NEF	LDGLIYSK	171	8	15	23		11497
NEF	GLDGLIYSK	125	9	16	25		11498
NEF	GGLDGLIYSK	124	10	16	25		11499
NEF	KGGLDGLIYSK	122	11	16	25		11500
NEF	RFPLTFGWCF	216	11	16	25		11501
NEF	FFPDWQNY	199	8	17	27		11502
NEF	LLIIPMSQII	257	8	17	27		11503
NEF	GFPPDWQNY	198	9	17	27		11504
NEF	YTPGQIRY	207	9	17	27		11505
NEF	FDSFLKEK	112	10	17	27		11506
NEF	QGFPPDWQNY	196	10	17	27		11507
NEF	AFDLSFLKEK	111	11	17	27		11508
NEF	FDSFLKEK	112	8	18	28		11509
NEF	LLIIPICQII	257	8	18	28		11510
NEF	AFDLSFLKEK	111	9	18	28		11511
NEF				18	28		11512

Table XVII
IIIY A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
NEF	QNYTPGPGIR	205	10	18	28		11513
NEF	GGLEGLIY	124	8	19	30		11514
NEF	KGLEGLIY	122	9	19	30		11515
NEF	DLDLWVY	185	8	20	31		11516
NEF	YTPGPGIR	207	8	20	31		11517
NEF	QDILDWVY	184	9	20	31		11518
NEF	QNYTPGPGTR	205	10	20	31		11519
NEF	GGLDGLIY	124	8	21	33		11520
NEF	WYIITQGY	191	8	21	33		11521
NEF	YTPGPGTR	207	8	21	33		11522
NEF	KGGLDGLIY	122	9	21	33		11523
NEF	DLWVYIITQGY	188	10	21	33		11524
NEF	LDLWVYIITQGY	187	11	21	33		11525
NEF	LSFLKEK	114	8	22	34		11526
NEF	ELIPEYTK	124	8	22	34		11527
NEF	DLWVYIITQGY	188	10	22	34		11528
NEF	GLIYSKKR	173	8	22	34		11529
NEF	LSIIFLKEK	114	8	23	36		11530
NEF	DLWVYIITQGY	188	10	23	36		11531
NEF	ELIPEYTK	124	8	27	42		11532
NEF	DLWVYIITQGY	188	10	27	42		11533
NEF	ELIPEYTK	124	8	27	42		11534
NEF	DLWVYIITQGY	188	10	27	42		11535
NEF	ELIPEYTK	124	8	27	42		11536
NEF	DLWVYIITQGY	188	10	27	42		11537
NEF	ELIPEYTK	124	8	27	42		11538
NEF	DLWVYIITQGY	188	10	27	42		11539
NEF	ELIPEYTK	124	8	27	42		11540
NEF	DLWVYIITQGY	188	10	27	42		11541
NEF	ELIPEYTK	124	8	27	42		11542
NEF	DLWVYIITQGY	188	10	27	42		11543
NEF	ELIPEYTK	124	8	27	42		11544
NEF	DLWVYIITQGY	188	10	27	42		11545
NEF	ELIPEYTK	124	8	27	42		11546
NEF	DLWVYIITQGY	188	10	27	42		11547
NEF	ELIPEYTK	124	8	27	42		11548
NEF	DLWVYIITQGY	188	10	27	42		11549
NEF	ELIPEYTK	124	8	27	42		11550
NEF	DLWVYIITQGY	188	10	27	42		11551
NEF	ELIPEYTK	124	8	27	42		11552
NEF	DLWVYIITQGY	188	10	27	42		11553
NEF	ELIPEYTK	124	8	27	42		11554
NEF	DLWVYIITQGY	188	10	27	42		11555
NEF	ELIPEYTK	124	8	27	42		11556
NEF	DLWVYIITQGY	188	10	27	42		11557
NEF	ELIPEYTK	124	8	27	42		11558
NEF	DLWVYIITQGY	188	10	27	42		11559
NEF	ELIPEYTK	124	8	27	42		11560
NEF	DLWVYIITQGY	188	10	27	42		11561
NEF	ELIPEYTK	124	8	27	42		11562

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ETWETWTE	588	10	10	16		11563
POL	VSLDTTNQK	659	10	10	16		11564
POL	ENLAFPGGEAR	4	11	10	16		11565
POL	TGKYARKMTA	543	11	10	16		11566
POL	VVSLDTTNQ	658	11	10	16		11567
POL	QTKELQKQIK	961	11	10	16		11568
POL	QIRANSPTKR	21	10	11	18		11569
POL	TNNETGIR	324	9	11	17		11570
POL	TNNETGIRY	324	10	11	17		11571
POL	LDGDKAQEDII	754	11	11	17		11572
POL	IGGFIVK	137	8	11	17		11573
POL	RIGPENPY	238	8	11	17		11574
POL	TAITNDVK	551	8	11	17		11575
POL	QLTEVVQK	559	8	11	17		11576
POL	IDKAEQEDII	757	8	11	17		11577
POL	VVPRRKVK	1012	8	11	17		11578
POL	KIKDYCK	1019	8	11	17		11579
POL	GIGGFIVK	136	9	11	17		11580
POL	SLDTTNQK	660	9	11	17		11581
POL	GIDKAEQEDII	756	9	11	17		11582
POL	SNFTSTTVK	871	9	11	17		11583
POL	KVPRRKVK	1011	9	11	17		11584
POL	GIGGFIVK	135	10	11	17		11585
POL	ISRIGPENPY	236	10	11	17		11586
POL	STNETGIR	323	10	11	17		11587
POL	ESWTYNDIQK	439	10	11	17		11588
POL	ETTNQKTELH	663	10	11	17		11589
POL	DGIDKAEQEDII	755	10	11	17		11590
POL	GSNFTSTTVK	870	10	11	17		11591
POL	GIOQEFQIPY	886	10	11	17		11592
POL	SDIQKELQK	958	10	11	17		11593
POL	FNFPQITLWQR	85	11	11	17		11594
POL	IGGIGGFIVK	134	11	11	17		11595
POL	KISRIGPENPY	235	11	11	17		11596
POL	PTNNETGIR	322	11	11	17		11597
POL	STNETGIRY	323	11	11	17		11598
POL	VVSLTETTNQ	658	11	11	17		11599
POL	NGSNFTSTTV	869	11	11	17		11600
POL	AGIQQEFQIPY	885	11	11	17		11601
POL	IDIASDIQTK	953	11	11	17		11602
POL	VDIATDIQTK	951	11	11	17		11603
POL	ASDIQKELQK	957	11	11	17		11604
POL	NSEKVVPRRK	1007	11	11	17		11605
POL	QIRANSPTSR	21	10	12	19		11606
POL	IKIQNFR	969	8	12	19		11607
POL	QIYFGIKVK	458	9	12	19		11608
POL	QDQWTYQIY	526	9	12	19		11609
POL	IKIQNFRVY	969	10	12	19		11610
POL	ASQIYFGIKVK	456	11	12	19		11611
POL	IKIQNFRVYVY	969	11	12	19		11612

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	AFPOGEAR	7	8	12	19		11613
POL	TNOKTELIH	665	8	12	19		11614
POL	KTELQAIY	668	8	12	19		11615
POL	LAFPOGEAR	6	9	12	19		11616
POL	EINLPQKWK	122	9	12	19		11617
POL	TTNOKTELIH	664	9	12	19		11618
POL	QIKIQNFR	968	9	12	19		11619
POL	VIQDNSEIK	1003	9	12	19		11620
POL	NSEIKVVPR	1007	9	12	19		11621
POL	VLEEINLPQK	119	10	12	19		11622
POL	VVIQDNSEIK	1002	10	12	19		11623
POL	DNSEIKVVPR	1006	10	12	19		11624
POL	NSEIKVVPRR	1007	10	12	19		11625
POL	TVLEINLPQK	118	11	12	19		11626
POL	EINLPQKWKPK	122	11	12	19		11627
POL	QGDQWYQI	524	11	12	19		11628
POL	RMRGATINDV	548	11	12	19		11629
POL	TNOKTELQAIY	665	11	12	19		11630
POL	QIKIQNFRVY	968	11	12	19		11631
POL	AVVIQDNSEIK	1000	11	12	19		11632
POL	DNSEIKVVPR	1005	11	12	19		11633
POL	DNSEIKVVPRR	1006	11	12	19		11634
POL	ELOKQIK	964	8	13	21		11635
POL	KTGKYARMR	542	9	13	21		11636
POL	NLKTGKYARM	540	11	13	21		11637
POL	EDINLPQK	121	8	13	20		11638
POL	TGKYARMR	543	8	13	20		11639
POL	YARMRGAR	546	8	13	20		11640
POL	QVREQAEII	916	8	13	20		11641
POL	DINLPQKWK	122	9	13	20		11642
POL	VLEDINLPQK	119	10	13	20		11643
POL	EDINLPQKWK	121	10	13	20		11644
POL	RAKJELREII	388	10	13	20		11645
POL	TVQPIVLPEK	429	10	13	20		11646
POL	AGRWPVKTHI	857	10	13	20	5.60000	11647
POL	IGQVREQAEH	914	10	13	20		11648
POL	QVREQAEIILK	916	10	13	20		11649
POL	TLWQRLVTV	91	11	13	20		11650
POL	LVTIKIGGQLK	97	11	13	20		11651
POL	TVLEDINLPQK	118	11	13	20		11652
POL	DINLPQKWK	122	11	13	20		11653
POL	KIEELREIILK	390	11	13	20		11654
POL	WTVQPIVLPEK	428	11	13	20	0.0510	11655
POL	TGKYARMRGA	543	11	13	20		11656
POL	LAGRWPVKTI	856	11	13	20		11657
POL	IIGQVREQAEH	913	11	13	20		11658
POL	EIKVVRKAK	1009	11	13	20		11659
POL	EFSEQTR	16	8	14	22		11660
POL	QIVPGIKVR	458	9	14	22		11661
POL	ASQIYPGIKVR	456	11	14	22		11662

Table XVII
HIV-1 M1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SIQ ID NO.
POL	IATESISVWGK	567	11	14	22		11663
POL	ILIECGK	149	8	14	22		11664
POL	LIEICGK	150	8	14	22		11665
POL	QNPDIIVY	363	8	14	22		11666
POL	NFTSTIVK	872	8	14	22		11667
POL	IASDIQTK	956	8	14	22		11668
POL	DSRDPLWK	981	8	14	22		11669
POL	QILIECGK	148	9	14	22		11670
POL	ILIEICGK	149	9	14	22		11671
POL	IASDIQTK	955	9	14	22		11672
POL	RDSRDLWK	980	9	14	22		11673
POL	QILIECGK	148	10	14	22		11674
POL	QNPDIIVY	363	10	14	22		11675
POL	RTKIELRQII	388	10	14	22		11676
POL	PGKVRQLCK	461	10	14	22		11677
POL	DIASDIQTK	954	10	14	22		11678
POL	RDPLWKGPAK	983	10	14	22		11679
POL	FSPTQILWQK	85	11	14	22		11680
POL	YDQILIECGK	146	11	14	22		11681
POL	KTPKFLINQK	577	11	14	22		11682
POL	GIDKAQEEIER	756	11	14	22		11683
POL	QTRANSPTK	21	9	15	24		11684
POL	LYEICTEMEK	221	10	15	24	0.0120	11685
POL	ELRQILLR	393	8	15	23		11686
POL	OGDQDWTY	524	8	15	23		11687
POL	KTELQAIH	668	8	15	23		11688
POL	EIKVVPKPK	1009	9	15	23		11689
POL	LGHQAQPDK	695	10	15	23		11690
POL	VDKLVSAQIR	740	10	15	23		11691
POL	IDKAQEEIER	757	10	15	23		11692
POL	ALVEICTEMEK	220	11	15	23		11693
POL	KIELRQILLR	390	11	15	23		11694
POL	TNQTTELQAIH	665	11	15	23		11695
POL	ALGHQAQPDK	694	11	15	23		11696
POL	LYNQIEQLIK	709	11	15	23		11697
POL	QVDKLVSAQIR	739	11	15	23		11698
POL	VDKLVSAQIR	740	11	15	23		11699
POL	IDKAQEEIER	757	11	15	23		11700
POL	KAEIEIER	759	8	16	25		11701
POL	KAEIEIER	759	9	16	25		11702
POL	NLAFOQGEAR	5	10	16	25		11703
POL	KAEIEIER	759	10	16	25		11704
POL	AFQQGEAR	7	8	16	25		11705
POL	RANSPTK	26	8	16	25		11706
POL	SAITINDVK	551	8	16	25		11707
POL	IIQAQPDK	697	8	16	25		11708
POL	KLVSAQIR	742	8	16	25		11709
POL	LVSAGIRK	743	8	16	25		11710
POL	EIKVVPKPK	1009	8	16	25	0.0054	11711
POL	LAFQQGEAR	6	9	16	25		11712

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GIQAQMDR	696	9	16	25		11713
POL	KLVSAGIRK	742	9	16	25	0.0770	11714
POL	ENLAFQGGEA	4	11	16	25		11715
POL	RANSPTR	26	8	17	27		11716
POL	KIELRQII	390	8	17	27		11717
POL	ELREILLK	393	8	17	27		11718
POL	WGKTPKFK	575	8	17	27		11719
POL	TIKIGGQLK	99	9	17	27		11720
POL	VTIKIGGQLK	98	10	17	27	0.0330	11721
POL	TVQMIQLPEK	429	10	17	27	0.2100	11722
POL	VIWGRTPKFK	573	10	17	27		11723
POL	TLWQRPLVTI	91	11	17	27		11724
POL	WTVQPIQLPEK	428	11	17	27		11725
POL	VIWGRTPKFK	572	11	17	27		11726
POL	YFSVPLDKDFR	304	11	18	27		11727
POL	NLKTGKYAKM	540	11	18	29		11728
POL	PDIVIVQY	365	8	18	29		11729
POL	SVPLDKDFR	306	9	18	28		11730
POL	FSVPLDKDFR	305	10	18	28		11731
POL	SVPLDKDFR	306	10	18	28		11732
POL	AGIKVKQLCK	461	10	18	28		11733
POL	VNQHEQLIK	710	10	18	28		11734
POL	FSVPLDKDFR	305	11	18	28		11735
POL	SVPLDKDFR	306	11	18	28		11736
POL	YAGIKVKQLCK	460	11	18	28		11737
POL	LVSQHEQLIK	709	11	18	28		11738
POL	VNQHEQLIK	710	11	18	28		11739
POL	PLDKDFR	308	8	19	30		11740
POL	PLDKDFRKY	308	9	19	30		11741
POL	KTGKYAKMR	342	9	19	30		11742
POL	LKDPRKY	309	8	19	30		11743
POL	KIELREI	390	8	19	30		11744
POL	TKGYAKMR	343	8	19	30		11745
POL	GAITNDVK	551	8	19	30		11746
POL	LTDITNQK	661	8	19	30		11747
POL	PLWKGPAK	985	8	19	30		11748
POL	GIKVRQLCK	462	9	19	30		11749
POL	RGAITNDVK	550	9	19	30		11750
POL	KVRQLCKLLR	464	10	19	30		11751
POL	ATESIWIWK	568	10	19	30		11752
POL	VSQHEQLIK	710	10	19	30	0.0370	11753
POL	MAGDDCVASR	1028	10	19	30		11754
POL	VSQHEQLIK	710	11	19	30		11755
POL	QMAGDDCVAS	1027	11	19	30		11756
POL	QIYAGIKVK	458	9	20	32		11757
POL	KVYLAWVPAH	722	10	20	32	0.0016	11758
POL	KAACWVAGIK	879	10	20	32	0.0740	11759
POL	ASQIYAGIKVK	456	11	20	32		11760
POL	KVYLAWVPAH	722	11	20	32	2.3000	11761
POL	KFKLPIQK	580	8	20	31		11762

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GDGCVASR	1010	8	20	31		11763
POL	AGDDCVASR	1029	9	20	31		11764
POL	VSLTETINQK	639	10	20	31		11765
POL	LLKLAGRWV	853	11	20	31		11766
POL	YFSVPLDK	304	8	21	33		11767
POL	ACWWAGIK	881	8	21	33		11768
POL	SLTETTNQK	660	9	21	33		11769
POL	AACWWAGIK	880	9	21	33		11770
POL	DYFSVPLDK	302	10	21	33	0.0470	11771
POL	DLHIGIIRTK	381	10	21	33		11772
POL	QLCKLLRGTK	467	10	21	33		11773
POL	IFAIKKKDKTK	249	11	21	33		11774
POL	GDAYFSVPLD	301	11	21	33		11775
POL	SDLEIGIIRTK	380	11	21	33		11776
POL	SDNLPPIVAK	776	11	21	33		11777
POL	AGIKQEGIPY	885	11	21	33		11778
POL	EIGIIRTK	383	8	22	34		11779
POL	RTKIEELR	388	8	22	34		11780
POL	YLAWVPPIH	724	8	22	34		11781
POL	YLAWVPPIH	725	8	22	34		11782
POL	YLAWVPPIH	724	9	22	34	0.0570	11783
POL	NFQITLWQR	86	10	22	34		11784
POL	MTKILEPFRK	353	10	22	34	0.0380	11785
POL	AGRWPKVH	857	10	22	34		11786
POL	GIKQEGIPY	886	10	22	34		11787
POL	SMTRILEPFRK	352	11	22	34	0.0002	11788
POL	KTKPKRLPIQK	577	11	22	34		11789
POL	LAGRWPKVI	856	11	22	34		11790
POL	KVYLSWVPPIH	722	10	23	37		11791
POL	KVYLSWVPPIH	722	11	23	37		11792
POL	KILEPFRK	355	8	23	36		11793
POL	KVILVAVH	823	8	23	36		11794
POL	SFPQITLWQR	86	10	23	36		11795
POL	DFNLPPIVAK	777	10	23	36		11796
POL	EGKVLVAVH	821	10	23	36		11797
POL	LLKWGFTTPD	398	11	23	36		11798
POL	LLRWGFTTPD	398	11	23	36		11799
POL	IDIIATDIQTK	953	11	23	36		11800
POL	NTPIFAIK	246	8	24	38		11801
POL	GDGCVAGR	1030	8	24	38		11802
POL	YNTPIFAIK	245	9	24	38		11803
POL	NTPIFAIKK	246	9	24	38		11804
POL	LCKLLRGTK	468	9	24	38	0.0001	11805
POL	AGDDCVAGR	1029	9	24	38		11806
POL	YNTPIFAIKK	245	10	24	38		11807
POL	NTPIFAIKK	246	10	24	38		11808
POL	MAGDDCVAGR	1028	10	24	38		11809
POL	YNTPIFAIKK	245	11	24	38		11810
POL	QQQQWYTIQI	524	11	24	38		11811
POL	KLKAGYVTD	643	11	24	38		11812

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	TAYFLKLAG	849	11	24	38		11813
POL	OMAGDDCVAG	1027	11	24	38		11814
POL	OGOWTYQIV	526	9	25	40	0.0001	11815
POL	RIFAIKKK	248	8	25	39		11816
POL	QGQGWYTY	524	8	25	39		11817
POL	FLKLKLAGR	852	8	25	39		11818
POL	YFLKLKLAGR	851	9	25	39		11819
POL	QLCKLLRGAK	467	10	25	39		11820
POL	LGKAGYVTDK	644	10	25	39		11821
POL	IDKAEIEIEK	757	10	25	39		11822
POL	PSKDLIAEIQK	513	11	25	39		11823
POL	GIDKAEIEIEK	756	11	25	39		11824
POL	IDKAEIEIEKY	757	11	25	39		11825
POL	SDENLPVAVK	776	11	25	39		11826
POL	RAKIEELR	388	8	26	41		11827
POL	KFRLPIQK	580	8	26	41		11828
POL	NLPPIVAK	779	8	26	41		11829
POL	LCKLLRGAK	468	9	26	41		11830
POL	FNLPPVAK	778	9	26	41		11831
POL	SNFTSAVK	871	9	26	41		11832
POL	DFNLPVAVK	777	10	26	41		11833
POL	GSNFTSAVK	870	10	26	41		11834
POL	TGQETAYFLL	845	11	26	41		11835
POL	NGSNFTSAVV	869	11	26	41		11836
POL	KAQEEIEK	759	8	27	43		11837
POL	ASQIYAGIK	456	9	27	43	0.3400	11838
POL	KAQEEIEKY	759	9	27	43		11839
POL	KAQEEIEKYII	759	10	27	43		11840
POL	INLPKWK	123	8	27	42		11841
POL	EICTEMEK	223	8	27	42		11842
POL	EIQIIRAK	383	8	27	42		11843
POL	LVSSGIRK	743	8	27	42		11844
POL	NLPVAVK	779	8	27	42		11845
POL	KLVSIGIRK	848	8	27	42	0.0430	11846
POL	FNLPPVAVK	742	9	27	42		11847
POL	INLPKWKPK	778	9	27	42		11848
POL	DLEIGIIRAK	123	10	27	42		11849
POL	WASQIYAGIK	381	10	27	42		11850
POL	KVKQLCKLLR	455	10	27	42		11851
POL	EICTEMEKEGK	464	10	27	42		11852
POL	SDLEIGIIRAK	223	11	27	42		11853
POL	VDKLVSSGIRK	380	11	27	42		11854
POL	ASQIYAGIK	740	11	27	42		11855
POL	KDLIAEIQK	456	9	28	44		11856
POL	NLKTGKYAK	515	9	28	44		11857
POL	DLIAEIQK	540	9	28	44		11858
POL	IVGAETFY	516	8	28	44		11859
POL	NFTSAVK	626	8	28	44		11860
POL	CTEMEKEGK	872	8	28	44		11861
POL		225	9	28	44	0.0001	11862

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GIKVKQLCK	462	9	28	44		11863
POL	PIVGAETFY	625	9	28	44		11864
POL	OLIKKEKVV	716	9	28	44		11865
POL	ICTEMEKEGK	224	10	28	44		11866
POL	WASQIVIGIK	455	10	28	44		11867
POL	KNLTKGVAK	539	10	28	44		11868
POL	NLTKGVAR	540	9	29	46		11869
POL	KLVSSGIR	742	8	29	45	0.0001	11870
POL	KNLTKGVAR	539	10	29	45		11871
POL	VIWGTTPKFR	573	10	29	45		11872
POL	VDKLVSSGIR	740	10	29	45		11873
POL	IVIWGKTPKFR	572	11	29	45		11874
POL	QVDKLVSSGIR	739	11	29	45		11875
POL	WGKTPKFR	575	8	30	47		11876
POL	LTETTNQK	661	8	30	47		11877
POL	ANRETILGK	638	9	30	47	0.0001	11878
POL	AAARETKLGG	637	10	30	47	0.0016	11879
POL	IEQLIKKEK	713	10	30	47	0.0003	11880
POL	GAANREIKLG	636	11	30	47		11881
POL	QHEQLIKKEK	712	11	30	47		11882
POL	ILKLGRWPFV	853	11	30	47		11883
POL	KIILVAVII	823	8	31	48		11884
POL	ETAYFILK	848	9	31	48		11885
POL	YFILKLGR	851	8	31	48		11886
POL	EGKILVAVII	821	10	31	48		11887
POL	PSINNETGIR	322	11	31	48		11888
POL	TQGETAYFILK	845	11	31	48		11889
POL	TAYFILKLGR	849	11	31	48		11890
POL	INNETGIR	324	9	32	51		11891
POL	INNETGIRY	324	10	32	51		11892
POL	FILKLGR	852	8	32	50		11893
POL	SINNETGIR	323	10	32	50		11894
POL	SINNETGIRY	323	11	32	50		11895
POL	SSMTKILEPFR	351	11	32	50		11896
POL	QTKELQKQITK	961	11	32	50	0.0100	11897
POL	EMEKEGKISK	229	10	33	52	0.0001	11898
POL	DVKQLTEAVQ	556	11	33	52	0.0240	11899
POL	DIATDIQTK	934	10	34	53	0.0130	11900
POL	ELQKQITK	964	8	35	56		11901
POL	LIKKEKVV	717	8	35	55		11902
POL	DSRDPIWK	981	8	35	55		11903
POL	ETKLKAGY	641	9	35	55		11904
POL	IATDIQTK	955	9	35	55	0.0980	11905
POL	QITKIQNR	968	9	35	55	0.0045	11906
POL	RDSRDPWK	980	9	35	55		11907
POL	TDIQTKELOK	938	10	35	55	0.0001	11908
POL	RDPWKGPAP	983	10	35	55		11909
POL	ATDIQTKELOK	937	11	35	55	0.1800	11910
POL	QITKIQNRVY	968	11	35	55		11911
POL	ITKIQNR	969	8	36	57		11912

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ITKIQNERVY	969	10	36	57	0.0012	11913
POL	ITKIQNERVY	969	11	36	57		11914
POL	IATDIQTK	956	8	36	56		11915
POL	PIWKGPAK	985	8	36	56		11916
POL	NLPKGWPK	124	9	36	56		11917
POL	AIQSSMTK	347	9	36	56	0.9600	11918
POL	PAIFQSSMTK	346	10	36	56	0.0830	11919
POL	VFAIKKKDSTK	249	11	36	56		11920
POL	NTVFAIK	246	8	37	58	0.0003	11921
POL	PVFAIKK	248	8	37	58	0.0001	11922
POL	QLTEAVQK	559	8	37	58		11923
POL	QIEQLIK	712	8	37	58		11924
POL	IEQLIK	713	8	37	58		11925
POL	YLSWVPAI	724	8	37	58		11926
POL	LSWVPAIK	725	8	37	58		11927
POL	YNTVFAIK	245	9	37	58	0.0002	11928
POL	NTVFAIKK	246	9	37	58	0.0600	11929
POL	QIEQLIK	712	9	37	58	0.1600	11930
POL	YLSWVPAIK	724	9	37	58		11931
POL	VIQNSDIK	1003	9	37	58	0.0068	11932
POL	YNTVFAIKK	245	10	37	58		11933
POL	NTVFAIKK	246	10	37	58	0.0046	11934
POL	VVIQNSDIK	1002	10	37	58	0.0210	11935
POL	YNTVFAIKK	245	11	37	58		11936
POL	AVVIQNSDIK	1000	11	37	58	0.0150	11937
POL	IFQSSMTK	348	8	38	59	0.0073	11938
POL	ILKEPVIGVY	498	11	38	59		11939
POL	LDGIDKAQEEH	754	11	39	62		11940
POL	AGYVTDGR	647	9	39	61		11941
POL	YVTDGRQK	649	9	39	61	0.0010	11942
POL	KAGYVTDGR	646	10	39	61		11943
POL	LGIIQAQPDK	695	10	39	61		11944
POL	DGIDKAQEEH	755	10	39	61	0.0001	11945
POL	PVHGVYDPS	505	11	39	61		11946
POL	AGYVTDGRQ	647	11	39	61		11947
POL	ALGIQAQPDK	694	11	39	61		11948
POL	DIKVYTRKAK	1009	11	39	61		11949
POL	VTDGRQK	650	8	40	63	0.0065	11950
POL	IIQAQPDK	697	8	40	63		11951
POL	GIQAQPDK	696	9	40	63	0.0400	11952
POL	GIDKAQEEH	756	9	40	63		11953
POL	NSDIKVPR	1007	9	40	63		11954
POL	ILKEPVIGVY	498	10	40	63		11955
POL	DNSDIKVPR	1006	10	40	63		11956
POL	NSDIKVPR	1007	10	40	63	0.0001	11957
POL	ELKEPVIGVY	497	11	40	63		11958
POL	WTYQVQEPF	529	11	40	63	0.0540	11959
POL	QIQEPEKLNK	532	11	40	63	0.2900	11960
POL	QNSDIKVPR	1005	11	40	63		11961
POL	DNSDIKVPR	1006	11	40	63		11962

Table XVII
HIV All Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SIQ ID NO.
POL	NSDIKVPRRK	1007	11	40	63		11963
POL	ESIVWGKTPK	570	11	41	65		11964
POL	QYQEPFK	532	8	41	64	0.0013	11965
POL	IDKAQEEH	757	8	41	64		11966
POL	KAKIRDY	1017	8	41	64		11967
POL	KAKIRDYGK	1017	10	41	64	0.0018	11968
POL	KISKIGPENFY	235	11	41	64		11969
POL	KAGYVTDK	646	8	42	66		11970
POL	ISKIGPENFY	236	10	42	66		11971
POL	SMTRILEPFR	352	10	42	66	0.0004	11972
POL	SIVWGKTPK	571	10	42	66		11973
POL	IVIVQYMDLKY	367	11	42	66		11974
POL	VVPRKAKIIR	1012	11	42	66		11975
POL	GVYDPSK	508	8	43	67		11976
POL	SCDKCQLK	791	8	43	67		11977
POL	MTKILEPFR	353	9	43	67	0.0160	11978
POL	IIGVYDPSK	507	9	43	67	0.0001	11979
POL	ASCDKCOLK	790	9	43	67	0.0140	11980
POL	DSWTVNDIQK	439	10	43	67	0.0002	11981
POL	TFYVDGAANR	631	10	43	67	0.0008	11982
POL	VASCDKCOLK	789	10	43	67	0.0004	11983
POL	KDSWTVNDIQ	438	11	43	67		11984
POL	ETFYVDGAAN	630	11	43	67		11985
POL	IVASCDKCOLK	788	11	43	67		11986
POL	SDIKVVR	1008	8	44	69	0.1000	11987
POL	SDIKVVR	1008	9	44	69	0.0001	11988
POL	VDGAANRETK	634	10	44	69		11989
POL	IGQVRDQAEH	914	10	44	69		11990
POL	QVRDQAEHLK	916	10	44	69	0.0093	11991
POL	SDIKVVRPRK	1008	10	44	69	0.0001	11992
POL	ENBEIKERVII	494	11	44	69		11993
POL	YVDGAANRET	633	11	44	69		11994
POL	IGQVRDQAEH	913	11	44	69		11995
POL	VAKIVASCDK	784	11	45	71		11996
POL	GAANIRETK	636	8	45	70		11997
POL	EIVASCDK	787	8	45	70		11998
POL	DGAANRETK	635	9	45	70		11999
POL	PFKNLTKGY	537	10	45	70	0.0002	12000
POL	PLVRLWYQLE	613	11	45	70		12001
POL	EILKEIVII	497	8	46	72		12002
POL	KLWYQLEK	616	8	46	72		12003
POL	RDAEHLK	918	8	46	72		12004
POL	PFKNLTKGK	537	9	46	72		12005
POL	DIQTKELQK	959	9	46	72	0.0006	12006
POL	LVKLWYQLEK	614	10	46	72	0.0020	12007
POL	KVKQWPLTEE	207	11	46	72	0.0330	12008
POL	VWGKTPK	573	8	48	75		12009
POL	QVRDQAEH	916	8	48	75		12010
POL	DIKVVPR	1009	8	48	75		12011
POL	IVIWGKTPK	572	9	48	75	0.3700	12012

Table XVII
 HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	DIKVVHRRK	1009	9	48	75	0.0001	12013
POL	KVLFLDGIDK	750	10	48	75	0.7800	12014
POL	KCQLKGEAMII	794	10	48	75		12015
POL	VVESMNKELK	902	10	48	75		12016
POL	GVVESMNKEL	901	11	48	75		12017
POL	VVESMNKELK	902	11	48	75		12018
POL	GVVESMNK	901	8	49	77		12019
POL	QGVVESMNK	900	9	49	77		12020
POL	KLKPGMDGPK	197	10	49	77	0.0760	12021
POL	QSQGVVESMIN	898	11	49	77		12022
POL	ESIVWGG	570	8	50	79		12023
POL	YVDGAANR	633	8	50	78		12024
POL	LAGRWPK	856	8	50	78	0.0001	12025
POL	KIIRDYGG	1019	8	50	78		12026
POL	KLGRWPK	855	9	50	78	0.0690	12027
POL	QNFVYRDS	973	11	50	78		12028
POL	GMGPKVK	201	8	51	80		12029
POL	KIGPENPY	238	8	51	80	0.0004	12030
POL	NNETPGIR	325	8	51	80		12031
POL	FTTPDKKI	403	8	51	80		12032
POL	PGMDGPKVK	200	9	51	80	0.0001	12033
POL	NNETPGIRY	325	9	51	80		12034
POL	GFTHDCKII	402	9	51	80		12035
POL	VLFLDGIDK	751	9	51	80		12036
POL	VIYQYMDDLV	368	10	51	80	0.0320	12037
POL	WGFTTPDKKII	401	10	51	80	0.0090	12038
POL	FTTPDKKIQQ	403	10	51	80		12039
POL	NNETPGIRYQY	325	11	51	80	0.0150	12040
POL	GFTHDCKIIQ	402	11	51	80		12041
POL	PAGLKKKK	286	8	51	81		12042
POL	SDLEIGQII	380	8	52	81		12043
POL	DLEIGQIR	381	8	52	81		12044
POL	WGFTTPDK	401	8	52	81		12045
POL	GFTHDCK	402	8	52	81		12046
POL	KIQNRIVY	971	8	52	81		12047
POL	VVPRRKAK	1012	8	52	81	0.0001	12048
POL	ETPGIRYQY	327	9	52	81		12049
POL	GSDLEIGQII	379	9	52	81	0.0001	12050
POL	SDLEIGQIR	380	9	52	81	0.0039	12051
POL	WGFTTPDKK	401	9	52	81		12052
POL	KIQNRIVY	971	9	52	81	0.0039	12053
POL	KVPRRKAK	1011	9	52	81		12054
POL	VGSDLEIGQII	378	10	52	81		12055
POL	GSDLEIGQIR	379	10	52	81		12056
POL	KIQNRIVYR	971	10	52	81	0.2100	12057
POL	NFRVYRDSR	974	10	52	81		12058
POL	ICGIGGFIKVR	134	11	52	81		12059
POL	VGFTPNIGR	164	11	52	81		12060
POL	YVGSLEIGQH	377	11	52	81		12061
POL	VGSDLEIGQHR	378	11	52	81		12062

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GIPIIPAGLKKK	282	11	53	84		12063
POL	IGGFIKVR	137	8	53	83		12064
POL	GEIKVRQY	139	8	53	83		12065
POL	PIETVPVK	190	8	53	83		12066
POL	ETVPVKLK	192	8	53	83	0.0001	12067
POL	ELELAENR	489	8	53	83		12068
POL	QLKGEAMH	796	8	53	83		12069
POL	ESMNKELK	904	8	53	83		12070
POL	SMNKELKK	905	8	53	83		12071
POL	GGGFIKVR	136	9	53	83	0.0005	12072
POL	GGFIKVRQY	138	9	53	83	0.0001	12073
POL	ESMNKELKK	904	9	53	83		12074
POL	GGGFIKVR	135	10	53	83	0.0002	12075
POL	GGGFIKVRQY	137	10	53	83	0.0002	12076
POL	ISPIETVPVK	188	10	53	83	0.0310	12077
POL	PIETVPVKLK	190	10	53	83	0.0001	12078
POL	EAELELAENR	487	10	53	83		12079
POL	LVAIVIVASGY	826	10	53	83		12080
POL	GIGGFIKVRQY	136	11	53	83		12081
POL	ISPIETVPVK	187	11	53	83		12082
POL	ILVAVIVASGY	825	11	53	83		12083
POL	FVNTPLPVK	608	9	54	86	0.0660	12084
POL	GIPIIPAGLKK	282	10	54	86	0.1700	12085
POL	LGPIIPAGLKK	281	11	54	86		12086
POL	QNERVYYR	973	8	54	84		12087
POL	PTFVNIUR	166	9	54	84		12088
POL	LAENREIK	492	9	54	84	0.0001	12089
POL	ELAENREIK	491	10	54	84	0.0003	12090
POL	EFVNTPLPVK	607	10	54	84	0.0003	12091
POL	PLTEKIK	212	8	55	86		12092
POL	LFLDGIDK	752	8	55	86		12093
POL	GIPIIPAGLK	282	9	56	89		12094
POL	LGPIIPAGLK	281	10	56	89	0.0650	12095
POL	QLGPIIPAGLK	280	11	56	89	0.0150	12096
POL	VTVLVDVGDY	295	10	56	88		12097
POL	ELKKIIGQVR	909	10	56	88	0.0004	12098
POL	DFWEVOLGPIH	275	11	56	88		12099
POL	SVTVLDVGDA	294	11	56	88		12100
POL	KTAYQMAVFI	925	11	56	88		12101
POL	VNTPLPVK	609	8	57	89		12102
POL	AIKKKDKSTK	251	9	57	89	0.0086	12103
POL	TVLDVGDY	296	9	57	89	0.0036	12104
POL	TPDKKIIOK	404	9	57	89	0.0042	12105
POL	FAIKKDKSTK	250	10	57	89	0.0002	12106
POL	NTPLVLKLVY	610	10	57	89		12107
POL	AIKKKDKSTK	251	11	57	89		12108
POL	VNTPLVLKLV	609	11	57	89		12109
POL	MAVFIHFKR	930	11	57	89		12110
POL	GGIGYSAGER	941	11	57	89		12111
POL	KDSTKWRK	255	8	58	91		12112

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	EVQLGPIH	278	8	58	91		12113
POL	GGNEQVDK	735	8	58	91		12114
POL	FIINFKRK	933	8	58	91		12115
POL	GGYSAGER	944	8	58	91		12116
POL	RVYRDSR	976	8	58	91		12117
POL	IGGNEQVDK	734	9	58	91	0.0001	12118
POL	VFILNFKRK	932	9	58	91	0.0003	12119
POL	IGGYSAGER	943	9	58	91	0.0001	12120
POL	GIGGNEQVDK	733	10	58	91	0.0001	12121
POL	PAETQETAY	842	10	58	91	0.0001	12122
POL	AVFIINFKRK	931	10	58	91	0.8500	12123
POL	GIGGYSAGER	942	10	58	91	0.0001	12124
POL	STKWRKLVDF	257	11	58	91		12125
POL	KGIGGNEQVDK	732	11	58	91		12126
POL	AVIIVASGY	828	8	59	92		12127
POL	ETGQETAY	844	8	59	92		12128
POL	GIWQLDCTH	811	9	59	92		12129
POL	VAVIVASGY	827	9	59	92	0.0001	12130
POL	KGPAKLLWK	988	9	59	92	0.0007	12131
POL	EVNIVTSQY	684	10	59	92		12132
POL	PGIWQLDCTH	810	10	59	92		12133
POL	TAVQMAVFH	926	10	59	92	0.0110	12134
POL	VGKLNWASQI	450	11	59	92		12135
POL	NFKRKGIGGY	936	11	59	92		12136
POL	QLDCTHLEQK	814	10	60	95	0.0003	12137
POL	DFRELNR	265	8	60	94		12138
POL	VLDVGDAY	297	8	60	94		12139
POL	KNLKTGY	539	8	60	94		12140
POL	VDFRELNR	264	9	60	94		12141
POL	MGVELIIPDK	419	9	60	94		12142
POL	KLWNASQIY	452	9	60	94	0.0960	12143
POL	AVQMAVFH	927	9	60	94	0.0006	12144
POL	MAVFIINFK	930	9	60	94		12145
POL	LVDFRELNR	263	10	60	94	0.3000	12146
POL	WMGYELIIPDK	418	10	60	94	0.0004	12147
POL	QMAVFIINFK	929	10	60	94		12148
POL	MAVFIINFKR	930	10	60	94	0.6400	12149
POL	KLVDRELNR	262	11	60	94	0.0083	12150
POL	QMAVFIINFK	929	11	61	95		12151
POL	LNWASQIY	453	8	61	95		12152
POL	NDIQKLVGK	444	9	61	95		12153
POL	LDCTHLEQK	815	9	61	95		12154
POL	VNDIQKLVGK	443	10	61	95		12155
POL	TVNDIQKLVGK	442	11	61	95	0.1700	12156
POL	VDFRELNR	264	8	62	97		12157
POL	WTVNDIQK	441	8	62	97	0.0001	12158
POL	DIQKLVGK	445	8	62	97		12159
POL	NIYVTSQY	686	8	62	97		12160
POL	DCTHLEQK	816	8	62	97		12161
POL	AVFIINFK	931	8	62	97	0.0380	12162

Table XVII
HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	VFIHFKR	932	8	62	97		12163
POL	LVDFRELNK	263	9	62	97	0.0300	12164
POL	VNIYDSQY	685	9	62	97		12165
POL	AVFIHFKR	931	9	62	97	1.8000	12166
POL	MIGGIGGFIK	133	10	62	97	0.0550	12167
POL	KLVDRELNK	262	10	62	97	0.0900	12168
POL	KMIGGIGGFIK	132	11	62	97	0.7000	12169
POL	NVLIQGWK	336	8	63	100	0.0012	12170
POL	IGGIGGFIK	134	9	63	98	0.0037	12171
POL	YNVLIQGWK	335	9	63	98	0.0001	12172
POL	GGIGGFIK	135	8	64	100		12173
POL	FLWMGYELII	416	9	64	100		12174
POL	PELWMGYELII	415	10	64	100		12175
REV	GTRQTRKNR	37	9	01	50		12176
REV	TTRQARNR	37	9	01	50		12177
REV	GTRQTRKNR	37	10	01	50		12178
REV	TTRQARNR	37	10	01	50		12179
REV	GTRQTRKNR	37	11	01	50		12180
REV	TTRQARNR	37	11	01	50		12181
REV	GTETGVGR	103	8	06	19		12182
REV	QGTETGVGR	102	9	06	19		12183
REV	LLKTVRLIK	12	9	10	16		12184
REV	GDSDELLK	6	9	11	17		12185
REV	PLQPHR	76	9	11	17		12186
REV	SGDSDELLK	5	10	11	17		12187
REV	RSQDSDELLK	4	11	11	17		12188
REV	PVPLQPHR	74	11	11	17		12189
REV	RAQRQR	30	8	12	19		12190
REV	DSDELLK	7	8	12	19		12191
REV	ILSTCLGR	63	8	12	19		12192
REV	RLSTCLGR	62	9	12	19		12193
REV	SNPTSPGTR	27	11	12	19		12194
REV	AVHIKILY	17	9	13	20		12195
REV	OLPPLERLI	78	9	13	20		12196
REV	PSPECTROAR	31	10	13	20		12197
REV	RNRRRWRER	43	10	13	20		12198
REV	PSPECTROAR	31	11	13	20		12199
REV	PLQPLERLI	76	11	13	20		12200
REV	GTRQARKNR	36	11	14	22		12201
REV	RAQRQHI	50	8	15	24		12202
REV	GTRQARKNR	36	9	15	23		12203
REV	GTRQARKNR	36	10	15	23		12204
REV	QARKNRNR	40	9	16	25		12205
REV	QARKNRNR	40	11	16	25		12206
REV	QARKNRNR	40	8	17	27		12207
REV	IKILYQSNPY	20	11	18	28		12208
REV	KNRRRWRA	43	10	19	30		12209
REV	KNRRRWRA	43	8	21	33		12210
REV	RNRRRRWRA	43	10	23	36		12211
REV	KILYQSNPY	22	9	26	41		12212

Table XVII
 HIV Δ11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
REV	ILYQSNPY	23	8	27	42		12213
REV	EGTRQAIR	35	8	27	42		12214
REV	EGTRQARRNR	35	10	27	42		12215
REV	EGTRQARRNR	35	11	27	42		12216
REV	GTROARRNR	36	9	34	53		12217
REV	GTROARRNR	36	10	34	53		12218
REV	GTROARRNR	36	11	34	53		12219
REV	PVPLQLPTLR	74	11	34	53		12220
REV	PLQLPTLR	76	9	35	55		12221
REV	QARRNR	40	11	37	58		12222
REV	QARRNR	40	8	38	59		12223
REV	QARRNR	40	9	38	59		12224
REV	RNRNRNR	43	8	40	63		12225
TAT	PGGYTRK	104	8	01	50		12226
TAT	AGPGGYPRR	102	9	01	50		12227
TAT	TGPGGQPCII	102	9	01	50		12228
TAT	ETGPGQPCII	101	10	01	50		12229
TAT	KAGPGGYPR	101	10	01	50		12230
TAT	AGPGGYPRR	102	10	01	50		12231
TAT	KAGPGGYPRR	101	11	01	50		12232
TAT	GGYPRKGGSC	105	11	01	50		12233
TAT	ACTNLCYCK	24	8	10	16		12234
TAT	TACTNLCYCK	23	9	10	16		12235
TAT	CNLCYCK	25	8	11	17		12236
TAT	YCKKCCFI	29	8	11	17		12237
TAT	YCKKCCYII	29	8	11	17		12238
TAT	VDPRLEPWK	4	9	11	17		12239
TAT	ACNNCYCKK	24	9	11	17		12240
TAT	PVDPRLEPWK	3	10	11	17	0.0001	12241
TAT	VDPRLEPWKII	4	10	11	17		12242
TAT	TACNNCYCKK	23	10	11	17		12243
TAT	PVDPRLEPWK	3	11	11	17		12244
TAT	RGDPTGPKES	84	11	11	17		12245
TAT	GDPTGPKESK	85	11	11	17		12246
TAT	ESKKKVESK	93	9	12	19		12247
TAT	GDPTGPKESK	85	10	12	19		12248
TAT	PTGPKESKKK	88	10	12	19		12249
TAT	TGPKESKKK	89	9	13	20		12250
TAT	LNKGLGISY	42	9	14	22		12251
TAT	FLNKGLGISY	41	10	14	22		12252
TAT	PVDNLEPWNI	3	11	14	22		12253
TAT	CFLNKGLGISY	40	11	14	22		12254
TAT	LNKGLGISYGR	42	11	14	22		12255
TAT	WNHFGSQPK	14	9	15	23		12256
TAT	RGDPTGPK	84	8	16	25		12257
TAT	VDNLEPWNI	4	10	16	25		12258
TAT	PNLEPWNI	9	8	17	27		12259
TAT	ACNNCYCK	24	8	17	27		12260
TAT	TACNNCYCK	23	9	17	27		12261
TAT	PTGPKESKK	88	9	18	28		12262

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
TAT	TGPKESKK	89	8	19	30		12263
TAT	PTGPKESK	88	8	20	31		12264
TAT	YGRKKRRQRR	50	11	22	34		12265
TAT	YGRKKRRQRR	50	10	38	39		12266
TAT	ISYGRKKRRQRR	48	11	39	61		12267
TAT	YGRKKRRQRR	50	9	41	64		12268
TAT	GISYGRKKRR	47	10	45	70	0.0001	12269
TAT	LGISYGRKKRR	46	11	45	70		12270
TAT	ISYGRKKRR	48	9	46	72	0.0005	12271
TAT	GLGISYGRKKRR	45	11	54	86		12272
TAT	GLGISYGR	45	8	55	87		12273
TAT	GLGISYGRKK	45	9	55	87	0.0006	12274
TAT	GLGISYGRKK	45	10	55	87		12275
TAT	KGLGISYGR	44	9	55	86	0.0180	12276
TAT	KGLGISYGRKK	44	10	55	86	0.0007	12277
TAT	GISYGRKKRR	47	11	57	89		12278
TAT	LGISYGRKKRR	46	10	57	89	0.0015	12279
TAT	LGISYGRKK	46	8	58	91		12280
TAT	GISYGRKK	47	8	58	91		12281
TAT	ISYGRKKRR	48	8	58	91		12282
TAT	LGISYGRKK	46	9	58	91		12283
VIF	LIVWQVDR	8	8	10	16	0.0005	12284
VIF	RMKINTWK	15	8	10	16		12285
VIF	LIKPKKK	158	8	10	16		12286
VIF	KGWFFRIIHY	36	9	10	16		12287
VIF	ALIKPKKK	157	9	10	16		12288
VIF	VDRMINTWK	13	10	10	16		12289
VIF	GVSEWRLRR	87	10	10	16		12290
VIF	QVDRMINTWK	12	11	10	16		12291
VIF	RLVITYWGL	65	11	10	16		12292
VIF	QTGERDWIILG	75	11	10	16		12293
VIF	GVSEWRLRR	87	11	10	16		12294
VIF	IDPDLADQLHI	103	11	10	16		12295
VIF	LVIEDRWNKIQ	178	11	10	16		12296
VIF	SEWRLRR	89	8	11	16		12297
VIF	TALIKPKK	156	8	11	17		12298
VIF	LVIEDRWNK	178	8	11	17		12299
VIF	VSIEWRLRR	88	8	11	17		12300
VIF	SEWRLRRY	89	9	11	17		12301
VIF	LTALIKPKK	155	9	11	17		12302
VIF	KLVEDRWNK	177	9	11	17		12303
VIF	VSIEWRLRRY	88	10	11	17		12304
VIF	GLADQLIIMHI	106	10	11	17		12305
VIF	ALTALIKPKK	154	10	11	17		12306
VIF	WNKPKQTRGHI	183	10	11	17		12307
VIF	PGLADQLIIMHI	105	11	11	17		12308
VIF	GLADQLIIMHI	106	11	11	17		12309
VIF	LALTALIKPKK	153	11	11	17		12310
VIF	WNKPKQTRGH	183	11	11	17		12311
VIF							12312

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	WFYRIIYESR	3R	11	12	19		12313
VIF	KGWFRIRII	36	8	12	19		12314
VIF	WGLQGER	72	8	12	19		12315
VIF	QTGERDWII	75	8	12	19		12316
VIF	IVWQVDRMK	9	9	12	19		12317
VIF	KIRTWNSLYK	17	10	12	19		12318
VIF	LVKIHIMYVSK	24	10	12	19		12319
VIF	GLQTGERDWII	73	10	12	19		12320
VIF	TGERDWIILGH	77	10	12	19		12321
VIF	HGVSEWRLR	86	10	12	19		12322
VIF	IVWQVDRMKI	9	11	12	19		12323
VIF	KIRTWNSLYK	17	11	12	19		12324
VIF	SLVKIHIMYVS	23	11	12	19		12325
VIF	LVKIHIMYVSK	24	11	12	19		12326
VIF	WGLQTGERD	72	11	12	19		12327
VIF	WFYRIIYESR	3R	10	13	21		12328
VIF	QVDRNKIR	12	8	13	20		12329
VIF	HIPLGDAR	56	8	13	20		12330
VIF	ADQLIHIMII	10R	8	13	20		12331
VIF	CFDSAIR	119	8	13	20		12332
VIF	FSDSAIRK	120	8	13	20		12333
VIF	SLOYLALK	149	8	13	20		12334
VIF	LTALIKPK	155	8	13	20		12335
VIF	LADQLIHIMII	107	9	13	20		12336
VIF	ADQLIHIMY	108	9	13	20		12337
VIF	CFDSAIRK	119	9	13	20		12338
VIF	GSLQYLALK	148	9	13	20		12339
VIF	ALTALIKPK	154	9	13	20		12340
VIF	SVKKLTDAR	174	9	13	20		12341
VIF	EVHPLGDAR	54	10	13	20		12342
VIF	LADQLIHIMY	107	10	13	20		12343
VIF	DCFSAIRK	118	10	13	20		12344
VIF	VGSLQYLALK	147	10	13	20		12345
VIF	LALTALIKPK	153	10	13	20		12346
VIF	PSVKKLTEDR	173	10	13	20		12347
VIF	DCFSAIRK	117	11	13	20		12348
VIF	YLALTALIKPK	152	11	13	20		12349
VIF	FSESARK	120	8	14	22		12350
VIF	IVSPRCEY	133	8	14	22		12351
VIF	GVSEWRLR	87	9	14	22		12352
VIF	ADQLIHILY	108	9	14	22		12353
VIF	CFESAIRK	119	9	14	22		12354
VIF	VDRMRITWK	13	10	14	22		12355
VIF	LADQLIHILY	107	10	14	22		12356
VIF	RCDYQAGHINK	137	10	14	22		12357
VIF	QVDRMRITW	12	11	14	22		12358
VIF	RIRTWNSLVK	17	11	14	22		12359
VIF	RMRTWK	15	8	15	23		12360
VIF	RTWKSIVK	19	8	15	23		12361
VIF	VSIEWRLR	88	8	15	23		12362

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SI:Q ID NO.
VIF	ADQLILY	108	8	15	23		12363
VIF	RTWKSIVKII	19	9	15	23		12364
VIF	QGVSEWRK	86	9	15	23		12365
VIF	LADQLILY	107	9	15	23		12366
VIF	AIRKAILGII	124	9	15	23		12367
VIF	CDYQAGINK	138	9	15	23		12368
VIF	RIRTWKSLVK	17	10	15	23		12369
VIF	RIRTWKSLVK	17	10	15	23		12370
VIF	RTWKSIVKIII	19	10	15	23		12371
VIF	SAIRKAILGII	123	10	15	23		12372
VIF	RIRTWKSLVK	17	11	15	23		12373
VIF	LQGVSEWR	84	11	15	23		12374
VIF	VDPGLADQLII	103	11	15	23		12375
VIF	ITTYWGLII	68	11	15	23		12376
VIF	GVSIEWRK	87	8	16	25		12377
VIF	RCYQAGII	137	8	16	25		12378
VIF	LALALIK	153	8	16	25		12379
VIF	VITYWGLII	67	9	16	25		12380
VIF	YLALALIK	152	9	16	25		12381
VIF	KTKGIKGSII	188	9	16	25	0.0001	12382
VIF	LVITYWGLII	66	10	16	25		12383
VIF	WNKPKTKGII	183	10	16	25		12384
VIF	WNKPKTKGII	183	11	16	25		12385
VIF	EDRWKPKTK	180	11	17	27		12386
VIF	WNKPKTK	183	8	18	28		12387
VIF	KSLVKIIIMY	22	9	18	28		12388
VIF	EDRWKPKTK	180	11	18	28		12389
VIF	RCEYQAGINK	137	10	19	30		12390
VIF	RIPLGEAR	56	8	20	31		12391
VIF	WNKPKTR	183	8	20	31		12392
VIF	EVIIPLGEAR	54	10	20	31		12393
VIF	IITGERDWII	75	8	21	33		12394
VIF	DLADQLII	106	8	21	33		12395
VIF	PLADQLII	105	9	21	33		12396
VIF	GLITGERDWII	73	10	21	33		12397
VIF	WGLITGERD	72	11	21	33		12398
VIF	VSPRCEYQAG	134	11	21	33		12399
VIF	LTEDRWKPKQ	178	11	21	33		12400
VIF	GSIIIMNGII	194	8	22	34	0.0130	12401
VIF	RGSIIIMNGII	193	9	22	34		12402
VIF	TTYWGLITGE	69	11	22	34		12403
VIF	ILGIICVSEW	83	11	22	34		12404
VIF	NSLVKIIIMY	22	9	24	38		12405
VIF	WNSLVKIIIM	21	10	24	38		12406
VIF	QGVSEWR	86	8	25	39		12407
VIF	LQGVSEWR	84	10	25	39		12408
VIF	ILQGVSEW	83	11	25	39		12409
VIF	RCEYQAGII	137	8	26	41		12410
VIF	RTWNSLVKII	19	9	26	41		12411
VIF	RTWNSLVKIII	19	10	26	41		12412

Table XVII
HIV A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
VIF	RTWNSLVK	19	8	27	42		12413
VIF	IIGVSEWR	86	8	27	42		12414
VIF	GLADQLIH	106	8	27	42		12415
VIF	PLGADQLIH	105	9	27	42		12416
VIF	LGHGVSEWR	84	10	27	42		12417
VIF	YFDCFSASIR	116	11	27	42		12418
VIF	WGLIHGIR	72	8	28	44		12419
VIF	DCFSASIR	118	9	28	44		12420
VIF	FDCFSASIR	117	10	28	44		12421
VIF	WNSLVKIH	21	8	29	45		12422
VIF	CFESASIR	119	8	29	45		12423
VIF	KLTEDRWNK	177	9	29	45	0.2700	12424
VIF	LTEDRWNK	178	8	31	48	0.0045	12425
VIF	IVWQVDRMIR	9	11	33	52		12426
VIF	QVDRMRIR	12	8	34	53		12427
VIF	EDRWNKIQK	180	9	39	61		12428
VIF	VMIVWQVDR	7	11	41	64		12429
VIF	QVMIVWQVDR	6	10	43	67		12430
VIF	MIVWQVDRM	8	10	43	67	0.0001	12431
VIF	AGINKVGSLSQ	142	11	43	67		12432
VIF	SLYKIHMY	23	8	44	69		12433
VIF	VMIVWQVDR	7	9	44	69	0.0220	12434
VIF	MIVWQVDR	8	8	46	72		12435
VIF	IVWQVDRMR	9	9	47	73	0.0007	12436
VIF	INKVGSLSQ	144	9	47	73		12437
VPR	ALPCRRGR	85	8	01	50		12438
VPR	NIRGRVR	85	8	01	50		12439
VPR	WALELLELK	18	10	09	15		12440
VPR	QLLFYIIR	66	8	10	16		12441
VPR	HSRIGIR	79	8	10	16		12442
VPR	RIGTRQR	81	8	10	16		12443
VPR	IGTRQR	82	8	10	16		12444
VPR	ALELLELK	19	9	10	16		12445
VPR	RIGTRQR	81	9	10	16		12446
VPR	HSRIGTRQR	79	10	10	16		12447
VPR	HSRIGTRQR	79	11	10	16		12448
VPR	WLHGLQY	38	8	11	17		12449
VPR	IFRIGCRH	71	8	11	17		12450
VPR	HSRIGTR	79	8	11	17		12451
VPR	FIHFRIGCR	69	9	11	17		12452
VPR	LFHFRIGCR	68	10	11	17		12453
VPR	FIHFRIGCRH	69	10	11	17		12454
VPR	FVIFRIGCOH	69	10	11	17		12455
VPR	HFIRIGCRISR	71	10	11	17		12456
VPR	LFHFRIGCR	67	11	11	17		12457
VPR	LFHFRIGCRH	68	11	11	17		12458
VPR	LFVIFRIGCCII	68	11	11	17		12459
VPR	RIGCRISR	74	8	12	19		12460
VPR	LQIIINYTY	42	9	13	20		12461
VPR	LQYIYETY	42	9	13	20		12462

Table XVII
HIV All Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPR	IFPRWLII	33	8	14	22		12463
VPR	KSEAVRIIFPR	27	10	14	22		12464
VPR	AVRIIFRIWL	30	11	14	22		12465
VPR	ELKSEAVR	25	8	16	25		12466
VPR	ACVEAIR	55	8	16	25		12467
VPR	ELKSEAVRII	25	9	16	25		12468
VPR	WAGVEAIR	54	9	16	25		12469
VPR	LEELKSEAVR	22	11	16	25		12470
VPR	DTWAGVEAIR	52	11	16	25		12471
VPR	ELKNEAVR	25	8	17	27		12472
VPR	ELKNEAVRII	25	9	17	27		12473
VPR	LGOHIYETY	42	9	17	27		12474
VPR	LEELKNEAVR	22	11	17	27		12475
VPR	EGVEAIR	55	8	18	28		12476
VPR	DTWEGVEAIR	52	11	18	28		12477
VPR	KANGASIR	93	8	19	30		12478
VPR	KNEAVRIIFPR	27	10	19	30		12479
VPR	WLIIGLQHI	38	8	20	31		12480
VPR	HGLGQHIY	40	8	20	31		12481
VPR	WLIIGLQHIY	38	10	20	31		12482
VPR	LFIIFRIGCQH	68	11	29	45		12483
VPR	FIIFRIGCQH	69	10	30	47		12484
VPR	IFPRWLII	33	8	31	49		12485
VPR	AVRIIFRIWL	30	11	31	48		12486
VPR	ILQQLFIIFR	63	11	31	48		12487
VPR	ILQQLFIH	62	10	36	56		12488
VPR	EDQGIQREPY	6	9	37	58		12489
VPR	QAPEDQGIQPR	3	10	37	58		12490
VPR	WTLELLELK	18	10	39	62		12491
VPR	QGIQREPY	8	8	42	69		12492
VPR	QLFIIFR	66	8	43	68		12493
VPR	IFRIGCQH	71	8	44	69		12494
VPR	TLELLELK	19	8	44	69		12495
VPR	IFRIGCQISR	71	9	44	69		12496
VPR	RIGCQISK	74	8	44	69		12497
VPR	EAVRIIFPR	29	8	47	73		12498
VPR	LVQRKQDR	43	8	59	92		12499
VPR	VTLLSSK	94	8	01	50		12500
VPR	LVQRKQDRR	43	9	01	50		12501
VPR	LVTLSSK	91	9	01	50		12502
VPR	RIKEIRDDSDY	64	11	01	50		12503
VPR	RIKEIRDDSDY	64	11	01	50		12504
VPR	RIKEIRDDSDY	64	11	01	50		12505
VPR	WTIVFIYR	34	9	10	16		12506
VPR	TIVFIYR	35	8	10	16		12507
VPR	IDRLDIR	54	9	10	16		12508
VPR	RLDIRIR	56	9	10	16		12509
VPR	KIDLDIR	52	10	10	16		12510
VPR	VWTVFIYR	31	11	10	16		12511
VPR	WTIVFIYR	34	8	12	19		12512

Table XVII
HIV All Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VP1	IVFIEYRK	36	8	12	19		12513
VP1	VVWTVFIEY	31	10	12	19		12514
VP1	IVVWTVFIEY	30	11	12	19		12515
VP1	LIDRIERK	58	8	14	22		12516
VP1	KIHRLIDR	52	8	15	23		12517
VP1	ILRQKIDR	46	9	15	23		12518
VP1	KLRQKIDR	45	10	15	23	0.0001	12519

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SIQ ID NO.
ENV	IIMQLTVW	650	8	10	16		12520
ENV	WFDITNWL	767	8	10	16		12521
ENV	WFDITNWLW	767	9	10	16		12522
ENV	IYCTIAGFAI	262	10	10	16		12523
ENV	IWNMTWME	717	10	10	16		12524
ENV	WFDITNWLW	767	11	10	16		12525
ENV	SYIIRLDLLI	864	11	10	16		12526
ENV	IYCTIAGF	262	8	11	17		12527
ENV	FYATGDIKDI	367	11	11	17		12528
ENV	FYATGDIH	367	8	12	19		12529
ENV	WMEWEREI	723	8	12	19		12530
ENV	GWEALKYL	896	8	12	19		12531
ENV	GWEGLKYL	896	8	12	19		12532
ENV	TWMEWEREI	722	9	12	19		12533
ENV	SYIIRLDLLI	864	10	12	19		12534
ENV	NMTWMEWER	720	11	12	19		12535
ENV	YWGOELKNSA	909	11	12	19		12536
ENV	LYKYKVEI	561	9	13	20		12537
ENV	SYIIRLDIF	864	9	13	20		12538
ENV	SYIIRLDIFL	864	10	13	20		12539
ENV	VMISFNCGRH	432	11	13	20		12540
ENV	LFSYIIRLDIF	862	11	13	20		12541
ENV	LFSYIIRLDLL	862	11	13	20		12542
ENV	SYIIRLDLL	864	9	14	22		12543
ENV	KYWWNLQY	901	10	14	22		12544
ENV	WWNLQYW	903	8	15	23		12545
ENV	YWWNLQYW	902	9	15	23		12546
ENV	KWASLWNWF	760	11	15	23		12547
ENV	SFNCGRGF	437	8	16	25		12548
ENV	SFNCGRGF	437	9	16	25		12549
ENV	KWLWYIKIF	772	9	16	25		12550
ENV	KWLWYIKIF	772	10	16	25		12551
ENV	RYLIHQQLL	671	9	17	27	0.23100	12552
ENV	RYLIHQQLLGI	671	11	17	27		12553
ENV	RYLIHQQL	671	11	18	28		12554
ENV	SYIIRLDIF	864	8	18	28		12555
ENV	AYDTEVINWV	73	10	18	28		12556
ENV	LFSYIIRLDIF	862	10	18	28		12557
ENV	KWLWYIKI	772	8	19	30		12558
ENV	AWDDLKSL	853	8	20	31	0.00004	12559
ENV	NMVEQMIEDI	112	10	20	31		12560
ENV	AWDDLKSLCL	853	10	20	31		12561
ENV	NMVEQMIEDII	112	11	20	31		12562
ENV	AWDDLKSLCL	853	11	20	31		12563
ENV	FYCNTSGL	445	8	21	33		12564
ENV	FYCNTSGL	444	9	21	33		12565
ENV	FYCNTSGL	445	9	21	33		12566
ENV	EFFYNTSGL	443	10	21	33		12567
ENV	FFYNTSGL	444	10	21	33		12568
ENV	EFFYNTSGLF	443	11	21	33		12569

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SiQ ID NO.
ENV	VWKEATITL	55	9	22	34	0.03100	12570
ENV	VWKEATITLF	55	10	22	34	0.27100	12571
ENV	LFSYIRLRDL	862	10	22	34		12572
ENV	SYIRLRDL	864	8	23	36		12573
ENV	NWLWYIKI	772	8	25	39		12574
ENV	NWLWYIKIF	772	9	25	39		12575
ENV	KYKVVKEIPL	563	10	25	39		12576
ENV	NWLWYIKIFI	772	10	25	39		12577
ENV	GELALAWDDL	848	10	25	39		12578
ENV	RYLKDQQLGI	671	11	25	39		12579
ENV	KWASLWNW	760	8	26	41		12580
ENV	KWASLWNWF	760	9	26	41		12581
ENV	IYCAPAGF	262	8	27	42		12582
ENV	IYCAPAGFAI	262	10	27	42		12583
ENV	IYCAPAGFAIL	262	11	27	42		12584
ENV	QMIHDIISL	116	9	27	45		12585
ENV	LYKYKVVKI	561	9	29	45	0.02100	12586
ENV	RYLKDQQL	671	9	29	45	0.76100	12587
ENV	QMIHDIISLW	116	10	29	45		12588
ENV	GYSPLSFOTL	806	10	29	45		12589
ENV	RYLKDQQL	671	8	30	47		12590
ENV	IFIMVGGI	779	10	33	52		12591
ENV	IMVGGI	781	10	34	54		12592
ENV	IMVGGI	781	8	35	56		12593
ENV	IFIMVGGI	779	9	35	55		12594
ENV	IFIMVGGI	779	10	36	56		12595
ENV	IFIMVGGI	779	9	37	58		12596
ENV	IFIMVGGI	779	9	39	61		12597
ENV	WYIKIFIM	775	9	41	64		12598
ENV	WYIKIFIMI	774	9	43	67		12599
ENV	WYIKIFIMI	774	10	43	67		12600
ENV	WYIKIFIMI	774	8	48	73		12601
ENV	WYIKIFIMI	774	9	48	75		12602
ENV	WYIKIFIMI	774	8	49	77		12603
ENV	WYIKIFIMI	774	8	55	86	0.0270	12604
ENV	WYIKIFIMI	774	8	55	86		12605
ENV	WYIKIFIMI	774	10	59	17		12606
ENV	WYIKIFIMI	774	11	59	17		12607
ENV	WYIKIFIMI	774	9	10	16		12608
ENV	WYIKIFIMI	774	9	10	16		12609
ENV	WYIKIFIMI	774	8	11	17		12610
ENV	WYIKIFIMI	774	8	13	20		12611
ENV	WYIKIFIMI	774	10	13	20		12612
ENV	WYIKIFIMI	774	11	13	20		12613
ENV	WYIKIFIMI	774	8	14	22		12614
ENV	WYIKIFIMI	774	8	14	22		12615
ENV	WYIKIFIMI	774	9	14	22		12616
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ENV	WYIKIFIMI	774	8	16	25		12639
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ENV	WYIKIFIMI	774	8	16	25		12663
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ENV	WYIKIFIMI	774	8	16	25		12759
ENV	WYIKIFIMI	774	8	16	25		12760
ENV	WYIKIFIMI	774					

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
GAG	KYRLKILVW	29	9	16	25		12620
GAG	RFVNPGLL	45	9	16	25	0.0100	12621
GAG	LYCVIQR	87	8	18	25		12622
GAG	GWNTNPPH	269	9	18	28	0.0140	12623
GAG	RFALNPL	45	8	20	31		12624
GAG	WNTNPPH	270	8	20	31		12625
GAG	RFALNPL	45	9	20	31		12626
GAG	LYNTVATL	80	8	22	34		12627
GAG	AWVKVIEKA	175	11	24	38		12628
GAG	AMQMLKETI	218	9	26	41		12629
GAG	IMMQRGNF	408	8	27	42		12630
GAG	DYVDRFKTL	319	10	27	42		12631
GAG	CFNCGKEGHI	425	10	27	42		12632
GAG	CFNCGKEGHI	425	10	27	42		12633
GAG	DYVDRFYKTL	319	10	28	44		12634
GAG	AWVKVIEKA	175	11	28	44	0.0010	12635
GAG	NYPIVQNL	152	8	31	48		12636
GAG	AMQMLKDTI	218	9	33	52		12637
GAG	PFNDYVDRFF	316	10	33	55		12638
GAG	NWMTETLL	339	8	35	56		12639
GAG	RMSPVSILDI	299	11	36	59		12640
GAG	RMSPVSI	299	8	38	63		12641
GAG	RMSPVSIL	299	9	40	63		12642
GAG	MYSPVSILDI	300	10	40	63		12643
GAG	MYSPVSIL	300	8	42	66		12644
GAG	QMRPRGSDI	248	10	44	69		12645
GAG	VWASKELERF	36	10	45	70		12646
GAG	AFSTEVIPIMF	184	10	50	78	0.0078	12647
GAG	IYKRWIL	285	8	54	84		12648
GAG	IYKRWILGL	285	10	54	84	0.0140	12649
GAG	RWILGLNKL	288	10	56	88		12650
GAG	PFNDYVDRF	316	9	63	98		12651
NEF	PMYKGF	105	8	12	19		12652
NEF	TYKGF	107	8	12	19		12653
NEF	PMYKGFADL	105	10	12	19		12654
NEF	VYIITQGF	192	8	13	20		12655
NEF	LWVYITQGF	190	9	13	20		12656
NEF	LWVYITQGF	190	10	13	20		12657
NEF	NYITGPTGF	206	10	13	20		12658
NEF	VYIITQGF	192	11	13	20		12659
NEF	RFPLTFGWCF	216	10	17	27		12660
NEF	IYKKRQEL	175	9	18	29		12661
NEF	AFDLSFL	175	10	18	29		12662
NEF	DWQNYTPGPG	111	8	18	28		12663
NEF	RFPLTFGW	203	11	18	28		12664
NEF	NYITGPGI	216	8	20	32		12665
NEF	KWSKSSIVGW	206	8	20	31		12666
NEF	RYPLTFGWCF	4	10	20	31		12667
NEF	VYIITQGYF	216	10	21	33		12668
NEF		192	8	21	33		12669

Table XVIII
 HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SFQ ID NO.
NEF	LWVYITQGYF	190	10	21	33		12670
NEF	VYIITQGYFD	192	11	21	33		12671
NEF	SFFLKXKGGI	115	10	22	34		12672
NEF	FFLKXKGGI	116	9	26	41		12673
NEF	RYPLTFGW	216	8	27	43		12674
NEF	IFLKXKGGI	116	9	29	45		12675
NEF	TFGWCFKL	222	8	40	63		12676
NEF	GFPVIRQVPL	93	10	48	75		12677
POL	AFRQGEAREF	7	10	10	16		12678
POL	NMLTQLGCTL	175	10	10	16		12679
POL	TWETWWTY	589	10	10	16		12680
POL	TWWTYDWOA	592	11	10	16		12681
POL	CWWAGIQQEF	882	10	11	17		12682
POL	IWGXIKPF	574	8	11	17		12683
POL	WYQLETERI	618	9	11	17		12684
POL	WWAGIQQEF	883	9	11	17		12685
POL	IYPIKVKQL	439	10	11	17		12686
POL	LWYQLETERI	617	10	11	17		12687
POL	WWAGIQQEF	883	11	11	17		12688
POL	QYDQINIEI	145	9	12	19		12689
POL	KWTVQMVVL	427	9	12	19		12690
POL	LWQRPLVTVK	92	11	12	19		12691
POL	TWWTYDWOA	592	11	12	19		12692
POL	SFSFRONTLW	84	10	13	20		12693
POL	SFSFRONTL	84	9	14	22		12694
POL	WYQLEKDI	618	9	14	22		12695
POL	YYRDSRDIPL	978	9	14	22		12696
POL	WWTDYWQAT	593	10	14	22		12697
POL	LWYQLEKDI	617	10	14	22		12698
POL	YYRDSRDIPL	977	10	14	22		12699
POL	YYRDSRDIPL	978	10	14	22		12700
POL	LWQRPLVTIKI	92	11	14	22		12701
POL	PFKKNPDVI	359	11	14	22		12702
POL	WWTDYWQAT	593	11	14	22		12703
POL	GYSAGERIVDI	945	11	14	22		12704
POL	YYRDSRDIPL	977	11	14	22		12705
POL	FFREDLAF	1	8	15	23		12706
POL	IYPIKVKRQL	459	10	15	23		12707
POL	PFKKNPDI	359	9	16	25		12708
POL	RWKPKMIGGI	128	10	17	27		12709
POL	IWGTIPKFKL	574	10	17	27		12710
POL	YFSVPLDKDF	304	10	18	29		12711
POL	LWKGPAKLL	986	9	18	28		12712
POL	NMLTIQICTL	175	10	18	28		12713
POL	IYAGIKVKQL	459	10	18	28		12714
POL	LWKGPAKLLW	986	10	18	28		12715
POL	AYFSVPLDKDF	303	11	18	28		12716
POL	AMASDFNLPI	773	11	18	28		12717
POL	LWKGPAKL	986	8	19	30		12718
POL	DYWQATWIPE	596	11	19	30		12719

Table XVIII
 HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	DYQATWI	596	8	20	31		12720
POL	KFLPIQKETW	580	11	20	31		12721
POL	CWVAGIKQEF	882	10	21	33		12722
POL	LWQPLVTI	92	9	21	33	0.0190	12723
POL	WWAGIKQEF	883	9	21	33	0.0120	12724
POL	WWAGIKQEF	883	11	21	33		12725
POL	NFQITLW	86	8	22	34		12726
POL	AWVPAIKGI	726	9	22	34		12727
POL	SPQITLW	86	8	23	36		12728
POL	WWTEYWOAT	593	10	23	36		12729
POL	WWTEYWOAT	593	11	23	36		12730
POL	PYNTIFAI	244	9	24	38		12731
POL	YELLKLAGRW	851	10	25	39		12732
POL	AYFLKLAGR	850	11	25	39		12733
POL	KFLPIQKETW	580	11	26	41		12734
POL	QYDQILIEI	145	9	27	42		12735
POL	NWASQIYAGI	434	10	27	42		12736
POL	KWTVQML	427	9	28	44		12737
POL	NWASQIYPGI	434	10	29	45		12738
POL	IWKTKPKFRL	574	10	30	47		12739
POL	WYOLEKEPI	618	9	31	48	0.0001	12740
POL	VYDPSKDLI	509	10	31	48	0.0150	12741
POL	LWYOLEKEPI	617	10	31	48		12742
POL	YFLKLAGRW	851	10	31	48		12743
POL	AYFLKLAGR	850	11	31	48		12744
POL	EMEKEGKISKI	229	11	32	50		12745
POL	EYWOATWPIE	596	11	33	52		12746
POL	YRDSRDP	978	9	34	53		12747
POL	VYRDSRDP	977	10	34	53		12748
POL	VYRDSRDP	978	10	34	53		12749
POL	VYRDSRDP	977	11	34	53		12750
POL	VYDPSKDLI	510	9	35	55		12751
POL	IWKGPAKLL	986	9	35	55		12752
POL	IWKGPAKLLW	986	10	35	55		12753
POL	IWKGPAKL	986	8	36	56		12754
POL	EYWOATWI	596	8	37	58	0.0310	12755
POL	PYNTIPVFAI	244	9	37	58		12756
POL	SWVPAIKGI	726	9	37	58		12757
POL	KYTAFTPSI	315	10	37	58		12758
POL	IFQSSMTKI	348	9	38	59	0.0029	12759
POL	IFQSSMTKIL	348	10	38	59	0.0002	12760
POL	VYDPSKDL	509	9	39	61	0.0004	12761
POL	IYQEPFKNL	533	9	40	63	0.0520	12762
POL	GYSAGERHDI	945	11	40	63		12763
POL	FFRENLA	1	8	41	64		12764
POL	GYSAGERII	945	9	41	64		12765
POL	GKVRQYDQI	139	11	41	64		12766
POL	NWRAMASDF	770	11	41	64		12767
POL	EMEKEGI	229	8	42	66		12768
POL	DFRKYTAF	312	8	42	66		12769

Table XVIII
HIV A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	TYQYQEPF	530	9	42	66	0.3000	12770
POL	KWKPKMIGGI	128	10	42	66		12771
POL	DFRKYTAFTI	312	10	42	66		12772
POL	QWTYQYQEP	528	11	42	66		12773
POL	YYDPISKDL	510	8	43	67		12774
POL	SMTKILEPF	352	9	43	67	0.0110	12775
POL	NWRAMASDF	770	9	43	67	0.0016	12776
POL	AMASDFNL	773	8	45	70		12777
POL	IWGRTKPF	574	8	48	75		12778
POL	EWFEFNTPL	605	10	50	78		12779
POL	GMIDGPKVKQ	201	10	51	80		12780
POL	TWIPEWEF	601	8	52	81		12781
POL	YWQATWIPE	597	10	52	81	0.0660	12782
POL	SMNKLKKI	905	9	53	83		12783
POL	SMNKLKKII	905	10	53	83		12784
POL	EFVNTPL	607	8	54	84		12785
POL	GYIEAEVI	834	8	54	84		12786
POL	SWTVNDIOKL	440	10	54	84		12787
POL	EFVNTPLVKL	607	11	54	84		12788
POL	QWPLTEKI	210	9	56	88		12789
POL	DFWEVOLGI	275	9	56	88		12790
POL	FWEVQLGI	276	8	57	89		12791
POL	GYSAGERI	945	8	57	89		12792
POL	LYVGSDEL	376	9	58	91		12793
POL	KWRKLVDF	259	8	59	92		12794
POL	GWKGSFAT	341	8	59	92		12795
POL	GWKGSFAIF	341	9	59	92	0.0095	12796
POL	IWQLDCTIIL	812	9	59	92		12797
POL	LWKGEAVVI	994	10	59	92		12798
POL	KWRKLVDFRE	259	11	59	92		12799
POL	NFKRKGGI	936	8	60	94		12800
POL	GYELHPDKW	420	9	60	94	0.0001	12801
POL	QMAVFIHNF	929	9	60	94	0.0190	12802
POL	WMGYELIHPDK	418	11	60	94		12803
POL	IYQYMDIDL	369	8	61	95		12804
POL	YMDLTVGSD	372	11	61	95		12805
POL	KMIGGIGCF	132	9	62	97	0.0011	12806
POL	KMIGGIGFI	132	10	62	97	0.0001	12807
POL	QYNVLPQGW	334	9	63	98	0.0036	12808
POL	RYQYNVLPQG	332	11	63	98		12809
POL	PFLWMGYEL	415	9	64	100		12810
REV	RWRERQRI	48	9	11	17		12811
REV	RWRARQRI	48	9	35	55		12812
TAT	CYCKKCCF	28	8	11	17		12813
TAT	CFHCQVCF	34	8	11	17		12814
TAT	CFLNKLGLI	40	9	14	22		12815
VIF	RWQVLIVW	4	8	10	16		12816
VIF	RYSTQVDFGL	98	10	10	16		12817
VIF	CFSDSARKAI	119	11	10	16		12818
VIF	QYLALKAL	151	8	11	17		12819

Table XVIII
HIV Δ24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ ²⁴⁰¹	SIQ ID NO.
VIF	QYLALAAAL	151	8	12	19		12870
VIF	RMKIRTWNSL	15	10	12	19		12821
VIF	YWGLOIGERD	71	11	12	19		12822
VIF	CFSESARKAI	119	11	12	19		12823
VIF	CFSESARKAI	119	11	12	19		12824
VIF	VWQVDRMKI	10	9	13	20		12825
VIF	IMIIYDFCF	113	8	13	23		12826
VIF	RMRIITWKS	15	10	15	23		12827
VIF	RMRIITWNSL	15	10	15	23		12828
VIF	DWILGQVSI	81	10	18	28		12829
VIF	YFDFCFSES	115	11	31	31		12830
VIF	DWILGHIGVSI	81	10	21	33		12831
VIF	YWGLHTGERD	71	11	22	34		12832
VIF	QYLALTALI	151	9	28	44		12833
VIF	YFDFCFSES	116	10	28	44		12834
VIF	QYLALTAL	151	8	33	52		12835
VIF	RWQVMIVW	4	8	43	67		12836
VIF	VWQVDRMRI	10	9	48	75		12837
VPR	IIFRIWLISL	33	10	10	16		12838
VPR	IIFRIGCHISRI	71	11	11	17		12839
VPR	PWLIHGLGQII	37	10	12	19		12840
VPR	QYIYETYGDT	44	11	14	22		12841
VPR	TWEGVEAIRI	53	11	14	22		12842
VPR	TWAGVEAIRI	53	11	15	23		12843
VPR	TWAGVEAI	53	8	16	25		12844
VPR	TWAGVEAIL	53	9	16	25		12845
VPR	INTYGDITW	46	9	18	28		12846
VPR	TWEGVEAI	53	9	19	30		12847
VPR	TWEGVEAI	53	9	20	31		12848
VPR	IIFRIPWLIIQL	33	10	24	38		12849
VPR	PYNEWTLLEL	14	9	30	47	0.1400	12850
VPR	INTYGDITW	46	10	30	47		12851
VPR	EWTLLELEFL	17	9	31	48	0.0580	12852
VPR	IIFRIGCQISRI	71	10	40	63		12853
VPU	NYELAVGAL	5	11	44	69		12854
VPU	NYELAVGAL	5	9	01	25		12855
VPU	DYKLGVGALI	10	10	01	25		12856
VPU	DYKLGVGALI	10	9	02	29		12857
VPU	DYRLGVGALI	10	10	02	29		12858
VPU	DYRLGVGALI	10	9	03	43		12859
VPU	EMGHIAFW	89	10	03	43		12860
VPU	VFIEYRKI	37	8	11	17		12861
VPU	EYRKILQRKI	41	8	12	19		12862
VPU	EYRKILQRKI	41	11	13	21		12863

Table XIXa
III DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VSTQLLNG	61	95	KPVVSTQLLNGSLA	299	29	45	12864
ENV	VVSTQLLN	60	94	IKPVVSTQLLNGSL	298	29	45	12865
ENV	LVSTQIKQL	59	92	LLQLTVWGIKQLQAR	651	26	41	12866
ENV	LLSGIVQQQ	38	91	ARQLLSGVQQSNNL	627	22	34	12867
ENV	WATHACVPT	36	88	HNWVWATHACVPTDPN	79	44	69	12868
ENV	LGAAGSTMG	55	86	LGFLGAAAGSTMGAAS	605	36	36	12869
ENV	VRQGYSPLS	55	86	VNRVRQGYSPLSFQT	800	36	36	12870
ENV	LLNGSLAE	54	84	STQLLNGSLAEFEV	303	16	25	12871
ENV	VKLTPLCVT	53	83	KPCVKLTPLCVTLNC	130	29	45	12872
ENV	LRAIEAQHQ	51	80	NNLLRAIEAQHQILQ	639	18	28	12873
ENV	VSTVQCTHG	51	80	CKNVSTVQCTHGKIF	285	14	22	12874
ENV	LGIWGCCK	50	78	QQLGIWGCCKGLJC	676	46	72	12875
ENV	LWDQSLKPC	50	78	IISLWDQSLKPCVKL	121	35	55	12876
ENV	LGFLGAAGS	49	77	AVELGFLGAAGSTMG	602	19	30	12877
ENV	VWATHACVP	49	77	VHNVWATHACVPTDP	78	34	53	12878
ENV	WGKQLQAR	49	77	LTVWGKQLQARVLA	654	39	61	12879
ENV	LWYIKIFIM	43	67	TNWLWYIKIFIMIVG	771	11	17	12880
ENV	FCASDAKAY	42	66	TILECASDAKAYDTE	61	18	28	12881
ENV	IVGGLIGL	42	66	FIMIVGGLIGLIRVF	780	22	34	12882
ENV	IFIMIVGGL	41	64	YIKIFIMIVGGLIGL	776	30	47	12883
ENV	VYGVVVK	41	64	WVTYVYGVVVKKEAT	46	22	34	12884
ENV	IKQLQARVL	40	63	VWGIKQLQARVLA	656	31	49	12885
ENV	IKIFIMV	39	61	LWYIKIFIMIVGGLI	774	31	48	12886
ENV	MCAASTLT	39	61	GSTMCAASTLTIVQA	613	28	44	12887
ENV	YIKIFIMV	39	61	WLWYIKIFIMIVGGL	773	38	59	12888
ENV	ITGLLITRD	37	58	SSNITGLLITRDGGK	516	06	9	12889
ENV	IPHYCAPA	36	56	FEPIHYCAPAGFA	255	21	33	12890
ENV	MIYGLIGL	36	56	IFIMIVGGLIGLIRV	779	22	34	12891
ENV	VQARQLLSG	36	56	TLTVQARQLLSGIVQ	622	35	55	12892
ENV	FEPIHYC	35	55	KVSFEPIHYCAPA	252	17	27	12893
ENV	LRSLCLFSY	35	55	WDDLRLSLCLFSYIRL	854	28	44	12894
ENV	MWKNMVEQ	35	55	NFNMWKNMVEQMIIE	105	11	17	12895
ENV	VINWVATHA	35	55	DTEVINWVATHACVP	75	17	27	12896
ENV	WKNMVEQM	35	55	FNMWKNMVEQMHED	106	20	31	12897
ENV	YGVVWKE	35	55	VTVYVYGVVWKEATT	47	22	34	12898
ENV	LLQLTVWGI	34	53	QQHLLQLTVWGIKQL	648	34	53	12899
ENV	IEPLGVAPT	33	52	VVKIEPLGVAPTAKK	566	12	19	12900
ENV	IKPVVSTQL	33	52	THGIKPVVSTQLLN	295	32	50	12901
ENV	LQARVLA	33	52	IKQLQARVLAVERVL	659	32	50	12902
ENV	WDDLRLSL	33	52	ALAWDDLRLSLCLFSY	831	18	28	12903
ENV	INIHTPH	01	50	SRPINIHTPHREKR	581	01	2	12904
ENV	INIHPIRE	01	50	RPIINHPIREKRA	582	01	2	12905
ENV	ITQACPKVS	32	50	TSVITQACPKVSFEP	242	08	13	12906
ENV	IVQQSNLL	32	50	LSGIQQSQSNLLRAI	631	26	41	12907
ENV	LONNSTNST	01	50	NKTLONNSTNSTLON	131	01	2	12908
ENV	VISTRTHRE	01	50	ARPVISTRTHREKRA	580	01	2	12909
ENV	WRWGTFLG	01	50	QNLWRWGTFLGMLM	12	01	5	12910
ENV	WRWGTMLG	01	50	QILWRWGTMLGMLM	12	03	5	12911
ENV	FAVLSIVNR	31	48	RIVEFAVLSIVNRVQ	791	14	22	12912
ENV	LLNGSLAE	31	48	TQLLNGSLAEFEV	304	14	22	12913

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Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	LTPLCVTLN	29	45	CVKLTPLCVTLNCTD	132	11	17	12914
ENV	LYKYKVKI	29	45	RSELYKYKVKIEPL	538	23	36	12915
ENV	VPWNSWSN	29	45	TINVPWNSWSNKS	691	03	5	12916
ENV	YRLNCNTS	28	44	YKEYRLNCNTSAIT	232	01	8	12917
ENV	IHYCAPAGF	27	42	PIHIHYCAPAGF	258	26	41	12918
ENV	LKDQQLGI	27	42	ERYLKDQQLGIWGC	670	25	39	12919
ENV	YKYKVKIE	27	42	SELYKYKVKIEPLG	559	24	38	12920
ENV	IRPVSTQL	26	41	THIGIRPVSTQLLN	295	26	41	12921
ENV	LDKWSLWN	26	41	LLALDKWSLWNWED	755	08	13	12922
ENV	LRIVFAVS	26	41	LIGLRIVFAVSIN	787	10	16	12923
ENV	LNGSLAEE	25	39	QLLLNGSLAEEVVI	305	13	20	12924
ENV	YKVKIEPL	25	39	LYKYKVKIEPLGVA	561	23	36	12925
ENV	LKGLRLGWE	23	37	RSSLKGLRLGWEGLK	885	04	7	12926
ENV	FSTRRLDL	23	36	LCLFSYIIRLDILLI	860	08	13	12927
ENV	INCTRPNN	23	36	SYEINCTRPNNTRK	340	05	8	12928
ENV	VYKIEPLGV	23	36	KYKVKIEPLGVAPT	563	23	36	12929
ENV	WKEATITLF	23	36	VPWKEATITLFCAS	53	22	34	12930
ENV	IGLRIVEAF	22	34	GGUGLIRIVFAVLSI	785	12	19	12931
ENV	FFYCNISGL	21	33	GGEFFYCNISGLFNS	441	07	11	12932
ENV	FLGLALFLG	01	33	RAAFGLGALFLGFLG	594	01	2	12933
ENV	FYCNISGLF	21	33	GEFFYCNISGLFNS	442	07	11	12934
ENV	LIGLRIVFA	21	33	VGGILGRLIVFAVLS	784	17	27	12935
ENV	VGLGAVFLG	01	33	KRAVGLGAVFLGFLG	593	06	9	12936
ENV	VGLGMFLG	01	33	KRAVGLGMFLGVLS	594	01	2	12937
ENV	ICTTAVPWN	20	31	GKLICTTAVPWNSSW	686	09	14	12938
ENV	ICTTAVPWN	20	31	GKLICTTAVPWNSSW	686	08	13	12939
ENV	LGVAPTKAK	19	30	IEPLGVAPTAKRRV	589	15	23	12940
ENV	LICTTAVPW	19	30	SGKLICTTAVPWNSS	685	09	14	12941
ENV	LRDQQLGI	19	30	ERYLRDQQLGIWGC	670	17	27	12942
ENV	VELGHLGAA	19	30	LQAVFLGFLGAGST	600	09	14	12943
ENV	FSTRRLKDF	18	28	LCLFSYHRLRDFILI	860	08	13	12944
ENV	IPHYCTPA	18	28	FEPIPIHYCTPAGFA	255	10	16	12945
ENV	IVFAVLSIV	18	28	OLRIVFAVLSIVNRV	789	16	25	12946
ENV	VPWNASWSN	18	28	LRIVFAVLSIVNRV	790	16	25	12947
ENV	IGLRIFAV	17	27	TTAVPWNASWSNKS	691	06	9	12948
ENV	IRQAHCNIS	17	27	GGLIGLRIFAVLSI	785	11	17	12949
ENV	VAPTAKARR	17	27	IGDIRQAHCNISRAK	378	02	3	12950
ENV	FNQTGPKCN	16	25	PLGVAPTAKARRVQ	571	10	16	12951
ENV	IGPGQTFYA	01	25	DKXFNQTGPKCNVST	276	05	8	12952
ENV	IGSQAFYV	01	25	SVRIGPGQTFYATGD	335	03	5	12953
ENV	IRYNLVNQ	01	25	RYSGISGQAFYVTGK	338	01	2	12954
ENV	LIGLRIFA	16	25	QTAIRYNLVNQTEN	400	01	2	12955
ENV	LLQYWSQEL	16	25	VUGLIGLRIFAFLS	784	12	19	12956
ENV	LRNLCLFSY	16	25	WWNLQYWSQELKNS	903	09	14	12957
ENV	LYSGFLALA	16	25	WDDLRLNLCLFSYHRL	834	11	17	12958
ENV	VSGFLALAW	16	25	SIRLYSGFLALAWDD	842	09	14	12959
ENV	FDPIPIHYC	15	23	IRLYSGFLALAWDDL	843	09	14	12960
ENV	IIFAVLSIV	15	23	KYTFDPIPIHYCTPA	252	03	5	12961
ENV	LINCNTSAI	15	23	GLRIIFAVLSIVNRV	789	20	30	12962
ENV		15	23	EYRLINCNTSAITQA	234	04	9	12963

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	LLNATAIV	15	23	AVSLNATAIAVAEG	918	10	16	12964
ENV	LRIFAIVS	15	23	LIGLRIFAIVSIN	787	11	17	12965
ENV	VITQACPKV	15	23	NTSVITQACPKVSFE	241	08	13	12966
ENV	YVWNLLOYW	15	23	VLKYVWNLLOYWSQE	899	07	11	12967
ENV	FAILKCNDK	14	22	PAGFAILKCNDKFN	266	09	14	12968
ENV	IFAVLSYN	14	22	LRIFAIVLSYNVR	790	13	20	12969
ENV	INCNTSAIT	14	22	YRLINCNTSAITQAC	235	14	22	12970
ENV	LNATAIYA	14	22	VSLNATAIAVAEGT	919	10	16	12971
ENV	WNSSWSNKS	14	22	NVPWNSSWSNKSLE	693	03	5	12972
ENV	WNASWSNKS	13	21	NVPWNASWSNKSIED	693	02	3	12973
ENV	ICTTTVPWN	13	20	GKLICTTTVPWNASW	686	06	9	12974
ENV	LLKLTWVGI	13	20	QQHLLKLTWVGKQL	648	13	20	12975
ENV	LKYKVVEI	13	20	RSELYKYKVVEIKPL	558	05	8	12976
ENV	MFLGFLGAA	13	20	LGAMFLGFLGAAAGST	600	07	11	12977
ENV	MHSFNCGGE	13	20	EIVMHSFNCGGEFFY	430	13	20	12978
ENV	YWSQELKNS	13	20	LLQYWSQELKNSAVS	906	10	16	12979
ENV	ICAVFLGFL	12	19	AVGIGAVFLGFLGAA	595	09	14	12980
ENV	LIARTVEL	12	19	DFILIAARTVELLGH	870	04	6	12981
ENV	LICTTTVPW	12	19	SGKLICTTTVPWNAS	685	06	9	12982
ENV	LLNGSLAEG	12	19	TQLLNGSLAEGEII	304	03	5	12983
ENV	YWGQELKNS	12	19	LWYWGQELKNSAIS	906	02	3	12984
ENV	IAARTVELL	11	17	FILIAARTVELLGH	871	03	5	12985
ENV	FLGFLGAA	11	17	IGALFLGFLGAAAGST	600	06	9	12986
ENV	LKNSAVSL	11	17	SOELKNSAVSLLNAT	911	08	13	12987
ENV	VGIGAVFLG	11	17	KRAVGIGAVFLGFLG	593	11	17	12988
ENV	VSLNATAI	11	17	NSAVSLNATAIAVA	916	09	14	12989
ENV	YATGDIIGD	11	17	QITFYATGDIIGDIRQ	365	04	6	12990
ENV	IAIAVAEGT	10	16	LDIAIAVAEGTDRI	922	02	3	12991
ENV	IHYCTPAGF	10	16	PIPIHYCTPAGFAIL	258	08	13	12992
ENV	ILGLVIICS	10	16	QTLILGLVIICSASN	19	03	5	12993
ENV	IWNMTWME	10	16	VDEIWNMTWMEWER	714	01	2	12994
ENV	LGLVIICSA	10	16	TLIILGLVIICSA	20	04	6	12995
ENV	LRDFILIA	10	16	YIIRLDRDFILIAARTV	865	06	9	12996
ENV	LTPLCVTL	10	16	CVKLTPLCVTLCHN	132	03	5	12997
ENV	MLQLTVWGI	10	16	QQHMLQLTVWGIKQL	648	08	13	12998
ENV	VEINCTRN	10	16	NESVEINCTRPNNT	338	02	3	12999
ENV	VRQLLSUIV	10	16	TVQVRQLLSUIVQQQ	624	08	13	13000
ENV	LILGLVIIC	09	15	WOTLILGLVIICSA	18	07	11	13001
GAG	VGGHQAAMQ	60	94	LNTYGGHQAAMQMLK	209	47	73	13002
GAG	LLVQNANPD	59	92	TETLLVQNANPDCKT	342	26	41	13003
GAG	VQNANPDCK	59	92	TLLVQNANPDCKTIL	344	26	41	13004
GAG	LGLNKIVRM	58	91	WILGLNKIVRMYS	289	55	86	13005
GAG	LSEGATPDM	58	91	FSALSEGATPQDLNT	193	29	45	13006
GAG	WILGLNKI	57	89	YKRWILGLNKIVRM	286	34	84	13007
GAG	LEEMMTACQ	56	88	QATLEEMMTACQGVG	364	27	42	13008
GAG	YKRWIILQ	55	86	GEIYKRWIILGLNK	283	37	58	13009
GAG	VSQNYPIVQ	54	84	VGEIYKRWIILGLNK	282	37	58	13010
GAG	WEKIRLRPG	50	83	SSQVVSQNYPIVQNLQ	145	09	19	13011
GAG	IAGTTSTLQ	46	72	LDXWEKIRLRPGGKK	13	13	20	13012
				GSDIAGTTSTLQEQI	234	45	70	13013

Table XIX^a
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
GAG	WASRELERF	46	72	HLVWASRELERFALN	34	17	27	13014
GAG	IPMFSALE	45	70	PEVIMFSALESEGAT	187	44	69	13015
GAG	MFSALEGA	45	70	VIPMFSALESEGATQ	189	43	67	13016
GAG	VIPMFSALE	45	70	SPEVIMFSALEGA	186	40	63	13017
GAG	MYSPVSLD	41	64	IVRMYSVSLDIRQ	297	23	36	13018
GAG	IVRMYSVPS	40	63	LKIVRMYSVPSILD	294	39	61	13019
GAG	VRMYSVSLI	40	63	NKIVRMYSVPSILOI	295	38	59	13020
GAG	YSPVSLDI	40	63	VRMYSVPSILDIRQG	298	23	36	13021
GAG	MTETLLVQN	38	59	KNWMTETLLVQNANP	338	34	53	13022
GAG	WMTETLLVQ	37	58	VKNWMTETLLVQNAN	337	34	53	13023
GAG	ISPTLNAW	36	56	HQASPTLNAWVKV	337	27	42	13024
GAG	VKNWMTETL	36	56	TQEVKNWMTETLLVQ	334	14	22	13025
GAG	IKCFNCGKE	34	53	QKRUKCFNCGKEGHL	418	05	8	13026
GAG	IPVGEIKR	34	53	NPPIPVGEIKRWII	277	32	51	13027
GAG	YTAVMQRQ	02	50	KGOYTAVMQRQNP	399	02	3	13028
GAG	VATLYCVHQ	30	47	YNTVATLYCVHQRIE	81	07	11	13029
GAG	WDLRHVHA	29	45	AAEWDLRHVHAQPI	230	22	34	13030
GAG	FLQSRPEPT	28	44	PONFLQSRPEPTAPP	483	27	43	13031
GAG	FKTLRAEQA	27	42	DRFFKTLRAEQATQE	322	16	23	13032
GAG	VHQASPR	27	42	QGMVHQASPRTLN	160	26	41	13033
GAG	YKTLRAEQA	27	42	QGMVYKTLRAEQASQE	161	27	42	13034
GAG	VSILDIRQG	25	39	DRFYKTLRAEQASQE	322	12	19	13035
GAG	LAEAMSVQT	23	37	YSFVSLDIRQGPKE	301	24	38	13036
GAG	LQKIWFPSK	23	36	ARVLAEAMSVQVTNSA	384	08	13	13037
GAG	VKCFNCGKE	23	36	ANFLGKVFPSHKGRI	467	22	34	13038
GAG	YNTVATLYC	23	36	RKTVKCFNCGKEGHI	420	07	11	13039
GAG	LHPVHAQPI	22	34	RSLYNTVATLYCVHQ	78	11	17	13040
GAG	LYNTVATLY	22	34	WDLRHVHAQPIAG	233	15	23	13041
GAG	MTDTLLVQN	22	34	LSLYNTVATLYCVHI	77	13	20	13042
GAG	WMTDTLLVQ	22	34	KNWMTDTLLVQNANP	338	16	25	13043
GAG	IBYKDTKEA	21	33	VKNWMTDTLLVQNAN	337	07	25	13044
GAG	LQGMVHQHA	20	31	HQRIEYKDTKEALDK	91	16	11	13045
GAG	MTNPPPIV	20	31	VQNQQGMVHQHAISP	156	15	23	13046
GAG	IAPQMREP	19	30	IGWMTNPPPIVGEI	268	16	25	13047
GAG	VHAQPIPPG	18	28	QIGWMTNPPPIVGEI	267	16	25	13048
GAG	LGPATLEE	18	28	AGPIAPQMREPGRS	241	19	30	13049
GAG	VHAQPIPPG	17	27	LHPVHAQPIAGQMR	236	14	22	13050
GAG	LSPTLNAW	17	27	LRALGPATLEEAMT	358	09	14	13051
GAG	YRLKJLYWA	16	25	VHPVHAGPIPPGQMR	236	10	16	13052
GAG	LGPATLEE	16	25	AGPIPPGQMRPGRS	241	16	25	13053
GAG	IPQMREP	16	25	HQALSPTLNAWVKV	165	10	16	13054
GAG	YRLKJLYWA	16	25	KKKYRLKJLYWASRE	27	13	20	13055
GAG	LKALOPAA	16	25	LKALOPAALEEAMT	358	16	25	13056
GAG	LKALOPAA	16	25	KTLKALGPAAATLEE	355	16	25	13057
GAG	LKDKPEPLA	01	25	QEQLKDKBPPLASLR	532	01	2	13058
GAG	LSGGKLDW	16	25	ASVLSGGKLDWKEI	5	14	22	13059
GAG	MTSNPPPIV	16	25	IGWMTSNPPPIVGEI	268	06	9	13060
GAG	VKNWMTDTL	16	25	TQYVKNWMTDTLLVQ	334	11	17	13061
GAG	VSILDIKQG	16	25	YSPVVSILDIKQGPKE	301	16	25	13062
GAG	WMTSNPPPI	16	25	QIGWMTSNPPPIVGEI	267	06	10	13063

Table XIXa
MIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
GAG	ENTVATLYC	15	23	KSLFNTVATLYCVIIQ	78	07	11	13064
GAG	IPMFTALSE	15	23	PEVIPMFTALSEGAT	187	13	20	13065
GAG	LASLSKSLFG	15	23	LYPLASLSKSLFGNDP	544	06	11	13066
GAG	LERFAVNPG	15	23	SRELERFAVNPGLE	39	14	22	13067
GAG	LFNTVATLY	15	23	SRLELFAVNPGLE	77	07	11	13068
GAG	NFTALSEGA	15	23	LRSLFNTVATLYCVII	189	14	22	13069
GAG	WDRVHPVHA	15	23	YIPMFTALSEGATIQ	230	12	20	13070
GAG	IVRMYSPTS	14	22	AAEWDRVHPVHAIGH	294	13	19	13071
GAG	LQEQIAWMT	14	22	LNKIVRMYSPTSILD	39	14	22	13072
GAG	VHPVHAQPI	14	22	SRELERFALNPGLE	261	05	8	13073
GAG	VIPMFTALS	14	22	TSLTQEQIAWMTGNP	233	11	17	13074
GAG	VRMYSPST	14	22	WDRVHPVHAQPIPG	186	13	20	13075
GAG	LQEQIAWMT	14	22	SPEVIPMFTALSEGA	295	13	20	13076
GAG	VIPMFTALS	14	22	NKIVRMYSPTSILD	467	13	20	13077
GAG	LQEQIAWMT	14	22	ANFLGKIWPSNKGRI	544	04	7	13078
GAG	VRMYSPST	13	20	LYPLTSLKSLFGNDP	297	12	19	13079
GAG	LQEQIAWMT	13	20	IVRMYSPTSILDIRQ	27	08	13	13080
GAG	YKLSKSLFG	13	20	KKLYKLSKSLFGNDP	298	12	19	13081
GAG	YKLSKSLFG	13	20	VRMYSPSTILDIRQ	544	04	7	13082
GAG	YKLSKSLFG	13	20	LYPLTSLKSLFGNDP	204	12	19	13083
GAG	YKLSKSLFG	13	20	DIKMLNIVGHIQAA	91	03	5	13084
GAG	YKLSKSLFG	13	20	IQRIDYKDKTKEALDK	265	09	14	13085
GAG	YKLSKSLFG	13	20	QEQIGWMTSNPPIV	277	08	13	13086
GAG	YKLSKSLFG	13	20	NPPIVGDIYKRWII	541	06	10	13087
GAG	YKLSKSLFG	13	20	DKELYPLASLSKSLFG	161	07	11	13088
GAG	YKLSKSLFG	13	20	COMVHOALSPTLNA	45	11	17	13089
GAG	YKLSKSLFG	13	20	REAVNPGLLETSEGC	542	06	16	13091
GAG	YKLSKSLFG	13	20	KELYPLASLSKSLFG	483	10	25	13092
GAG	YKLSKSLFG	13	20	PONFLQNRPEPTAPP	405	01	3	13093
GAG	YKLSKSLFG	13	20	AAAJMMQKSNFKGPR	384	02	16	13094
GAG	YKLSKSLFG	13	20	ARVLAEMSQQVQQSN	467	10	13	13095
GAG	YKLSKSLFG	13	20	ANFLGKIWPSNKGRI	45	08	6	13096
GAG	YKLSKSLFG	13	20	REALNPGLLETAGCC	542	04	23	13097
GAG	YKLSKSLFG	13	20	KELYPLASLSKSLFG	200	15	36	13098
GAG	YKLSKSLFG	13	20	FDWQWYTTGPIQIRY	93	07	11	13099
GAG	YKLSKSLFG	13	20	GFVPRQVPLRPMTY	216	15	24	13100
GAG	YKLSKSLFG	13	20	RQVPLRPMTYKLGAF	182	12	19	13101
GAG	YKLSKSLFG	13	20	RYPLTFGWCFLVPV	222	07	11	13102
GAG	YKLSKSLFG	13	20	RQELDLWYHTQGY	186	21	33	13103
GAG	YKLSKSLFG	13	20	TFGWCFKLVPDPRE	2	05	8	13104
GAG	YKLSKSLFG	13	20	ILDLWYHTQGYFPD	182	05	9	13105
GAG	YKLSKSLFG	13	20	GGKWSKSSIVGWPAI	254	06	6	13106
GAG	YKLSKSLFG	13	20	RODILDWYHTQGY	254	06	9	13107
GAG	YKLSKSLFG	13	20	NNCLLHPMSQHGMD	210	06	16	13108
GAG	YKLSKSLFG	13	20	NNSLHPICQHGMD	50	13	20	13109
GAG	YKLSKSLFG	13	20	GPGRYPLTFGWCFL	186	06	9	13110
GAG	YKLSKSLFG	13	20	HGAITSNTAATNAD	103	06	9	13111
GAG	YKLSKSLFG	13	20	SRDLKXHGATSSNT	226	08	13	13112
GAG	YKLSKSLFG	13	20	ILDLWYHTQGYFPD				13113
GAG	YKLSKSLFG	13	20	LRPMYTKGAFDL				
GAG	YKLSKSLFG	13	20	CFKLVPDPREVEEA				

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
NEF	VGWPAIRER	10	17	SSVQGWPAIRERMR	8	03	5	13114
NEF	WCFKLVPVE	11	17	TEGWCFKLVPVEPK	222	04	6	13115
NEF	FDRLAFHH	10	16	EWFRDRLAFHHVAR	307	02	1	13116
NEF	KLVPVDPDR	10	16	GWCFKLVPVDPREVE	224	10	16	13117
NEF	VPLRMTFK	10	16	RPQVPLRMTFKGAF	98	04	6	13118
POL	LLDADDT	63	98	KEALLDADDTVLE	107	37	58	13119
POL	WMGYLHPD	63	98	PFLWMGYLHPDKWT	415	60	94	13120
POL	YQYNVLPQG	63	98	GIRYQYNVLPQWKG	330	52	81	13121
POL	FRKYTAFT	61	97	DKDFRKYTAFTPSI	310	10	16	13122
POL	WTVNDIQKL	62	97	KDSWTVNDIQKLVGK	438	43	67	13123
POL	LDCTHLEK	61	95	IWQLDCTHLEKIL	812	29	45	13124
POL	LDVGDAYS	61	95	VTVLDVGDAYSVPL	295	50	78	13125
POL	MDLLYVGS	61	95	YQVMDLLYVGSDEL	370	57	89	13126
POL	VIPAETGQE	61	95	EAEVIPAETGQETAY	837	57	90	13127
POL	WKGECAVVI	61	95	KLLWKGECAVVIQDN	992	53	83	13128
POL	WQLDCTHLE	61	95	PGIWQLDCTHLEKGI	810	32	50	13129
POL	VDFRELNKR	60	94	RKLVDFRELNKRQD	261	57	89	13130
POL	WPKVMIGGI	60	94	PGKWPKVMIGGIGF	126	39	61	13131
POL	IWQLDCTHL	59	92	SPGIWQLDCTHLEK	809	56	88	13132
POL	VAVHVASGY	59	92	IILVAVHVASGYEA	874	26	41	13133
POL	WKGSAIFQ	59	92	PQGWKGSAPFQSSM	339	42	66	13134
POL	IGGYSAGER	58	91	KGIGGYAGERIID	940	37	59	13135
POL	YALGIIQAO	58	89	DSOYALGIIQAOQDK	690	39	61	13136
POL	FWEVQLGIP	57	89	TODFWEVQLGIPHA	273	52	81	13137
POL	IKKKDSTRW	57	89	VFAIKKKDSTRWRKL	249	36	56	13138
POL	LOUQAQPD	57	89	QYALGIIQAOQDKSE	692	39	61	13139
POL	LGIPHPAGL	56	89	EVQLGIIPIHPAGLKK	278	51	80	13140
POL	VNTPLVKL	57	89	WEFVNTPLVKLWYQ	606	50	79	13141
POL	VTVLDVQDA	57	89	KXSVTVLDVGDVFS	292	49	77	13142
POL	FPISPIETV	56	88	TLNFPISPIETPVK	183	52	83	13143
POL	ISPIETPV	56	88	NFISPIETPVKLLK	185	52	81	13144
POL	FVNTPLVK	54	86	EFVFNTPPLVKLWY	605	50	78	13145
POL	LNFPISPIE	55	86	OCTLNFPISPIETVP	181	53	83	13146
POL	WEFNTPL	54	86	IFWFEFNTPLVKL	603	49	77	13147
POL	IQNFRVYR	52	84	ITKIQNFRVYRDSR	969	32	51	13148
POL	LVGTPVNI	54	84	GTVLVGTPTVNIQR	160	51	80	13149
POL	VQLGIPHPA	54	84	FWEVQLGIPHPAGLK	276	53	83	13150
POL	WQATWIPFW	54	84	TEYWQATWIPWFEFV	595	19	30	13151
POL	IBTPVKLK	53	83	ISPIETPVVKLKPGM	188	51	80	13152
POL	IGTVLQPT	53	83	KAIGTVLQPTPVN	156	22	34	13153
POL	LVAVHVASQ	53	83	KILVAVHVASGYIE	823	26	41	13154
POL	VLVQPTPVN	53	83	IGTVLVQPTPVNIIG	139	45	70	13155
POL	VIEABVIPA	53	83	ASGYIEABVIPAETG	332	52	81	13156
POL	YVGSLEIG	53	83	DDLTVGSLEIGQHR	374	52	81	13157
POL	MDGPKVKQW	52	81	KFGMDQPKVKQWPLT	199	47	73	13158
POL	VASQYIEAE	52	81	AVHVASQYIEAEVTP	828	52	81	13159
POL	VQPTPVNI	52	81	TVLVQPTPVNIQRN	161	51	80	13160
POL	VQWPLTEE	52	81	GPKVQWPLTEEKIK	205	45	70	13161
POL	VYVYRDSRDP	52	81	NFRVYVYRDSRDPWK	974	29	45	13162
POL	WGFTTPDKK	52	81	LLRWGFTTPDKKHQK	398	23	36	13163

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	VIVQYMDLL	51	80	PEIVVQYMDLLVYG	365	23	36	13164
POL	LKKKKSSTV	49	78	PAGLKKKSSTVLDV	286	46	72	13165
POL	VPRRKAKII	50	78	IKVVPRRKAKIIRDY	1010	41	64	13166
POL	FPQITLWQR	49	77	SESEFQITLWQRLV	84	09	14	13167
POL	VIWGTPTKE	47	73	ESIVWGTPTKFRLP	570	23	37	13168
POL	YVDGAANRE	46	72	ETFYVDGAANREKL	630	24	38	13169
POL	FKNLKTGKY	45	70	QEPFKNLKTGKYAKM	535	15	23	13170
POL	IQTKELQKQ	45	70	ATDIQTKELQKQITK	957	24	38	13171
POL	YQKQMGDD	45	70	IRDYQKQMGDDCVA	1021	41	64	13172
POL	WRAMASDFN	43	67	ISNWRAMASDFNLP	768	31	48	13173
POL	ISKIGPENF	42	66	EGKISKIGPENPYNT	233	40	63	13174
POL	LTOIGCTLN	41	64	RNLLTOIGCTLNFTI	174	21	33	13175
POL	IIQAOPDKS	40	63	ALGHQAOPDKSISE	694	38	59	13176
POL	LPEKDSWTV	40	63	PVLPEKDSWTVNDI	432	13	20	13177
POL	FQSSMTKIL	38	59	PAIFQSSMTKILEPI	346	32	50	13178
POL	FTIPSINNE	38	59	YTAFTIPSINNETPG	316	36	56	13179
POL	IFQSSMTKI	38	59	SPAIFQSSMTKILEP	345	33	52	13180
POL	IIELQIKKE	37	58	VSQIEQLIKKEKVV	710	19	30	13181
POL	LSWVPAHKG	37	58	KVYLSWVPAHKGIGU	722	23	37	13182
POL	YLSWVPAHK	37	58	KKVYLSWVPAHKGIG	721	15	24	13183
POL	YTAFTIPSI	37	58	PRKYTAFTIPSINNE	313	37	59	13184
POL	IIATDIQTK	35	55	IIIDIIATDIQTKELQ	952	22	34	13185
POL	IKWGFAPKLL	35	55	RDPIWGFAPKLLWKG	983	34	53	13186
POL	LQKQITKIQ	35	55	TKELQKQITKIQNFR	962	29	46	13187
POL	LKEALLDTG	34	53	GGQLKEALLDTGADD	103	31	48	13188
POL	VYLSWVPAH	33	52	KEKYLSWVPAHKGII	720	15	23	13189
POL	FILKLAGRW	32	50	TATFILKLAGRWPVK	849	27	42	13190
POL	LECKIILVA	31	48	CTILLEGKIILVAHVH	817	30	47	13191
POL	YFILKLAGR	31	48	ETAYFILKLAGRWFP	848	30	47	13192
POL	IIILVAHVH	30	47	EGKIILVAHVHVASGY	821	30	47	13193
POL	IWGTPTKFR	30	47	SIVIWGTPTKFRPLI	571	22	34	13194
POL	LAGRWPVKV	30	47	ILKLAGRWVVKVVIIT	853	19	30	13195
POL	VVAKEIVAS	30	47	LPPVVAKEIVASCDK	780	21	33	13196
POL	IDIIATDIQ	29	45	ERIIDIIATDIQTKKE	950	22	34	13197
POL	IIIGRNMLTQ	29	45	PVNIIGRNMLTQIGC	949	23	36	13198
POL	IKVKQLCKL	29	45	YAGIKVKQLCKLRG	168	11	17	13199
POL	VDKLVSSGI	29	45	NEQVDKLVSSGIRKY	460	18	28	13200
POL	IVGAETTV	28	44	KEPIVGAETTVYDGA	737	26	41	13201
POL	LPPVVAKEI	28	44	DFNLPPVVAKEIVAS	623	16	25	13202
POL	WTVQIQLP	28	44	PDKWTVQIQLPIEKD	777	26	41	13203
POL	FNLPPVAK	27	42	ASDFNLPPVVAKEIV	425	13	20	13204
POL	FTSAAVKAA	27	42	GSNFTSAAVKAACTW	775	25	39	13205
POL	LALQDSGLE	27	42	AHLALQDSGLEVNI	870	25	39	13206
POL	LPIVAKEL	27	42	DFNLPIVVAKEIVAS	673	15	23	13207
POL	LQDSGLEVN	27	42	HLALQDSGLEVNI	777	20	31	13208
POL	FNLPPVAK	26	41	ASDFNLPIVVAKEIV	675	13	20	13209
POL	IQGHRAKIE	26	41	DLEIQGHRAKIEELR	775	21	33	13210
POL	IIGRNLLTQ	26	41	PVNIIGRNLLTQIGC	381	23	36	13211
POL	LEVINIVTDS	26	41	DSGLEVINIVTDSQYA	168	26	41	13212
POL		26	41		680	26	41	13213

Table XIXa
 HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	LRGAKALTD	26	41	CKLLRGAKALTDIVP	469	12	19	13214
POL	LVSSGIRKV	26	41	VDKLVSSGIRKVLFL	740	25	39	13215
POL	FLKLAGRW	25	39	TATFLKLAGRWPK	849	19	30	13216
POL	LALQDSGE	25	39	AHIALQDSGSEVNI	673	08	13	13217
POL	LQDSSEVN	25	39	HIALQDSGSEVNI	675	08	13	13218
POL	VKVIHTDG	25	39	RWPVKVIHTDGSNF	859	33	33	13219
POL	WPKVIHTD	25	39	AGRWPVKVIHTDGS	857	20	31	13220
POL	YFLKLAGR	25	39	ETAYFLKLAGRPV	848	24	38	13221
POL	ICGKKAIGT	24	38	LIEICGKKAIGTVLV	150	12	19	13222
POL	IVAKEVAS	24	38	LPPIVAKEIVASCDK	780	22	34	13223
POL	LRWGFTTPD	24	38	QIILLRWGFTTPDKKH	396	12	19	13224
POL	LEQGVILVA	23	36	CTHLEQGVILVAIVH	817	23	36	13225
POL	LKWGFTTPD	23	36	EHLLKWGFTTPDKKH	396	13	20	13226
POL	VILVAIIVA	23	36	EGKVLVAIVIVASGY	821	21	33	13227
POL	LAVPAHKG	22	34	KVYLAVPAHKGIGG	722	20	32	13228
POL	YDQLIEIC	22	34	VRQYDQLIEICGK	143	08	13	13229
POL	IGQHRKIE	22	34	EKVYLAWPVPAHKGIG	721	20	32	13230
POL	IGRNLTKI	21	33	DLIEIGQHRKIEELR	381	19	30	13231
POL	LWQRPVTV	21	33	VNIGRNLTQIGCT	169	21	33	13232
POL	VSLETNQT	21	33	QITLWQRPVTVTKIG	89	11	17	13233
POL	YLAWPVPAH	21	33	QKVVSLTETNQTKE	656	10	16	13234
POL	ICGHKAIGT	20	31	KEKVYLAWPVPAHKG	720	20	31	13235
POL	LRGKALTE	19	30	LIEICGHKAIGTVLV	150	10	16	13236
POL	LVNQIEQL	19	30	CKLLRGKALTEVIP	469	11	17	13237
POL	YFSPDLKD	18	28	ESELVNVQIEQLIKK	706	13	20	13238
POL	IGRNLTKI	18	28	ESELVNVQIEQLIKK	706	13	20	13239
POL	IKVRQLCKL	18	28	QDAVYFSPDLKDIFRK	301	18	28	13240
POL	LWQRPVTV	18	28	VNIGRNLTQIGCT	169	12	19	13241
POL	YAGIKVKQL	18	28	YDGIKVRQLCKLRG	460	13	20	13242
POL	FWGKTPEK	17	27	QITLWQRPVTVTKIG	89	09	14	13243
POL	LRHLKRWG	17	27	SQIYAGIKVKQLCKL	457	18	28	13244
POL	VQPIQLPEK	17	27	SIVWQGTPEKFLPI	571	17	27	13245
POL	WQRPVTVK	17	27	IEELRGHLKRWGFTT	391	12	19	13246
POL	IQAPORS	16	25	KWTVPQIPEKDSW	427	13	20	13247
POL	LQAHILAQ	16	25	ITLWQRPVTVTKIG	90	11	17	13248
POL	LYBICTEME	15	24	ALGIQAPDRSESE	694	12	19	13249
POL	LRQHLLRWG	15	24	KTELQAHILALQDSG	668	15	23	13250
POL	VDKLVSAIGI	15	24	IKALVEICTEMEKEG	218	15	23	13251
POL	YPOIKVRQL	15	24	IEELRGHLKRWGFTT	391	12	19	13252
POL	FRKQNPDIW	14	22	RNMLTQLGCTLNPI	174	10	16	13253
POL	FSFQITLW	14	22	VDKLVSAIGIRKVLFL	740	14	22	13254
POL	FTSTTVKAA	14	22	NEQVDKLVSAIGIRV	737	14	22	13255
POL	IASDIQTK	14	22	SQIYPOIKVRQLCKL	457	12	19	13256
POL	LAGRWPVKT	14	22	LEPFRKQNPDIWYQ	357	14	22	13257
POL	VQKIATESI	14	22	TVSFFQITLWQRP	77	05	10	13258
POL				GSNFTSTTVKAAQWW	870	11	17	13259
POL				IIDIASDIQTKELQ	952	11	17	13260
POL				LLKLAGRWPVKTHT	853	09	14	13261
POL				TEAVQKIATESIWIW	561	10	16	13262

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	FTIPSTNNE	13	20	YTAFSTNNETPG	316	13	20	13264
POL	LEDINLPKX	13	20	DTVLEDNLPKXWK	117	13	20	13265
POL	LTDIVPLTE	13	20	AKALTDIVPLTERAE	475	13	13	13266
POL	LVTKIGGQ	13	20	QRPLVTIKIGGQKE	94	08	13	13267
POL	MKGHTNDV	13	20	YARMGAIHTNDVKQL	546	12	20	13268
POL	VKTIHTDNG	13	20	RWPVKTIHTDNGSNF	859	09	19	13269
POL	VQPIVLPKX	13	20	KWTVQPIVLPKXSW	427	12	19	13270
POL	WPKVTHITD	13	20	AGRWPVKVTHITDNGS	857	09	14	13271
POL	WQRPVTVK	13	20	ITLWQRPVTVKIGG	90	09	14	13272
POL	WTQPIVLP	13	20	PKWTVQPIVLPKED	425	12	19	13273
POL	YTAFIPST	13	20	FRKYTAFIPSTNNE	313	13	21	13274
POL	IDIASDIQ	12	19	ERIDIASDIQTK	950	11	17	13275
POL	IDIASDI	12	19	GERIDIASDIQTK	949	11	17	13276
POL	IVDIATDI	12	19	GERIVDIATDIQTK	949	10	16	13277
POL	LEEINLPKX	12	19	DTVLEEINLPKXWK	117	11	17	13278
POL	LQAYIALQ	12	19	KTELQAYIALQDSG	668	11	17	13279
POL	LQKQIKIQ	12	19	TKELQKQIKIQNER	962	09	14	13280
POL	VDIATDIQ	12	19	ERIVDIATDIQTK	950	10	16	13281
POL	FNFRQITLW	11	17	VRYDQIPIEIGCKX	143	05	8	13282
POL	YDQINIEIC	11	17	VPTFNFRQITLWQRP	79	01	17	13283
POL	IGNMLTQL	11	17	VNIIGNMLTQLGCT	169	10	16	13284
POL	ISRIGENP	11	17	EGKISRIGENPYNT	233	10	16	13285
POL	LTEVIFLTE	11	17	TKALTEVIFLTEEAE	475	10	16	13286
POL	MESIVIGK	11	17	KJAMESIVIGKTPK	566	07	11	13287
POL	VPRKVKII	11	17	IKVVPKVKIIRDY	1010	08	13	13288
POL	VSEFQIT	11	17	QGTVSEFQITLWQ	75	05	8	13289
POL	WTQLETEPI	11	17	VKLWYQLETEPIVGA	615	04	6	13290
POL	YFGKVKQL	11	17	SQYFGKVKQLGKL	457	09	14	13291
POL	FPQGEAREF	10	16	NLAPFPQGEAREFPE	5	05	8	13292
POL	LIEALLDTG	10	16	GGQLEALLDTGADD	103	09	14	13293
POL	VSLLDTTNG	10	16	QKVSLLDTTNGKTE	636	09	14	13294
POL	WETWTDYW	10	16	KETWETWTDYWQAT	587	09	14	13295
POL	YAKMRTAHT	10	16	TGKYAKMRTAHTNDV	543	09	14	13296
POL	YKMLTKGY	10	16	QEPYKMLTKGYARM	535	03	5	13297
REV	LQLPPLERL	36	56	PVPLQLPPLERLTD	74	13	20	13298
REV	VPLQLPPE	36	56	AEPVPLQLPPLERLT	72	10	16	13299
REV	LYQSNPPS	18	28	IKFLYQSNPPSPPEG	21	04	6	13300
REV	VRIKILYQ	16	25	LKAVRIKILYQSNP	13	06	9	13301
REV	YQSNPPSP	12	19	KFLYQSNPPSPSEGT	22	05	8	13302
REV	LQLPPIERL	11	17	PVPLQLPPIERLRD	74	04	6	13303
REV	VPLQLPPIE	11	17	AEPVPLQLPPIERLR	72	04	6	13304
TAT	WNHPSQPK	15	23	LEPNHPSQPKTAC	11	11	17	13305
TAT	FLNKGLGIS	14	22	QVCFLNKGLGISYGR	38	04	6	13306
TAT	WKHPGSQPK	13	20	LEPWKHPGSQPKTAC	11	11	17	13307
TAT	YCKKCCYHC	11	17	NNCTYCKKCCYHCQVC	26	04	6	13308
TAT	YCKKCCYHC	11	17	TNCYCKKCCYHCQVC	26	02	3	13309
TAT	WNHPSQPT	10	16	LEPNHPSQPTTAC	11	07	11	13310
VIF	MIVWQVDRM	46	72	WQVMIVWQVDRMR	5	28	44	13311
VIF	WQVMIVWQV	43	67	ENRWQVMIVWQVDRM	2	41	64	13312
VIF	WQVDRMRIR	34	53	MIVWQVDRMRIRTWK	8	14	22	13313

Table XIXa
 IIIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
VIF	LQYLALTA	33	52	VGSQYLALTAIKP	147	14	22	13314
VIF	LGHVSVIEW	31	48	DWHLGHVSVIEWRLR	81	11	17	13315
VIF	VDRMRRTW	31	48	VWQVDRMRRTWNSL	10	15	23	13316
VIF	YDFCESA	28	44	ILYYDFCESAIRN	113	08	13	13317
VIF	YWGLTGER	28	44	ITTYWGLTGERDWH	68	14	22	13318
VIF	IRTWNSLVK	27	42	RMRTWNSLVKIHIM	15	12	19	13319
VIF	LQGVSVIEW	26	41	DWHLQGVSVIEWRCK	81	07	11	13320
VIF	LVRHMYYS	21	33	WNSLVKHIMYYSKKA	21	07	11	13321
VIF	IPLGEARLV	19	30	EVHPLGEARLVVRT	54	05	8	13322
VIF	LYKHIMYIS	19	30	WKSLLVKHIMYISGKA	21	05	8	13323
VIF	YLALTAIK	16	25	SLOYLALTAIKPKK	147	11	17	13324
VIF	IRTWKSLVK	15	23	RMRTWNSLVKIHIM	15	14	22	13325
VIF	LADQLHL	15	23	DPDLADQLHLYYFD	104	07	11	13326
VIF	LALTALIKP	15	23	LQYLALTAIKPKKI	150	08	13	13327
VIF	VDPLADQL	15	23	STQVDPLADQLHIL	100	04	6	13328
VIF	LYYDFCSE	14	22	ILYYDFCSESAI	111	14	22	13329
VIF	FSESARKA	13	20	FDCFSARNAKALG	117	10	16	13330
VIF	LADQLHIMH	13	20	EPGLADQLHIMHYYFD	104	08	13	13331
VIF	WQVDRMKIR	13	20	LIVWQVDRMKIRTN	8	09	14	13332
VIF	FSDSAIRKA	12	19	FDCFSASAIRKAILG	117	05	8	13333
VIF	FSESARNA	12	19	FDCFSASARNAILG	117	12	19	13334
VIF	IVSPCEYQ	12	19	LGHVSPCEYQNGII	130	06	9	13335
VIF	LQYLALAA	12	19	VGSQYLALAAALTP	147	04	6	13336
VIF	VORAKIRTW	12	19	VWQVDRMKIRTNWNSL	10	12	19	13337
VIF	YWGLTGER	12	19	IKTYWGLTGERDWH	68	08	13	13338
VIF	IPLGDARLV	11	17	EVHPLGDARLVITT	54	06	9	13339
VIF	LQYLAKAL	11	17	VGSQYLAKALALVTP	147	08	13	13340
VIF	WQVDRMRN	11	17	MIVWQVDRMRNRTWK	8	08	13	13341
VIF	IKPKKPKP	10	16	TALIKPKKPKPLPS	156	08	13	13342
VIF	VDRMRNTW	10	16	VWQVDRMRNTWNSL	10	09	14	13343
VPR	IGCQHSRIG	46	72	HFRIGCQHSRIGITR	71	08	13	13344
VPR	WTLELLEL	42	69	YNEWTLLELLELKE	15	12	19	13345
VPR	ILQLLFIH	37	58	IIRLQLLFIHFR	60	31	48	13346
VPR	FINFRIGCQ	30	47	QLLFIHFRIGCQHSR	66	29	45	13347
VPR	YNEWTLLEL	30	47	REPYNEWTLLEEL	12	27	42	13348
VPR	FRPWHLGL	24	38	VRHFRPWHLGLQHI	31	12	19	13349
VPR	WEGVEAIR	18	28	GDTWEGVEAIRILQ	51	14	22	13350
VPR	LEELKSEAV	16	25	LELEELKSEAVRHF	20	15	23	13351
VPR	WAGVEAIR	16	25	GDTWAGVEAIRILQ	51	15	23	13352
VPR	YODTWAGVE	16	25	YETYODTWAGVEAI	47	16	25	13353
VPR	IGCRIISRIQ	12	19	HFRIGCRHSRIGITR	71	03	5	13354
VPR	FINFRIGCR	11	17	QLLFIHFRIGCRHSR	66	11	17	13355
VPR	FVIFRIGCO	11	17	QLLFVIFRIGCQHSR	66	10	16	13356
VPR	YODTWGVE	11	17	YETYODTWGVEAI	47	04	6	13357
VPR	FRPWHLHSL	10	16	VRHFRPWHLHSLQHI	31	05	8	13358
VPR	WALELLEL	09	15	YNEWALELLEELKNE	15	03	5	13359
VPU	LVTLSSSK	01	50	EWLVTLSSSKLDQ	87	01	2	13360
VPU	VTLSSSKL	01	50	EWLVTLSSSKLDQ	89	01	2	13361
VPU	IIAIVVWTI	23	36	VVAIAIVVWTIVEI	20	02	3	13362
VPU	VDRIVIVA	01	3	LAKVDYRIVIVARIV	5	01	25	13363

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VP1	LRQRKIDRL	17	27	RKLRQRKIDRLDR	44	11	17	13364
VP1	IVVWTIVFI	15	23	IIAIVVWTIVFIEYR	27	07	11	13365
VP1	VVWTIVFIE	14	22	IAIVVWTIVFIEYRK	28	06	9	13366
VP1	IEYRKILRQ	13	21	IVFIEYRKILRQRKI	36	07	11	13367
VP1	ILAIVALVV	11	17	SLYLAIIVALVVAII	3	01	2	13368
VP1	WTIVFIEYR	10	16	IVVWTIVFIEYRKIL	30	05	8	13369
VP1	LAIVALVA	09	15	LQILAIVALVVAIII	4	02	3	13370

Table XIX¹
HIV DR Super Motif Peptides with Binding Information

[illegible]

Table XIX^b
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
VSTQLLNG	KPVVSTQLLNGSLA						12864
VYSTQLLN	IKPVVSTQLLNGSL						12865
LTWGIKQL	LLQLTWGIKQLQAR		0.0180				12866
LSGIVQOQ	ARQLLSGIVQOQSNL						12867
WATHACVPT	INWVWATHACVPTDPN						12868
LGAAGSTMG	LGFLGAAGSTMGAAS		-0.0007				12869
VRQYSPLS	VNRVQOYSPLSFQT						12870
LLNGSLAE	STQLLNGSLAEDEV						12871
VKLTPLCVT	KPCVKLTPLCVTLNC						12872
LRAIEAQH	NLLRAIEAQHILLQ		0.0150				12873
VSTVQCTHG	CKNVSTVQCTHGKIP						12874
LGWGCCGK	QQLLGIWGCCGKJIC						12875
LWDQSLKPC	IISLWDQSLKPCVKL		0.0012				12876
LGFLGAAGS	AVFLGFLGAAGSTMG						12877
VWATHACVP	VHNVWATHACVPTDP						12878
WGKQLQAR	LTWGIKQLQARVLA						12879
LWYIKIFIM	TNWLWYIKIFIMVIG						12880
FCASDAKAY	TTLFCASDAKAYDTE						12881
IVGGLIGLR	FIMVGGILGILRVF						12882
IFIMVGGI	YKIFIMVGGILGIL						12883
VYGVVPVWK	WYVYGVVPVWKEAT	-0.0004	0.0310	0.0049	0.4600		12884
IKQLQARVL	VWGIKQLQARVLAVE						12885
IKIFIMVG	LWYIKIFIMVGGIL						12886
MGAASITLT	GSTMGAASITLTVOA						12887
YIKIFIMV	WLWYIKIFIMVGGI						12888
ITGLLTRD	SSNITGLLTRDGGK						12889
IPHYCAPA	PEPIPHYCAPAGFA						12890
MIYGLIGL	IFIMVGGILGILRV						12891
VQARQLLSG	TLTYQARQLLSGIVQ						12892
FEPIPHYC	KVSFEPIPHYCAPA						12893
LRSLCLFSY	WDDLRSCLFSYIIRL						12894
MKNMVEQ	NFNMKNMVEQMHIE						12895
VHNVWATHA	DTEVHNVWATHACVP						12896
WKNMVEQM	FRMWKNMVEQMIED						12897
YGVVPVWKE	VTVYGVVPVWKEATT		0.0160	0.0210	0.5100		12898
LLQLTWGI	QQILLQLTWGIKQL	0.0180	0.3900				12899
IEPLGVAPT	VVKIEPLGVAPTAK						12900
IKPVSTQL	THGIKPVVSTQLLN						12901
LQARVAVE	IKQLQARVLAVERYL						12902
WDDLRSCL	ALA WDDLRSCLFSY						12903
INIHTPHR	SRPINIHTPHREKR						12904
INIHTPRE	RPINIHTPREKRA						12905
ITQACPKVS	TSVITQACPKVSFEP						12906
IVQQSNLL	LSGIVQQSNLLRAI						12907
LGNSTNST	NKTLGNSTNSTLGN						12908
VISTRHRE	ARPVISTRHREKRA						12909
WRWGTFLG	QNLWRWGTFLGMLM						12910
WRWGTMLLG	QHLWRWGTMLLGMLM						12911
FAVLISVNR	RIVFAVLISVNRVQ						12912
LLNGSLAE	TQLLNGSLAEDEV						12913

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LTPLCVTLN	CVKLTPLCVTLNCTD						12914
LYKYVVKI	RSELYKYKYVVKIEPL						12915
VPWNSWSN	TTNVPWNSWSNKSLS						12916
YRLNCNTS	YKEYRLNCNTSAIT						12917
IHCAPAGF	PIPIHCAPAGFAIL						12918
LKQQLLGI	ERYLKQQLLGIWGC						12919
YKYVVKJE	SELYKYKYVVKIEPLG						12920
IRPVSTQL	THGIRPVSTQLLN						12921
LDKWASLWN	LLALDKWASLWNWFD						12922
LRVFAVLS	LIGLRVFAVLSVNI						12923
LNGSLAEE	QLLNGSLAEEVVI						12924
YKVKIEPL	LYKYKYVVKIEPLGVA						12925
LKGLRLGWE	RSSLKGLRLGWECLX						12926
FSYHRLDL	LCLFSYHRLRDLII						12927
INCTRPNN	SVENCTRPNNRTK						12928
VYKIEPLOV	KYKYVVKIEPLGVAPT						12929
WKEATITLF	VPVWKEATITLFCAS				0.4700		12930
IGLRVFAV	GGILGLRVFAVLSI			0.0086			12931
FFYCNTSGL	GGEFFYCNTSGLFNS						12932
FGLQALFLG	RAAFGLQALFLGRLO						12933
FYCNISGLF	GGEFFYCNISGLFNST						12934
LIGLRVFA	VGGILGLRVFAVLS						12935
VGLQAVFLG	KRAYVGLQAVFLGFLG						12936
VGLGMLFLG	KRAYVGLGMLFLGVLS						12937
ICTTAVPVN	GKLICTTAVPVNSSW						12938
ICTNVPWN	GKLICTNVPWNSSW						12939
LGVATKAK	IEPLGVAPTAKAKRV						12940
LICTTAVPW	SGKLICTTAVPWNSS						12941
LRDQQLLGI	ERYLRDQQLLGIWGC						12942
VFLGFLGAA	LGA VFLGFLGAAAGST						12943
FSYHRLRDF	LCLFSYHRLRDFILI						12944
IPHYCTPA	FEPIHYCTPAGFA						12945
IVFAVLSIV	GLRVFAVLSIVNRV						12946
VFAYLSIVN	LRVFAVLSIVNRVR						12947
VPWNASWSN	TTAVPWNASWSNKSLS						12948
IGLRJFAV	GGILGLRJIJFAVLSI						12949
IRQAHNIS	IGDIRQAHNISRAK						12950
VAPTKARR	PLGVAPTAKARRVVQ						12951
FNQTGCKRN	DKKFNQTGCKNVST						12952
IGPQQTFFA	SVRIGPQQTFFATGD						12953
IGSGQAFYV	RYSGSGQAFYVITGK						12954
IRYLNLYNQ	QTAIRYLNLYNQTEN						12955
LIGLRIFA	VGGILGLRIFAIVLS						12956
LLQYWSQEL	WWNLLQYWSQELKNS						12957
LRNCLFSY	WDDLNRNCLFSYHRL						12958
LVSGFLALA	SIRLVSGFLALAWDD						12959
VSGFLALAW	IRLVSGFLALAWDD						12960
FDPIHYC	KVTFDPIHYCTPA						12961
IIFAVLSIV	GLRIFAIVLSIVNRV						12962
LINCNTSAI	EYRLINCNTSAITQA						12963

Table XIXb
HIV DR Super Motif Peptides with Binding Information

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
LLNATAIV	AVSLNATAIAVAG						12964
LRIIFAVLS	LGLRUFVLSIVN						12965
VTQACKV	NTSVITQACKVSE						12966
YWNLLQYW	VLKYWNLLQYWSQE						12967
FAIKCNDE	PAGFAIKCHDKKN						12968
IFAVLSVN	LRIIFAVLSIVNRV						12969
INNTSAIT	YRLNNTSAITQAC						12970
LNATAIVA	VSLNATAIAVAEGT						12971
WNSSWSNKS	NVPWNSSWSNKSUDE						12972
WNASWSNKS	NVPWNASWSNKSIED						12973
ICTTTVWN	GKLICTTTVWNASW						12974
LLKYVVEI	QOHLKLTWVGKQL						12975
MLQFLQAA	ESELYKYKVEIKPL						12976
MHSFNCGE	LGAMFLGFLQAGST						12977
YWSQELKNS	LLQYWSQELKNSAVS						12978
IGAVFLGL	AVGIGAVFLGFLGAA						12979
LIARTVEL	DFILIAARTVELLGH						12980
LICTTVPW	SGKLICTTVPWNAS						12981
LLNGSLAEG	TQLLNGSLAEGEH						12982
YWGQELKNS	LVWYWGQELKNSAIS						12983
IAARTVELL	FILIAARTVELLGHIS						12984
LFGLGAA	IGALFLGLGAAAGST						12985
LKNSAVSL	SQELKNSAVSLNAT						12986
VGIGAVFLG	KRAVGIGAVFLGFLG						12987
VSLNATAI	NSAVSLNATAIAVA						12988
YATGDHGD	QTFYATGDHGDIRQ						12989
IAIAVAEGT	LDIAIAVAEGTDRI						12990
IHYCTPAOF	PIPIHYCTPAOFAIL						12991
ILGLVICS	GTILGLVICSASN						12992
IWNNTWME	VDEIWNNTWMEWER						12993
LGLVICS	TLILGLVICSASN						12994
LRDFILIA	YHRLRDFILIAARTV						12995
LTPLCVTD	CVKLTPLCVTDGIN						12996
MLQLTWGI	QOHLMLQLTWVGKQL						12997
VENCTRN	NESVEINCTRNNT						12998
VRQLLSGIV	TVQVRQLLSGIVQQQ						12999
LILGLVHC	WGTLILGLVHCAS						13000
VGHQAAHQ	LNTVGHQAAHQMLK						13001
LVQNANPD	TETLLVQNANPDCKT						13002
VQNANPDCK	TLVQNANPDCKTIL						13003
LGLNKIVRM	WILGLNKIVRMYS						13004
LSEGATPD	FSALSEGATPDQDNT						13005
WILGNKI	YKRWILGNKIVRM						13006
LEEMTACQ	GATLEEMTACQVVG						13007
YKRWILGL	GENYKRWILGLNKI						13008
YKRWILGL	YGEIYKRWILGLNKL						13009
VSNQYPIVQ	SSQVSNQYPIVQNLQ						13010
WEKILRPG	LDKWEKILRPGGKK						13011
IAGTSTLQ	QSDIAGTSTLQEQI						13012
							13013

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
WASLERERF	HLVWASLERERFALN						13014
IPMFSALE	PEVPMFSALESEGT						13015
MFSALESEGA	VIPMFSALESEGTQ						13016
VIPMFSALE	SPVPMFSALESEGA			0.0130	0.0130		13017
MYSPVSLD	IVRMYSVPSILDIRQ	0.0007	-0.0007				13018
VRMYSPVS	LNKIVRMYSVPSILDI						13019
VRMYSPVSI	NKIVRMYSVPSILDI						13020
YSPVSLDI	VRMYSPVPSILDIRQ						13021
MTETLLVQN	KNWMTETLLVQNANP						13022
WMTETLLVQ	VKNWMTETLLVQNAN						13023
ISPTLLNAV	QKAIPTLLNAVYKV	0.0032	0.0230	0.0008	0.0053		13024
VKNWMTETL	TQEVKNWMTETLLVQ						13025
IKFCNCGKE	QKRJKFCNCGKEGHL						13026
IPVGEIKR	NPPIPVGEIKRWII						13027
YTAVERMQR	KGGYTAVERMQRQNP						13028
VATLYCVHQ	YNTVATLYCVHQRIE						13029
WDRLHPVHA	AAEWDRLHPVHAGPI						13030
FLQSRPEPT	FGNQLSRPEPTAPP		0.0130				13031
FKTLRAEQ	DRFFKTLRAEQATQE						13032
MVHOAISPR	QGMVHOAISPRTLN			0.0067	0.6400		13033
VHQASPR	QGMVHOAISPRTLNA	0.0085	0.0550				13034
YKTLRAEQ	DRFYKTLRAEQASQE	-0.0001	-0.0007		-0.0015		13035
VSILDIRQ	YSPVSILDIRQPKKE		0.0028				13036
LAEMSQT	ARVLAEMSQTYNISA						13037
LKGJWPSHK	ANFLKGJWPSHKGRP						13038
VKFCNCGKE	RKTVKFCNCGKEGHI						13039
YNTVATLYC	RSLYNTVATLYCVHIQ						13040
LHPVHAGPI	WDRLHPVHAGPIAPG						13041
LYNTVATLY	LRSLYNTVATLYCVHI						13042
MTDTLLVQN	KNWMTDTLLVQNANP						13043
WMTDTLLVQ	VKNWMTDTLLVQNAN						13044
IEVKDTKEA	IQRIEYKDTKEALOK						13045
LOGQMVHQA	VQNLOGQMVHQAISP						13046
MTNPPPIV	IGWMTNPPPIPVGEI						13047
WMTNPPPI	QIGWMTNPPPIPVGE						13048
IAPQMREP	AGPIAPQMREPRGS						13049
VHAGPIAPQ	LHPVHAGPIAPQGMNR						13050
LGPATLEE	LRALGPATLEEAMNT						13051
VHAGPIPG	VIPVHAGPIPGQMR						13052
IPQGMR	AGPIPGQMRREPRGS						13053
LSPTLLNAV	HQALSPTLLNAVWVW						13054
YRLKHLVWA	KKKYRLKHLVWASRE						13055
LCPAATLEE	LKALGPAATLEEAMT						13056
LKALGPAAT	KTILKALGPAATLEE						13057
LKDKPEPLA	QEQLKDKPEPLASLR						13058
LSGGKLDW	ASVLSGGKLDWAKI						13059
MTSNPPPV	IGWMTSNPPPIPVGEI						13060
VKNWMTDTL	TQDVKNWMTDTLLVQ		0.0006				13061
VSILDKQG	YSPVSILDKQGPKE						13062
WMTSNPPPI	QIGWMTSNPPPIPVGE						13063

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FNTVATLYC	KSLFNTVATLYCVIIQ						13064
IPMTFALSE	PEVIPMTFALSEGAT						13065
LASLSLFG	LYPLASLSLSLFGNDP						13066
LERFAYNPQ	SRELERFAYNPGLLE						13067
LFNTVATLY	LRLSNTVATLYCVII						13068
MFTALSEGA	VIPMTFALSEGA TPQ						13069
WDRVHPVHA	AAEWDRVHPVHA GPI						13070
VRMYSPTS	LNKIVRMYSPTSILD						13071
LERFALNPG	SRELERFALNPG LLE						13072
LQEQIAWMT	TSTLQEQIAWMTGNP						13073
VHPVILAGPI	WDRVHPVHAGPIPG						13074
VIPMTALS	SPEVIPMTALSEGA						13075
VRMYSPTSI	NKIVRMYSPTSILD						13076
LGRWFSNK	ANFLGRWFSNKG RFP						13077
LTSLSLFG	LYPLTSLSLSLFGNDP						13078
MYSPTSILD	IVRMYSPTSILDIRQ						13079
YKLKHVWA	KKKYKLKHVWASRE						13080
YSPTSILDI	VRMYSPTSILDIRQG						13081
LTSLSLFG	LYPLTSLSLSLFGNDP						13082
MMLNIVGGH	DLNMLNIVGGIQA A						13083
IDVYKDTKEA	HQRIDVYKDTKEALDK						13084
IGWMTSNPP	QEIQWMTSNPPPV						13085
IPVGDYKR	NPIPVGDYKRVII						13086
LYPLASLS	DKELYPLASLSLFG						13087
VHQALSPT	QQM VHQALSPTLMA						13088
VNPLGLET	RFAVNPLGLETSEGC						13089
FLQNRPEPT	PGNFLQNRPEPTAPP						13090
IMMOKSNFK	AAAIMMOKSNFKGPR						13091
LAEMSQVQ	ARVLAEMSQVQQSN						13092
LGRWFSNK	ANFLGRWFSNKG RFP						13093
LNPLGLETA	RNALNPLGLETAEGC						13094
YPLASLSL	KELYPLASLSLFG						13095
WQNYTPGPG	FPDWQNYTPGPGIRY						13096
VRQVPLRP	GFPVRQVPLRPNTY						13097
VPLRPMYK	RQVPLRPMYKGA F						13098
LTFGWCFKL	KYPLTFGWCFKLVPV						13099
ILDLYVYHT	RQEILDLYVYHTQGY						13100
WCFKLVPVD	TFQWCFKLVPVDPRE						13101
LWVYHTQGY	ILDLYVYHTQGYFPD						13102
WSKSSVGVW	GCKWSKSSVGVWPAI						13103
ILDLYVYNT	RQDILDLYVYNTQGY						13104
LLHPMSQHG	NNCLLHPMSQHGMD						13105
LLHPICQHG	NNSLHPICQHGMD						13106
IRYPLTFQW	QPGIRYPLTFQWCFK						13107
ITSSNTAAT	HGAITSNTAATNAD						13108
LEKHGATS	SHDLEKHGATSNT						13109
LWYHTQGF	ILDLYVYHTQGFPPD						13110
MTYKGAFDL	LRPMTYKGAFDLFF						13111
LVPVDPREV	CFKLVPVDPREVEEA						13112

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
VGVPAIRER	SSIVGWPAIRERMRR						13114
WCFKLVVE	TFGWCFKLVPEPEK						13115
FDSRLAFHH	EWREDSRLAFHHVAR						13116
FKLVPVDR	GWCFKLVVPVDPREVE						13117
VPLRPMIFK	RPQVPLRPMIFKGAFF						13118
LLDTGADDT	KEALLDTGADDTYLE						13119
WMGYELIPD	PFLWMGYELHPDKWT		-0.0003				13120
QYQNVLPQG	GIRYQYQNVLPQGWKG						13121
FRKTYAFTI	DKDPRKTYAFTPSI						13122
WTVNDIQKL	KDSWTVNDIQKLQCK		-0.0005				13123
LDCTHLEGR	IWQLDCTHLEGRKIL						13124
LDVGDAYES	VTVLDVGDAYESVPL		-0.0005				13125
MDLLVYGS	YQYMDLLVYGSDELEI		-0.0005				13126
VIPAEIGQE	FAEVIPAEIGQETAY						13127
WKGEGAYVI	KLLWKEGEGAVVIQDN	0.0450	0.2400	0.0450	0.2100		13128
WQDCTHLE	PGIWQDCTHLEGKI						13129
VDRELNRK	RKLVDRELNRKTQD						13130
WPKMIGGI	PGKWKPKMIGGIGGF						13131
IWQLDCTHL	SPGWQLDCTHLEGG		-0.0009				13132
VAVHVASGY	IILVAVHVASGYIEA						13133
WKGSPAFIQ	PQGWKGSPAFIQSSM		0.0087				13134
IGGYSAGIER	KGGIGGYSAGIERIID						13135
YALGIQDAQ	DSQYALGIQDAQOPDK						13136
FWVEYQLGIP	TQDFWEYQLGIPHPA						13137
IKKJDSKXW	YFAIKKJDSKXWRKL						13138
LGIPHAQPD	QYALGIQDAQPDKSE		-0.0005				13139
LGIPHPAGL	EVQLGIPHPAGLKKK		1.7000	0.1400	1.9000		13140
VNTPLVKL	WEFVNTPLVKLWYQ	0.0150	-0.0005	-0.0005	0.0016		13141
VTVLDVGDA	KKSVTVLDVGDAYES	0.0150	0.0640	-0.0005	0.0046		13142
FPISPIETV	TLNFPISPIETVPVK		0.1500	0.0008			13143
ISPIETPV	NFRISPIETVPVKLK						13144
FVNTPLVK	EWEFVNTPLVKLWY						13145
LNFPSPIE	GCTLNFPSPIETVP	0.0230	0.0380	0.2600	2.6000		13146
WEFVNTPL	IPWEFVNTPLVKL		1.4000				13147
IQNERVYVR	ITKIQNERVYVRDSR						13148
LVGPTPVI	GTVLVGPPTVNIQR	0.0290	0.0820	-0.0005	0.0180		13149
VQLGIPHPA	FWEVQLGIPHPAGLK		0.0024				13150
WQATWIFEW	TEYWQATWIFEWEIF						13151
LETVPVKLK	ISPIETVPVKLKPGM						13152
IGTVLVGPT	KKAIGTVLVGPTPVN		0.0150				13153
LVAHVASG	KILVAVHVASGYIE						13154
VLVGPTPVN	IGTVLVGPTPVNIIG	0.0400	0.0710	-0.0003	0.0320		13155
YIEAEVIPA	ASGYIEAEVIPAETG	0.0006	0.0120	0.0097	0.0480		13156
YVGSDEIG	DDLTVGSDEIGQHR						13157
MDGPKVKQW	KPGMDGPKVKQWPLT						13158
VASGYIEAE	AVHVASGYIEAEVIP						13159
VGPTPVNI	TVLVGPTPVNIQRN						13160
VQWPLTEE	GPKVQWPLTEEIKK						13161
VYRDSRDP	NFRVYRDSRDPWK		0.0150				13162
WGTTTPDKK	LLRWGTTTPDKKLIQK						13163

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR3w81	DR2w202	DR3	DR4w4	DR4w15	DR3w11	DR3w12	SEQ ID NO.
VIVQYMDLL	PEVIYQYMDLLVYG	0.0060								13164
LKKKKSVTV	PAGLKKKKSVTVLDV	0.0003		-0.0014		-0.0026		-0.0006		13165
VPRRKAKII	IKVPRRKAKIRDY	0.0027		0.0700		-0.0024		2.5000		13166
FPOITLWQR	SSEFQITLWQPLV					0.0130				13167
VIWGTGKPF	ESIVTWGKTPKFLP									13168
YVDGAANRE	ETFFYDGAANRETKL									13169
FKNLTKQY	QEPFNKLTGKYAKM									13170
IQTKELQKQ	ATDIQTKELQKQTK									13171
YDQMGAGDD	IRDYGKQMGAGDDCVA									13172
WRAMASDFN	HSNWRAMASDFNLPP	0.1300	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045	13173
ISKIGPENP	EGKISKIGPENPYNT									13174
LTOIGGCTLN	RNLLTQIGGCTLNFI									13175
IQAQPKDS	ALGIQAQPKDSISE	0.0001		-0.0014		-0.0026		-0.0007		13176
LPEKDSWTY	PIVLEKDSWTYNDI									13177
FOSSMTKIL	PAIFOSSMTKILEPF	0.0320	0.0320	0.0200	-0.0043	0.0058	0.6500	0.0660	-0.0045	13178
FTIPSNNE	YTAFTIPSNNETPG									13179
IFQSSMTKI	SPAIFQSSMTKILEP	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0770	0.0122	13180
IIQLIKKE	VSQIEQLIKKKEKYV									13181
LSWVPAAHG	KVYLSWVPAAHGKIGG									13182
YLSWVPAHIK	EKVYLSWVPAHIKIG									13183
YTAFTPSI	FRKYTAFTPSINNE	0.0270	0.1300	0.0048	-0.0043	0.1700	0.3800	0.0110	0.0039	13184
IIATDIQTK	IIIDIIATDIQTKELQ									13185
IWKGFALL	RDPIWKGFALLLWKQ									13186
LOKQITXIQ	TKELQKQITXIQNFR	0.0071	0.0210	0.0350		0.0340	0.0200	0.0330		13187
LKEALLDTG	GKQLKEALLDTGADD	0.0001		-0.0021		-0.0024		-0.0005		13188
VYLSWVPAH	KEKVYLSWVPAHIKGI									13189
FILKLAGRW	TAYFILKLAGRWPKYK									13190
LEGRIILVA	CTILEGRIILVAVIIV									13191
YFILKLAGR	ETAYYFILKLAGRWPY									13192
IILVAVHVA	EOKIILVAVHVASGY									13193
IWGTTPKFR	SIVIWGTTPKFLPI									13194
LGRWPVKV	ILKLGRWPVKVVIIT									13195
VVAKEIVAS	LPPVVAKEIVASCDK	0.0001		-0.0021		0.0043		-0.0010		13196
IIIDIIATDIQ	ERIIDIIATDIQTK									13197
IIIDIIATDIQ	GBRIIDIIATDIQTK									13198
IIGRNMLTQ	PVNIIGRNMLTQIGC									13199
IKVKQLCKL	YAGIKVKQLCKLLRG									13200
VDKLVSSGI	NEQVDKLVSSGIRKY									13201
IVGAETFYV	KEPIVGAETFYVQGA									13202
LPPVVAKEI	DFNLPPVVAKEIVAS	0.0042		-0.0021		-0.0024		0.0036		13203
WTVQIQLP	PDKWTVQIQLPEKD									13204
FNLPVPYAK	ASDFNLPPVVAKEIV	0.0026		-0.0021		-0.0028		-0.0006		13205
FTSAAVKAA	GSNFTSAAVKAACWV									13206
LALQDSGLE	AIHLALQDSGLEVNI									13207
LPPIVAKAI	DFNLPPVVAKEIVAS									13208
LQDSGLEVN	HLALQDSGLEVNIIVT									13209
FNLPPIVAK	ASDFNLPPVVAKEIV									13210
IGQIRAKIE	DLFIGQIRAKIEELR									13211
IIGRNLLTQ	PVNIIGRNLLTQIGC	0.0039		-0.0014		0.0043		0.0990		13212
LEVINIVTDS	DSGLEVINIVTDSQYA	0.0001		-0.0014		0.0350		-0.0007		13213

Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VTQYMDLL	PEIVYOYMDLLVVG						13164
LKKKSVTV	PAGLKKKSVTVLDV		0.0140				13165
VPRRKAJI	IKVVPRRKAIIRDY		0.0030				13166
FQITLWQR	SFSFPQITLWQRPLV		0.0006				13167
VIWGTPKF	ESVIWGTGTPKFRFP						13168
YVGGAAARE	ETFYVDGAANRETKL						13169
FRNLTKY	QEPFNLTGKYAKM						13170
IQTKELQK	ATDIQTKELQKQITK						13171
YKQMGDD	IRDYKQMGAGDDCVA						13172
WRAMASDFN	HSNWRAMASDFNLFP						13173
ISKIGPENP	EGKISKIGPENPYNT	0.0008	0.0530	0.0250	0.0860		13174
LTQIGCTLN	RNLLTQIGCTLNFI						13175
IIQAQPKDS	ALGIQAQPKDSSE		-0.0005				13176
LPEKDSWTV	PIVLPEKDSWTVNDI						13177
FQSSMTKIL	PAIFQSSMTKILEPF	0.1100	0.7300	0.0140	0.9100		13178
FTFSNN	YTAFTFSNNETPG						13179
IFQSSMTKI	STAFQSSMTKILEP	0.2800	0.1700	0.0150	2.3000		13180
IEQLKKE	VSQIEQLKKEKVV						13181
LSWVPAHKG	KVYLSWVPAHKGIG						13182
YLSWVPAHK	EKVYLSWVPAHKGIG						13183
YTAFTFSI	FRKYTAFTFSINNE	-0.0001	0.8400	0.0610	1.9000		13184
IIATDIQTK	IIIIATDIQTKELQ						13185
IKWGPALKL	RDIWKPALKLLWKG						13186
LQKQITKI	TKELQKQITKQNR						13187
LKEALLDTG	GGQLKEALLDTGADD	0.0050	0.0055	0.0250	0.0078		13188
VYLSWVPAH	KEKVYLSWVPAHIGI		-0.0009				13189
FILKLAGRW	TAYFILKLAGRWPK						13190
LEGKILVA	CTHLEGKILVAIVH						13191
YFILKLAGR	ETAYFILKLAGRWV						13192
ILVAVHVA	EGKILVAVHVASGY						13193
IWGTPKFR	SIVWQKTPKFRPLI						13194
LAGRWPKVY	ILKLAGRWPKVVIIT						13195
VYAKEIVAS	LPPVYAKEIVASCDK		-0.0009				13196
IIIIATDIQ	ERIIIIATDIQTK						13197
IIIIATDI	GERIIIIATDIQTK						13198
IGRNMLTQ	PYNIIGRNMLTQICG						13199
IKVKQLCKL	YAGIKVKQLCKLLRG						13200
VDKLVSSQI	NEQVDKLVSSGIRKY						13201
IVGAETFY	KEPIVGAETFYVDGA						13202
LPPVAKEL	DNLPVPAKEIVAS						13203
WTVPQIQLF	PDKWTVPQIQLPEKD		0.0530				13204
FNLPVPAK	ASDNLPVPAKEIV		0.0840				13205
FTSAAVKAA	GSNFTSAAVKAAACW						13206
LAQDSGLE	AIHLALQDSGLEVIN						13207
LPPVAKEL	DNLPVPAKEIVAS						13208
LQDSGLEVN	ILALQDSGLEVINI						13209
FNLPVPAK	ASDNLPVPAKEIV						13210
IQGHRAKIE	DLEIGQHRAKIEELR						13211
IGRNMLTQ	PYNIIGRNMLTQICG		-0.0005				13212
LEVINITDS	DSGLEVINITDSQYA		-0.0005				13213

Table XIXb

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDVYP						13214
LVSSGIRKV	VDKLVSSGIRKVLFL						13215
FLKLAGR	TAYFLKLAGRWPVK						13216
LALQDSGE	AHLALQDSGSEVNI						13217
LQDSGEVN	HLALQDSGSEVNI						13218
VYVITDNG	RWPVKVIHTDNGSNF						13219
WPVKVIHTD	AGRWPVKVIHTDNGS						13220
YFLKLAGR	ETAYFLKLAGRWPV		0.0041				13221
ICGKKAIGT	LIEICGKKAIGTVLV						13222
IVAKEIVAS	LPPIVAKEIVASCDK						13223
LRWGFTPD	QHLLRWGFTPDKKH						13224
LEGKVLVA	CHLLEGKVLVAVHV						13225
LKWGFTPD	EHLLKWGFTPDKKH						13226
VILVAVIVA	EGKVILVAHVAVSGY						13227
LAWVPAHKG	KVYLAWVPAHKGIGG			0.2500	0.3000		13228
YDQILEIC	VRQYDQILEICGCK	0.0014	0.1400	1.6000	0.5200		13229
YLAWVPAHK	EKYLAWVPAHKGIG	0.0010	1.4000				13230
IGQHRKIE	DLEIGQHRKIEELR		0.0012				13231
IGRNLLTQI	VNIORNLLTQIGCT						13232
LWQRPVLT	QITLWQRPVLTGIG						13233
VSLTITNQ	QKVSILTITNQKTE						13234
VYLAWVPAH	KEKVYLAWVPAHKG						13235
ICGKKAIGT	LIEICGKKAIGTVLV						13236
LRGAKALTE	CKLLRGAKALTEVIP						13237
LVNQIEQL	ESELVNQIEQLIKK		0.0040				13238
LVSQIEQL	ESELVSQIEQLIKK						13239
YFSVPLDK	GDAYFSVPLDKDFRK						13240
IGRNMLTQI	VNIORNMLTQIGCT						13241
IKVRQLCKL	YPGIKVRQLCKLLRG						13242
LWKOPAKLL	RDPWLKOPAKLLWKG						13243
LWQRPVLT	QITLWQRPVLTGIG						13244
YAGIKVKQL	SQIYAGIKVKQLCKL						13245
IWKTPFKK	SIVIWKTPFKKLPI						13246
LRHLLKWG	IEELREHLLKWGFTT						13247
VQPIQLPEK	KWTVPQPIQLPEKDSW						13248
WQRPVLTIK	ITLWQRPVLTIKIGG						13249
IQAQPDRS	ALGHQAQPDRESE						13250
LQAHILALQ	KTELQAHILALQDSG						13251
LVICTEME	IKALVEICTEMEKEG						13252
LRQHLLRWG	IEELRQHLLRWGFTT						13253
LTLQGLCTLN	RNMLTLQGLCTLNFI						13254
LVSAIRKV	NEQVLDLVSAIRKVL						13255
VDKLVSAIG	VDKLVSAIGIRKV		0.0120				13256
YPGIKVRQL	SQIYPGIKVRQLCKL	0.0028					13257
FRQNPDIV	LEPFRQNPDIVYQ						13258
FSFQITLW	TVSPFSFQITLWQRP						13259
FTSTTVKAA	GSNFTSTTVKAAACW						13260
IASDIQTK	IIDIASDIQTKELQ						13261
LAGRPVVK	LLKLAGRWPVKTIHT						13262
VQKIATESI	TEAVQKIATESIVW						13263

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w202	DR3	DR4w4	DR4w15	DR3w11	DR3w12	SEQ ID NO.
FTIPSTNNE	YTAFIPSTNNETPG								13264
LEEDNLPGK	DTVLEDNLPGKWKP								13265
LDIVPLTE	AKALTDIVPLTEAE								13266
LVTIKIGGQ	QRPLVTIKIGGQKE								13267
MRGAHTNDV	YARMGAHTNDVQQL								13268
VKTIHTDNG	RWPVKTIHTDNGSNF								13269
VQVILPEK	KWTVQVILPEKDSW								13270
WPVKTIHTD	AGRWPVKTIHTDNGS								13271
WQRPVTVK	ITLWQRPVTVKIGG								13272
WTVPVILP	PDKWTVPVILPEKD								13273
YTAFTIPST	FRKYTAFTIPSTNNE								13274
IDIASDIQ	ERIDIASDIQTK								13275
IIDIASDI	GERIIDIASDIQTK								13276
IVDIATDI	GERIVDIATDIQTK				0.0320				13277
LEENLPGK	DTVLEENLPGKWKP								13278
LOAIYALQ	KTELQAIYALALQDSG								13279
LOXQIUIQ	TKELQXQIUIQNF								13280
VUIATDIQ	HRVUIATDIQTK								13281
YDQIPIEC	VRQYDQIPIECGKK								13282
FRFPQITLW	VPTFRFPQITLWQRP								13283
IGRNMLTQL	VNIIGRNMLTQLCCT								13284
ISRGCPNP	EGKISRGCPNPYNT								13285
LTEVIPLTE	TKALTEVIPLTEAE								13286
MESIVWCK	KIAMESIVWCKTPK								13287
VPRKVKII	IKVPRKVKIIRDY								13288
VSEFPQIT	QGTVSEFPQITLWQ								13289
WYQLETEPI	VKLWYQLETEPIVGA								13290
YPCIKVKQL	SOIYPCIKVKQLCKL								13291
FPQGEAREF	NLAFPQGEAREFPE								13292
LIALLDYG	GGQLIALLDYGADD								13293
VSLDITNQ	QKYVSLDITNQKTE								13294
WETWTDYV	KETWETWTDYVQAT								13295
YAKMRTAHT	TOKYAKMRTAHTNDV								13296
YKNLTGKY	QEPYKNLTGKYARM								13297
LQLPLERL	PVQLPLPLERLTD								13298
VPLQLPPL	AEVPLQLPPLERLT								13299
LYQSNPPPS	IKFLYQSNPPPSPEG								13300
VRIKILYQ	LKAVRIKILYQSNP								13301
YQSNPPSP	KFLYQSNPPSPSPEGT								13302
LQPLPIEL	PVPLQPLPIELRLD								13303
VPLQLPPIE	AEVPLQLPPIELRL								13304
WNHPSQPK	LEPNWNHPSQPKTAC								13305
FLNKGGLIS	QVCFLNKGGLISYGR								13306
WKHPGSQPK	LEPWKHPSQPKTAC								13307
YCKKCCFHC	NNCYCKKCCFHCQVC								13308
YCKKCCYHC	TNCYCKKCCYHCQVC								13309
WNHPSQPT	LEPNWNHPSQPTTAC								13310
MIVWQVDRM	WQVMIVWQVDRMRIR								13311
WQVMIVWQV	ENRWQVMIVWQVDRM	1.3000	0.0036	-0.0043	0.0690	1.9000	0.0032	-0.0045	13312
WQVDRMRJR	MIVWQVDRMRJRRTWK								13313

Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FTIPSTNNE	YTAFTIPSTNNEPG						13264
LEDINLPKG	DTVLEDINLPKGWKP						13265
LTDPVPLTE	AKALTDPVPLTEAE						13266
LVTKIGGQ	QRPLVTIKIGGQKE						13267
MRGAIITNDV	YARMRGAIITNDVKQL						13268
VKTHITDNG	RWPVKTHITDNGSNF						13269
VQPIVLPEK	KWTVQPIVLPEKDSW						13270
WPKVTHID	AGRWPVKVTHIDNGS						13271
WQRLVTVK	ITLWQRLVTVVKIGG						13272
WTQVPIVLP	FDKWTQVPIVLPKED						13273
YTAFTIPST	FRKYTAFTIPSTNNE						13274
IDHIASDIQ	ERIHIDHIASDIQTK						13275
IDHIASDI	GERIHIDHIASDIQTK						13276
IVDIATDI	GERIVDIATDIQTK						13277
LEENLPKG	DTVLEENLPKGWKP		0.0026				13278
LQAIYLALQ	KTELQAIYLALQDSG						13279
LQKQIKIQ	TKELQKQIKIQNFR						13280
VNIATDIQ	ERIVDIATDIQTK						13281
YDQPIEIG	VRQYDQPIEIGGKK						13282
FNFPQITLW	VPTFNFPQITLWQRP						13283
IGRNMLTQL	VNIIGRNMLTQLGCT						13284
ISRUGPENP	EGKISRUGPENPYNT						13285
LTEVPLTE	TKALTEVPLTEAE						13286
MESIVWCK	KIAMESIVWCKTKY						13287
VPRKVKRII	IKVVPKVKVKIIRDY						13288
VSEFPQIT	QQTVSEFPQITLWQ						13289
WYQLETEPH	VKLWYQLETEPHVGA						13290
YPOIKVKQL	SOYPPOIKVKQLCKL						13291
FPQGEAREF	NLAFPQGEAREFPE						13292
LIEALDTG	GGQIEALDTGADD						13293
VSLDTTNO	OKVVSLLDTTNOKTE						13294
WETWTDYW	KETWETWTDYWQAT						13295
YAKMRTAHT	TOKYAKMRTAHTNDV						13296
YKNLKTGY	QEPYKKNLKTGYARM						13297
LQLPLERL	PVPLQLPLERLTL						13298
VPLQLPLE	AEPVPLQLPLELRT						13299
LYQSNPPS	IKELYQSNPPSPSEG						13300
VRIIKILYQ	LKAVRIIKILYQSNP						13301
YQSNPPSP	KFLYQSNPPSPSEGT						13302
LQLPIERL	PVPLQLPIERLRLD						13303
VPLQLPIE	AEPVPLQLPIERLR						13304
WNHPSQPK	LEPNWNHPSQPKTAC						13305
FLNKGGLIS	QVCFLNKGGLISYGR						13306
WKHPSQPK	LEPWKHPSQPKTAC						13307
YCKKCCFHC	NNCYCKKCCFHCQVC						13308
YCKKCCYHC	TNCYCKKCCYHCQVC						13309
WNHPSQPT	LEPNWNHPSQPTTAC						13310
MIVWQVDRM	WQVMIVWQVDRMRIR						13311
WQVMIVWQV	ENRWQVMIVWQVDRM	0.0018	0.1200	0.1500	0.2900		13312
WQVDRMRIR	MIVWQVDRMRIRTWK						13313

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DRI	DR2-w01	DR3-w202	DR3	DR4-w4	DR4-w15	DR3-w11	DR3-w12	SEQ ID NO.
LOYLALTAL	VGSLOYLALTALIKP									13314
LGHGVSEW	DWHLGHGVSEWRLLR									13315
VDRMRITW	VWQVDRMRITWNSL									13316
YDFCFESA	HLTYDFCFESAINR									13317
YWGLHTGER	ITTYWGLHTGERDWH									13318
IRTWNSLVK	RMRTWNSLVKHHM									13319
LQGVSEW	DWHLQGVSEWRKK									13320
LYKHMYVS	WNSLVKHMYVSKKA									13321
IPLGEARLV	EVHRLGEARLVYRT									13322
LYKHHMYIS	WKSLYKHHMYISGKA									13323
YLALTALIK	SLQYLALTALIKPKK									13324
IRTWKSLVK	RMRTWKSLSVKHHM									13325
LADQLIILY	DPDLADQLIILYFED									13326
LALTALIKP	LOYLALTALIKPKKI									13327
VNPLGADQL	STQVDPGLADQLIIL									13328
LYYDFCFSE	LIHLYYDFCFESAI									13329
FSESARKA	DFCFESARKAILG									13330
LADQLIIMH	EPGLADQLIIMHIYED									13331
WQVDRMKIR	LIVWQVDRMKIRTWN									13332
FDSAIRKA	FDGFSDAIRKAILG									13333
FSESARNA	FDGFSARINAILG									13334
IVSPRCEYQ	LGHIVSPRCEYQAGH									13335
LOYLALAAL	VGSLOYLALAALITP									13336
VDRMKIRTW	VWQVDRMKIRTWNSL									13337
YWGLQTOER	IKTYWGLQTOERDWH									13338
IPLGDARLV	EVHPLGDARLVIT									13339
LOYLALKAL	VGSLOYLALKALVTP									13340
WQVDRMRJN	MIVWQVDRMRJNTWK									13341
IKPKIKIPP	TALIKPKIKIPPLPS									13342
VDRMRITW	VWQVDRMRITWKSIL									13343
IGCQHSRIG	IFRGCQHSRIGITR									13344
WTLLELEL	YNFWTLELELEKSE									13345
ILQQLFIH	IIRILQQLFIHFRI									13346
FIHFRIGCO	QLLFIHFRIGCQHSR									13347
YNFWTLEL	REPYNFWTLELEL									13348
FRPWHLGL	VRHFRPWHLGLGOH									13349
WEGVENIR	GDTWEGVEAIRILQ									13350
LEELKSEAV	LELEELKSEAYRHF									13351
WAGVEAIR	GDTWAGVEAIRILQ									13352
YGDTWAGVE	YETYGDTWAGVEAIL									13353
IGCRHSRIG	IFRIGCRHSRIGITR									13354
FINFRIGCR	QLLFINFRIGCRHSR									13355
FVHFRIGCO	QLLFVHFRIGCQHSR									13356
YGDTWTGVE	YETYGDTWTGVEAIL									13357
FPRIWLHSL	VRHFPRIWLHSLGOII									13358
WALELEEL	YNFWALELEELKNE									13359
LVTLSSSK	BEWLVTLSSSKLDQ									13360
VTLSSSKL	EWLVTLSSSKLDQO									13361
IIAIVVWTI	VVAIAIVVWTIVFI									13362
VDRIVIVA	LAKVDYDRIVIVAFIV									13363

0.0200

0.0054

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LOYLALTAL	VGSLOYLALTALIKP						13314
LGHGVSEW	DWHLGHGVSEWRJR						13315
VDRMRITW	VWQVDRMRITWNSL						13316
YFDCFESA	HLIYFDCFESAIRN						13317
YWGLHTGR	ITTYWGLHTOERDWH						13318
IRTWNSLVK	RMRTWNSLVKHIIM						13319
LQQGVSEW	DWHLGQGVSEWRKK						13320
LVRHHMYVS	WNSLVKHIIMYVSKKA						13321
IFLGEARLV	EVHIFLGEARLVVRT						13322
LVKIHMYS	WKSIVKHIIMYISGKA						13323
YLALTALIK	SLQYLALTALIKPKK						13324
IRTWKSLVK	RMRTWKSLSVKHIIM						13325
LADQLIHL	DPDLADQLIHLIYFD						13326
LALTALIKP	LQYLALTALIKPKKI						13327
VDPLADQL	STQYDPLADQLIHL						13328
LYYFDCFE	LHLIYYFDCFESAI						13329
FSESARKA	FDCFESARKAILG						13330
LADQLIIMH	EPGLADQLIIMHIFD						13331
WQVDRMKIR	LIVWQVDRMKIRTW						13332
FSDSAIRKA	FDCFSDSAIRKAILG						13333
FSESARNA	FDCFSESARNAIIG						13334
IVSPCEYQ	LQHVSPCEYQAGH						13335
LOYLALAL	VGSLOYLALALITP						13336
VDRMKIRTW	VWQVDRMKIRTWNSL						13337
YWGLQTOER	IKTYWGLQTOERDWH						13338
PLGDARLV	EVHIFPLGDARLVIT						13339
LOYLALKAL	VGSLOYLALKALVTP						13340
WQVDRMRIN	MIVWQVDRMRINTWK						13341
IKPKIKPP	TALIKPKIKPPPLPS						13342
VDRMRINTW	VWQVDRMRINTWKS						13343
IGCHSRIG	IFRIGCHSRIGITR						13344
WTLLELLE	YNEWTLLELELKE						13345
ILQQLIYH	IRILQQLIYHIFRI						13346
FIHRIQCO	QLLIHFIHRIQCHSR						13347
YNEWTLLEL	REPNEWTLLELLEL						13348
FPKWLHGL	VRIHFPKWLHGLQHI						13349
WEGVEAIR	GDTWEGVEAIRILQ						13350
LEELKSEAV	LELLEELKSEAVRIH						13351
WAGVEAIR	GDTWAGVEAIRILQ						13352
YGDTWAGVE	YETYGDTWAGVEAII						13353
IGCHSRIG	IFRIGCHSRIGITR						13354
FIHRIQCO	QLLIHFIHRIQCHSR						13355
FVHFRIGCQ	QLLFVHFRIGCQHSR						13356
YGDTWTGVE	YETYGDTWTGVEAII						13357
FPRIWLHSL	VRIHFPRIWLHSLGQH						13358
WALELEEL	YNEWALELEELKNE						13359
LVTLLSSSK	EEWLVTLLSSSKLDQ						13360
VTLSSSKL	EWLVTLLSSSKLDQ						13361
IIAIVVWTI	VVAIIAIVVWTIVFI						13362
VDYRIVIVA	LAKVDYRIVIVAFIV						13363

0.0084

Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LRQRKIDRL	RKILRQRKIDRLIDR								13364
IVVWTVTFI	IIAIVVWTVTFIEYR								13365
VVWTVTFIE	IAIVVWTVTFIEYRK								13366
IEYRKILRQ	IVTEYRKILRQRKI								13367
IIAIVLVV	SLYLAIIVLVVAIL								13368
WTVTFIEYR	IVVWTVTFIEYRQL								13369
LAIVLVVA	LQILAIVLVVAGII								13370

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	I R6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
LRQRKIDRL	RKILRQRKIDRLIDR						13364
IVVWTIVFI	ILATVVTIVFIEYR						13365
VVWTIVFIE	IAIVVWTIVFIEYRK						13366
IEYRKILRQ	IVFIEYRKILRQRKQ						13367
ILAIVALVY	SLYILAIVALVVAII						13368
WTIVFIEYR	IVVWTIVFIEYRKIL						13369
LAIVALVA	LQILAIVALVYAGII						13370

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VPTDNPQE	53	83	HACVPTDNPQEVVL	85	12	19	13371
ENV	YLDQQLLG	31	48	VERYLDQQLLGW	669	18	28	13372
ENV	MHEDIISLW	29	45	VEQMHHEDISLWDQS	114	17	27	13373
ENV	VSFEPIPI	29	45	CPKVSFEPIPIIYCA	250	18	28	13374
ENV	LAVERYLKD	26	41	ARVLAVERYLKDQQL	664	15	23	13375
ENV	VKIEPLGVA	23	36	YKVKIEPLGVAPTK	564	15	23	13376
ENV	VVKEATTL	22	34	QVPVWKEATTLHCA	52	22	34	13377
ENV	LAWDDLRL	20	31	FLALAWDDLRLSLCLF	849	19	30	13378
ENV	LIESQNGQ	20	31	IYTLIESQNGQEN	737	07	11	13379
ENV	LOWEGLKYL	09	29	GLRLGWEGLKYLWNL	892	07	23	13380
ENV	LELDKWASL	18	28	QELLELDKWASLWNW	753	07	11	13381
ENV	YLRDQQLLG	18	28	VERYLRDQQLLGW	669	11	17	13382
ENV	MWQEVGKAM	15	23	INMWQEVGKAMYAP	492	12	19	13383
ENV	IEEGGERD	13	20	PEGIEEGGERDR	827	08	13	13384
ENV	MNENNTGN	01	20	INEMNENNTGNSTW	212	01	2	13385
ENV	IEEGGEQD	12	19	LGRIIEEGGEQDKNR	827	02	3	13386
ENV	LAEEVVR	12	19	NOSLAEEVVRIRSEN	309	04	6	13387
ENV	LALDKWASL	11	17	QDLLALDKWASLWNW	753	05	8	13388
ENV	LAVERYLKD	11	17	ARVLAVERYLKDQQL	664	10	16	13389
ENV	IRSENLTN	10	16	BIIRSENLTNNVKT	317	03	5	13390
ENV	MEWEREIDN	10	16	MTWMEWEREIDNYS	721	03	5	13391
GAG	ESPEVPMF	55	86	KETINEEAAEWDRHL	223	18	28	13392
GAG	VLAAMSQV	34	84	EKAFSPEVPMFSL	182	18	26	13393
GAG	MLKDTINEE	32	52	KARVLAAMSQVTS	383	09	14	13394
GAG	VVEEKAFSP	28	50	AMQMLKDTINEEAAE	218	30	47	13395
GAG	LRAEQATQE	27	44	WVKVVEEKAFSPEVI	176	28	44	13396
GAG	MLKETINEE	21	42	FKTLRAEQATQEVKN	325	09	14	13397
GAG	VVEEKAFSP	16	36	AMQMLKETINEEAAE	218	22	34	13398
GAG	VLAAMSQA	16	33	WVKVVEEKAFSPEVI	176	20	31	13399
GAG	LRAEQATQD	14	23	KARVLAAMSQA	383	03	5	13400
GAG	LRAEQATQD	14	22	LDKIEEQNKSKKA	103	09	14	13401
NEF	YFPDWQNT	12	19	FKTLRAEQATQDVKN	325	10	16	13402
NEF	FLKEKGLLE	36	56	YKTLRAEQASQEVKN	325	12	19	13403
NEF	FPDWQNT	30	47	TQGYFPDWQNTYTPP	195	33	52	13404
NEF	VSRDLKKG	26	41	LSHFLKEKGLGLLI	114	15	23	13405
POL	YMDLLYVGS	17	27	LSFFLKEKGLGLLI	114	14	22	13406
POL	IGPENYNT	11	17	TQGYFPDWQNTYTPP	195	17	27	13407
POL	LHPDKWTYQ	62	97	VGAVSRDLKKGAIT	46	11	17	13408
POL	IPAEQATQ	60	94	INQYMDLLYVGSLE	369	59	92	13409
POL	IPAEQATQ	59	94	ISKIOPENYNTPVF	236	28	44	13410
POL	LTEEKJAL	36	91	GYELHFDKWTVPQIQ	420	29	45	13411
POL	IAEEVPAE	55	88	EVNIVTDSQYALGII	684	58	91	13412
POL	LFLDIDRA	55	86	AEVPAETGQETAYF	838	55	86	13413
POL	VAKEIVASC	54	86	QWPLTEEKJALTEI	210	26	41	13414
POL	VGSLEIGQ	53	83	SGVIEAEVPAETGQ	833	51	80	13415
POL	IIRDYCKQM	50	78	RKVLFLDIDRAQEE	749	32	50	13416
POL				PPVAXEIVASCDC	781	22	34	13417
POL				KCOLGGEAMHGQVDC	794	47	73	13418
POL				DLYVGSLEIGQIRA	1017	28	44	13419
POL				KAKIIRDYCKQMAGD		36	56	13420

Table XXa
 IIIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	MASDFNLPT	47	73	WRAMASDFNLPPVVA	771	24	38	13421
POL	FYVDGAANR	43	67	AETFYVDGAANRETK	629	33	52	13422
POL	IHTDNGSNF	42	66	VKVIHTDNGSNFTSA	862	17	27	13423
POL	ILKEPVIGV	41	64	NREILKEPVHIGVYD	495	36	56	13424
POL	YYQEPFKNL	40	63	TYQNYQEPFKNLKTD	530	39	61	13425
POL	YYQEPFKNL	39	61	VIGVYDPSKDLAE	506	26	41	13426
POL	YYQEPFKNL	39	61	KAGYVTDGRQRKVS	646	19	30	13427
POL	YYQEPFKNL	39	61	IVPLTEAELELAEN	481	12	19	13428
POL	LTEEAEL	38	58	GAVYIQDNDIKVVP	999	37	58	13429
POL	VIQDNDIK	37	58	IDIAIDIQTKELQK	953	22	34	13430
POL	IATDIQTK	35	55	IPSNNETPGIRYQY	321	31	48	13431
POL	INNETPGIR	32	51	SKDLIAEIQKQCGQ	514	09	14	13432
POL	LIAEIQKQ	30	47	LVEICTEMEKEKIS	221	14	22	13433
POL	ICTEMEKEG	28	44	EPVGAETFYVDGAA	624	20	31	13434
POL	VGAETFYVD	28	44	RLPIQKETWETWTD	582	09	14	13435
POL	IQKETWETW	27	42	WAGIQKEFGIPYNPQ	884	21	33	13436
POL	IKQEFIPY	26	41	QKQMGDDCVAGRQD	1025	23	36	13437
POL	MAGDDCVAG	25	39	EQLIKKEKVIYLAWVP	715	19	30	13438
POL	IKKEKYLA	20	31	GKQMGDDCVASRQD	1075	19	30	13439
POL	MAGDDCVAS	19	30	YFSVPLDKDFRKYTA	304	18	29	13440
POL	VPLDKDFRX	18	28	WAGIQKEFGIPYNPQ	884	11	17	13441
POL	IQKEFGIPY	16	25	WYQLEKEPIVGAET	618	16	25	13442
POL	YQLEKEPIV	16	25	KLWYQLEKEPIVGAET	616	16	25	13443
POL	YQLEKEPIV	15	23	KLPIQKETWEAWWTE	582	05	8	13444
POL	ESSEOTRAN	14	22	AREFSSEQTRANSPT	14	10	16	13445
POL	IASDIQTK	14	22	IDIASDIQTKELQK	953	09	14	13446
POL	IATESIVTW	14	22	VQKIATESIVWGT	564	11	17	13447
POL	ILIEICGKK	14	22	YDQILIEICGKKAIG	146	13	20	13448
POL	VLEENLPO	14	22	DDTVLEEINLPKRWK	116	11	17	13449
POL	IKKEKYVLS	13	20	EQLIKKEKVIYLSWVP	715	07	11	13450
POL	VLEDNLP	13	20	DDTVLEDINLPKRWK	116	13	20	13451
POL	VLEKDSWT	12	20	QPIVLEKDSWTVND	431	13	20	13452
POL	VIQDSEIK	12	19	GAVYIQDSEIKVVP	999	12	19	13453
POL	IKDYGKQM	11	17	KAKIKDYQKQMAQA	1017	06	9	13454
TAT	VERETIDP	11	17	KKKVERETIDPAVQ	95	01	2	13455
VIF	YFEDCS	28	44	VKKLTEDRWNKPKQT	175	09	14	13456
VIF	YFEDCS	20	31	IIILYFEDCSAIR	112	14	22	13457
VIF	YFEDCS	11	17	VQKLVEDRWNKPKQT	175	04	6	13458
VIF	IDPDLADQL	10	16	STQIDPDLADQLIHL	100	10	16	13459
VPR	LKNEAVRHF	18	28	LEELKNEAVRHFRP	23	10	16	13460
VPR	LKSEAVRIIF	15	23	LEELKSEAVRIIFRI	23	07	11	13461
VPR	YIVETYGDT	14	22	LQQYIVETYGDTWAG	42	07	11	13462
VPR	LKQEAVRHF	11	17	LEELKQEAVRHFRP	23	06	9	13463

Table XXb
HEV DR 3a Malt Pentides with Binding Information

[illegible]

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VTPDPQOE	HACVPTDPNPQEVVL						13371
YLDKQQLLG	VERYLKDDQQLLGWQ						13372
MIEDIISLW	VEQMIEDIISLWDQS						13373
VSEFPIPH	CPKVSFENPIPHYCA						13374
LAVERYLKD	ARVLAVERYLKDQQL						13375
VKIEPLGVA	YKVVKIEPLGVAPTK						13376
VYKEATITL	GVPVWKEATITLFCF						13377
LAWDDLRL	FLALA WDDLRLSLCLF						13378
LIEESQNO	IYTLIEESQNOQEK						13379
LGWEGLYL	GLRLGWEGLYLWNL						13380
LELDKWSL	QELLELDKWSLWNW						13381
YLROOQLG	VERYLRDQQLLGWQ						13382
MWQEVKAM	IINMWQEVOKAMYAP						13383
IEEEGGERD	PEGIEEGGERDRDR						13384
MNNENNGTN	INEMNNENNGTNSW						13385
LAEEGVIR	LGRIEEGGEQDKNR						13386
LALDKWSL	NGSLAEEGVIRSEN						13387
LAVERYLRD	QDLLALDKWSLWNW						13388
IRSENLTNN	ARVLAVERYLRDQQL						13389
MEWEREIDN	EIIIRSENLTNNVKT						13390
INEEAAFD	MTWMEWEREIDNYTS						13391
FSFEVPMF	KETNEEAAEWDRLLH						13392
VLAEAMSQV	EKAFSPEVPMPSAL		0.0023				13393
MLKDTNEE	KARVLA EAMSQVTS		0.0025				13394
VVEEKAESP	AMQMLKDTNEEAAE						13395
LRAEQATQE	WVKVVEEKAESPVI		0.0003				13396
MLKETNEE	FKTLRAEQATQEVKN						13397
VVEEKAESP	AMQMLKETNEEAAE						13398
VLAEAMSQ	WVKVVEEKAESPVI						13399
IEEQNKSK	KARVLA EAMSQASGA						13400
LRAEQATQD	LQKIEEQNKSKKKA						13401
YFPDWQNT	FKTLRAEQATQDVKN						13402
FLKEGGLE	YKTLRAEQASQEVKN						13403
FPDWQNT	TQYFPDWQNTTGP						13404
YMRDLKVG	LSIFLKEGGLEGLI						13405
IGPENPNT	TQGFDPDWQNTTGP						13406
LHPDKWTVQ	VGAVSRDLKVGKAIT						13407
IVTDSQYAL	IYQYMDLLVGSLE						13408
IPAETQET	ISKIOPENPYNTPVF		-0.0005				13409
LTEEKIKAL	GYELHPDKWTVQPIQ	0.0108	-0.0014	-0.0009			13410
IEAEVIPAE	EVNIVTDSQYALQII						13411
VAKIVASC	AEVIPAETGOETAYE						13412
LKQEAAMHQ	QWPLTEEKIKALTEI						13413
VGSDLEIGQ	SGYIEAEVIPAETQ						13414
IIRDYOKQM	RKVLFLDGDIDKAQEF						13415
	PPVVAKEIVASCDC						13416
	KCOLKGEAMHGQVDC		0.0015				13417
	DLYYGSDDLKQHR						13418
	KAKIIRDYGRQMAQD						13419
							13420

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MASDFNLPP	WRA MASDFNLPPVVA						13421
FYVDGAANR	AETFYVDGAANRETK	-0.0002	-0.0014	0.0035			13422
IHTDNGSNF	YKVIHTDNGSNFSA						13423
ILKEPVHGV	NREILKEPVHGVYD	0.0120	0.0033	0.0010	0.0210		13424
YQEPFKNL	TYQIYQEPFKNLKTD						13425
VYDPSKDL	VHG VYDPSKDLAE						13426
YVDRGRQK	KAGVYVDRGRQK VVS						13427
LTEEAEL	IVPLTEEAELAEEN						13428
VIQDNDIK	GAVVIQDNDIKVVP	0.0447	-0.0014	-0.0009			13429
IATDIQTK	IDIIATDIQTKELQK						13430
INNETGIR	IPSINNETGIRYQY						13431
LIAIQKQG	SKDLIAIQKQGQKQ						13432
ICTEMEKEG	LYEICTEMEKEOKIS						13433
VGAETFYVD	EPIVGAETFYVDGAA						13434
IQKETWETW	RLPIQKETWETWTD						13435
IKQEFQIPY	WAGIKQEFQIPYNPQ	0.0123	-0.0014	-0.0009			13436
MAGDDCVAG	GKQ MAGDDCVAGRQD						13437
IKKEKYLLA	EQLIKKEKYLLAVVP				0.0011		13438
MAGDDCVAS	GKQ MAGDDCVASRQD	-0.3003	-0.0005	-0.0015			13439
VPLDKDFRK	YFSVPLDKDFRKYTA						13440
IQQEFQIPY	WAGIQQEFQIPYNPQ						13441
LEKEPIGA	WYQLEKEPIGAETE						13442
YQLEKEPIV	KLWYQLEKEPIVGAE						13443
IQKETWEAW	KLPIQKETWEAWWTE						13444
FSSEQTRAN	AREFSSEQTRANSPFT						13445
IASDIQTK	IDIIASDIQTKELQK						13446
IATESIVW	VOKIAATESIVWGT						13447
ILIEICOKK	YDQILIEICOKKANG						13448
VLEENLPG	DDTYVLEENLPGKWK						13449
IKKEKYLLS	EQLIKKEKYLLSVVP						13450
VLEDINLFO	DDTYVLEDINLPGWK						13451
VLPKDSWT	QPIVLPKDSWTYND						13452
VIQDNSEIK	GAVVIQDNSEIKVVP						13453
IKDYGKQM	KAKIHDYGKQMAGA						13454
VERETETDP	KERYERETETDPAVQ						13455
LTEDRWKNP	VKKLTEDRWKNPQKT						13456
LVEDRWKNP	VOKLVEDRWKNPQKT						13457
IDPDLADQL	STQIDPDLADQLIHL						13458
LKNEAVRIIF	LEELKNEAVRIIFPRP						13459
LKSEAVRHFF	LEELKSEAVRHFFPRJ						13460
YIYETYGDT	LQQYIYETYGDTWAG						13461
LKQEA VRHF	LEELKQEA VRHFPRP						13462
							13463

Table XXc
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	MRDNWRSEL	40	63	GCDMRDNWRSELYKY	550	37	58	13464
ENV	LTVQARQL	36	56	SITLTVQARQLLSGI	620	27	42	13465
ENV	IEAQOHLQ	35	55	LRAIEAQOHLQLTV	642	34	53	13466
ENV	IIGDIQAH	27	44	TGEIIGDIQAHICNI	370	07	11	13467
ENV	VEREKRAVG	23	37	RRVVEREKRAVGIGA	582	11	17	13468
ENV	MVEQMEDI	23	36	KNNMVEQMEDIISL	110	19	30	13469
ENV	AWDDLKSLC	20	31	LALA WDDLKSLCLES	850	18	28	13470
ENV	LEITTHSN	20	31	GGDLLEITTHSFNCRG	426	10	16	13471
ENV	YDTEVHNWV	18	28	AKAYDTEVINWVATHI	71	15	23	13472
ENV	AEQTDRIE	17	27	IAVAEGTDRIEVVQ	927	02	3	13473
ENV	VQREKRAVG	17	27	RRVQREKRAVGIGA	582	05	8	13474
ENV	AEQTDRIE	15	23	IAVAEGTDRIEVVQ	927	07	11	13475
ENV	IEAQOHLK	12	19	LRAIEAQOHLKLTIV	642	08	13	13476
ENV	LKCNCKFN	12	19	FAILKCNCKFNKGTG	269	05	8	13477
GAG	ANPDCKTL	45	70	VQNAINDCKTLKAL	347	27	42	13478
GAG	FYKTLRAEQ	28	44	VDRFYKTLRAEQASQ	321	19	30	13479
GAG	AFQGMREPR	27	42	GPIAFQGMREPRGSD	242	19	30	13480
GAG	FFKTLRAEQ	27	42	VDRFFKTLRAEQATQ	321	26	41	13481
GAG	IWPSHKGRP	23	36	LGLIWSHKGRGNF	470	22	34	13482
GAG	LAKNCRAPR	20	32	EGHLAKNCRAPRKKG	431	19	30	13483
GAG	IAKNCRAPR	18	29	EGHIAKNCRAPRKKG	431	10	16	13484
GAG	ATQEVKNWM	18	28	AEQAATQEVKNWMTET	330	14	22	13485
GAG	ATQDVKNWM	15	23	AEQAATQDVKNWMTET	330	11	17	13486
GAG	LAKNCRAPR	13	21	EGHIAKNCRAPRKKG	431	13	20	13487
GAG	IWPSHKGRP	13	20	LGLIWSHKGRGNF	470	13	20	13488
GAG	ANPDCKSIL	11	17	VQNAINDCKSILRAL	347	06	9	13489
GAG	ASQEVKNWM	11	17	AEQAASQEVKNWMTET	330	11	17	13490
GAG	TPWSSKGRP	10	16	LGLIWPSSKGRPGNF	470	10	16	13491
NEF	LIYSKKRQE	18	28	LDGLIYSKKRQEILD	171	11	17	13492
NEF	VPDPREVE	11	17	FKLVDPDPREVEAN	227	06	9	13493
NEF	MARELHPEY	10	16	FHHMARELHPEYYKD	316	04	6	13494
POL	MGYELHPDK	60	94	FLWMGYELHPDKWTY	416	60	94	13495
POL	FIHNFRRXK	58	91	MAVFIHNFRRXKOGIO	930	57	89	13496
POL	MNKLKXII	56	89	VESMNLKXIIKIQOV	903	45	70	13497
POL	IIGQVRDQA	44	69	LKKIIGQVRDQAHL	910	43	67	13498
POL	YHSNWRAMA	39	61	HEKYIHSNWRAMASDF	764	23	36	13499
POL	MEKEGKISK	36	56	CTIEMEKEGKISKGP	225	22	34	13500
POL	YTRDSKPT	34	53	FRYYTRDSKPTWKG	975	34	54	13501
POL	ANRETKLKG	30	47	DGAANRETKLKGAGY	635	28	44	13502
POL	IGGQLKEAL	25	39	TIKIGGQLKEALLDT	99	17	27	13503
POL	LDKDFKXYT	19	30	SVPLDKDFKXYTAFT	306	17	27	13504
POL	YTRDSKPL	14	22	FRYYTRDSKPLWKG	975	13	21	13505
POL	IIGQVRQA	13	20	LKKIIGQVRQAHL	910	13	20	13506
POL	YHNWRAMA	10	16	HEKYIHNWRAMASDF	764	06	9	13507
REV	ARNRRRW	39	61	TROARNRRRWRRAR	38	18	28	13508
REV	ARKNRBRW	18	28	TRQARKNRBRWRAR	38	13	20	13509
REV	LLKTVRLIK	10	16	DEELLKTVRLIKFLY	9	04	6	13510
VIF	ISSEVHIPL	27	42	HIPRISSEVHIPLGDA	48	08	13	13511
VIF	VSEVHIPL	27	42	HPKVSEVHIPLGEA	48	11	17	13512
VIF	VSIEWRLAR	11	17	OHGVSIIEWRLRRYST	85	05	8	13513

Table XXg
 HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservation (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
VPR	LPSNTRGRG	01	50	IGILPSNTRGRGRN	82	01	2	13514
VPR	LLEELKNEA	17	27	TLLEELKNEAVRI	19	12	19	13515
VPR	LLEELKSEA	16	25	TLLEELKSEAYRH	19	15	23	13516
VPU	AKVDYRVI	01	33	DLAKVDYRIVAF	3	01	2	13517
VPU	AKVDYRLGV	01	33	NFLAKVDYRLGVGAL	3	01	2	13518
VPU	ILRQRKIDR	15	23	YRKILRQRKIDRLID	42	12	19	13519

Table XXd
 HIV DR 1b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
MRDNWSEL	GDMRDNRWSELKYK								13464
LTVAQRQLC	SITLTVAQRQLLSGI								13465
IEAQQLLQ	LRAIEAQQLHLQLTV								13466
IIGDIRQAH	TGEIIGDIRQAHGNI								13467
VEREKRAVG	RNVVEREKRAVGIGA								13468
MYEQMHEDI	KNNMYEQMHEDIISL								13469
AWDDLRLC	LALA WDDLRLSLCLFS								13470
LEITTHISFN	GGDLLEITTHISFCRG								13471
YDTEVHNW	AKAYDTEVHNWATHI								13472
AEQTDRIE	LVAEQTDRIEVVQ								13473
VQREKRAVG	REVQREKRAVGIGA								13474
AEQTDRIE	LVAEQTDRIEVVQ								13475
IEAQQLLQ	LRAIEAQQLHLQLTV								13476
LKNDKXFN	FAILKNDKXFNFTG								13477
ANPDKCTL	VQNAVDPCKTILKAL								13478
FKYTLRAEQ	VDREYKTLRAEQASQ								13479
APQGMREPR	QPLAFQGMREPRGSD	0.0031		0.0049					13480
FFKTLRAEQ	YDRFFKTLRAEQATQ	-0.0017							13481
TPWSHKGRP	LQKIWPSHKGRPGNF								13482
LARNCRAPR	EGHLARNCRAPRKKG								13483
IARNCRAPR	EGHIAKNCRAPRKKG								13484
ATQEVKNWM	AEQATQEVKNWMTET								13485
ATQDVKNWM	ABQATQDVKNWMTDT								13486
IARNCRAPR	EGHIAKNCRAPRKKG								13487
TPWSHKGRP	LQKIWPSHKGRPGNF								13488
ANPDKCTL	VQNAVDPCKTILKAL								13489
ASQEVKNWM	AEQASQEVKNWMTET								13490
TPWSHKGRP	LQKIWPSHKGRPGNF								13491
LIYSKGRQE	LDGLIYSKGRQEILD								13492
VIVDPREVE	FKLVPVIVDPREVEAN								13493
MARELHPEY	FHIMARELHPEYTKD								13494
MGVELHPDK	FLWMGYELHPDKWTV								13495
FHNFKKGG	MAVFHNFKKGGIGQ								13496
MNKKELKII	VESMKNELKIKIGQY								13497
IIGQVRDQA	LKKIIGQVRDQAEHL								13498
YHSNWRAMA	HEKYIHSNWRAMASDF								13499
MEKEGKISK	CTEMEKEGKISKIGP								13500
YVRDSRDIPI	FRVYVRDSRDIPIWKG								13501
ANRETKLQK	DGANRETKLQKAGY								13502
IGGQLKEAL	TIKIGGQLKEALLDT								13503
LDKDFRYKT	SVPLDKDFRYKYTAPT								13504
YVRDSRDIPI	FRVYVRDSRDIPIWKG								13505
IIGQVRDQA	LKKIIGQVRDQAEHL								13506
YHNNWRAMA	HEKYHNNWRAMASDF								13507
ARKNNRRRW	TRQARKNNRRRWRRAR								13508
LLKTYRLIK	DEELLKTYRLIKELY								13509
ISSEVHIPL	HPRISSSEVHIPLQDA								13510
VSEVHIPL	HPKVSSEVHIPLGEA								13511
VSEVHIPL	HPKVSSEVHIPLGEA								13512
VSEVHIPL	HPKVSSEVHIPLGEA								13513

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MRDNRSEL	GQDMRDNRSELVYKY						13464
LTVQARQLL	SITLTVQARQLLSGI						13465
IEAQRIQLQ	LRAIEAQRIQLQLTV						13466
IIGDIRQAH	TGEIIGDIRQAHNCNI						13467
VEREKRAYG	RRVVEREKRAYGIGA						13468
MVEQMIEDI	KNNKVEQMIEDISL						13469
AWDDLRLC	LALA WDDLRLSLCLS						13470
LEITISFN	GGDLLEITHSFNCRG						13471
YDTEVHNW	AKAYDTEVHNWATHI						13472
AEQTDRIE	IAVAEGTDRIEIVVQ						13473
VQREKRAYG	RRVQREKRAYGIGA						13474
AEQTDRIE	IAVAEGTDRIEIVVQ						13475
IEAQRIQLL	LRAIEAQRIQLQLTV						13476
LKNDKFN	FAILKNDKFNKGTG						13477
ANPCKTIL	VQNAIPCKTILKAL						13478
FYKTLRAEQ	VDRFYKTLRAEQASQ						13479
APQMREPR	GPIAPQMREPRGSD						13480
FFKTLRAEQ	VDRFFKTLRAEQATQ						13481
IWTSKGRP	LGIWTSKGRPGNFG						13482
LARNCRAPR	EGHILARNCRAPRKKG						13483
IAKNCRAPR	EGHIAKNCRAPRKKG						13484
ATQDVKNWM	AEQATQDVKNWMTET						13485
ATQDVKNWM	AEQATQDVKNWMTDT						13486
IARNCRAPR	EGHIAARNCRAPRKKG						13487
IWTSKGRP	LGIWTSKGRPGNFG						13488
ANPCKSIL	VQNAIPCKSILRAL						13489
ASQEVKNWM	AEQASQEVKNWMTET						13490
IWTSKGRP	LGIWTSKGRPGNFG						13491
LIYSKXQE	LDQLIYSKXQEILD						13492
VPVDPREVE	FKLVPVDPREVEAN						13493
MARELHPY	FHTIMARELHPETTKD						13494
MGYELHFDK	FLWNGYELHFDKWTY						13495
FJHFKRXG	MAYFJHFKRXGGIG						13496
MNKLKXII	VESMKNELKXIIQVY						13497
IIGQVRDQA	LKKIIGQVRDQAEHL						13498
YHSNWRAMA	HEKYNHSNWRAMASDF						13499
MEKEGKISK	CTEMEKEGKISKIGP						13500
YVRDSRDP	FRVYVRDSRDPFWKG						13501
ANRETKLGK	DGAANRETKLGKAGY						13502
IGQQLKEAL	TIKIGQQLKEALLDT						13503
LKXDFRYT	SVPLDKXDFRYTFT						13504
YVRDSRDP	FRVYVRDSRDPFWKG						13505
IIGQVRDQA	LKKIIGQVRDQAEHL						13506
YHSNWRAMA	HEKYNHSNWRAMASDF						13507
ARNRRRRW	TROARNRRRRRWRR						13508
ARKNRRRRW	TROAKNRRRRWRR						13509
LLKTVRLIK	DEELLKTVRLIKFLY						13510
ISSEVHIPL	HPRISSSEVHIPLGDA						13511
VSEVHIPL	HPKVSEVHIPLGEA						13512
VSEWRLRR	GHGVSEWRLRRYST						13513

0.0048

Table XXd
 HIV DR3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w02	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LPSNTRGRG	IGILPSNTRGRGRN									13514
LLEELKNEA	TLELLEELKNEAYRH									13515
LLEELKSEA	TLELLEELKSEAYRH									13516
AKVDYRIV	DLAKVDYRIVIVAF									13517
AKVDYRLQV	NFLAKVDYRLQVGL									13518
ILRQRKIDR	YRKILRQRKIDRLID	0.0024	0.0740	0.0410	13.0000	-0.0055		0.1500		13519

Table XXd
HIV DR 3b Mott Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LPSNTRGRG	IGILPSNTRGRGRN						13514
LLEELKNEA	TLELLEELKNEAVRII						13515
LLEELKSEA	TLELLEELKSEAVRII						13516
AKVDYRIV	DLIAKVDYRIVIVAF						13517
AKVDYRLGV	NFLAKVDYRLGVGAL	0.0016	-0.0014	0.0270			13518
ILRQRKIDR	YRKILRQRKIDRLID						13519

TABLE XXI. Population coverage with combined HLA Supertypes

<u>HLA-SUPERTYPES</u>	<u>PHENOTYPIC FREQUENCY</u>					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
<u>a. Individual Supertypes</u>						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
<u>b. Combined Supertypes</u>						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

Table XXIII: Immunogenicity of HIV peptides

	Peptide	Sequence	Protein	Immunogenicity	
				patients	transgenic
A2 Supermotif	1261.04	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	AHRILQQL	HIV vpr 59	5/9	0/6
	1261.09	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	TTLFCASDAK	HIV env 61	3/6	
	1273.09	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	TVYYGVPVWK	HIV env 48		28/33
	1069.47	VTVYYGVPVWK	HIV env 47	6/6	
DR Supermotif	27.0313	KRWILGLNKIVRMV	HIV gag 298	3/13	
	27.0311	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27.0354	WEFVNTPLVKLWYQ	HIV pol 596	2/13	
	27.0377	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280.03	KVYLAWVPAHKGIG	HIV pol 712	3/13	
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171	4/13	
	27.0344	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27.0341	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27.0364	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide	
Species	Antigen	Allele	Cell line	Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	21.221 (transfecta	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVL
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL
	B27	B*2705	LG2	R 60s	FRYNGLIHR
	B35	B*3501	CIR, BVR	non-natural (B35CON2)	FPEKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	FPEKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	FPEKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
Mouse	B51		KAS116	non-natural (B35CON2)	FPEKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	FPEKYAAAF
	B54	B*5401	KT3	non-natural (B35CON2)	FPEKYAAAF
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL
	Cw6	Cw*0602	'21.221 transfecta	non-natural (C6CON1)	YRHDGGNVL
	Cw7	Cw*0702	'21.221 transfecta	non-natural (C6CON1)	YRHDGGNVL
	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	RGYVFEQGL
	D ^d		P815	HIV-IIIIB ENV G4->Y	RGPYRAFVTI
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI
	L ^d		P815	HBVs 28-39	IPQSLDSYWTSI

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LQ2	HA Y307-319	YPKYVVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAATAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	3M3107 or L416.:	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	AHAHAHAHAHAHAHA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^d		A20	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^k		CH-12	HEL 46-61	YNTDGSSTDYGILQNSR
	IA ^s		LS102.9	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^v		91.7	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purification.

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D ^b and L ^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-3	H-2 K ^b
10.3.6	H-2 IA ^k
14.4.4	H-2 IE ^d , IE ^k
MKD6	H-2 IA ^d
Y3JP	H-2 IA ^b , IA ^s , IA ^u

Table XXVI. The table lists the 64 fully represented aligned amino acid sequences that were identified for Motif analysis. Included are the aligned amino acid sequence ID number, the complete nucleotide sequence name it was derived from, the accession numbers for the sequence, the subtype, country and the total length of all nine sequences.

	ID Number	Name	Accession Numbers	Subtype	Country	Length
1	A.KE.Q23-CxC-CG	HIVQ2317	AF004885	A	KE	3584
2	A.SE.UGSE8891	AUGSE8891	AF069673	A	SE	3584
3	A.UG.92UG037	H92UG037	U51190	A	UG	3584
4	A.UG.U455	HIVU455A	M62320	A	UG	3584
5	AC.IN.21301	21301	AF067156	AC	IN	3584
6	AC.RW.92RW009	92RW009	U88823	AC	RW	3584
7	AC.ZM.ZAM184	ZAM184	U86780	AC	ZM	3584
8	ADI.ZR.MAL	HIVMALCG	K03456, X04415	ADI	ZR	3584
9	AE.CF.90CR402	HIV90CF402	U51188	AE	CF	3584
10	AE.TH.93TH253	H93TH253	U51 189	AE	TH	3584
11	AE.TH.CM240	HIV1CM240	U54771	AE	TH	3584
12	AG.DJ.DJ263	DJ263	AF063223	AG	DJ	3584
13	AG.DJ.DJ264	HDJ264	AF063224	AG	DJ	3584
14	AG.NG.92NG003	92NG003	U88825	AG	NG	3584
15	AG.NG.92NG083	H92NG083	U88826	AG	NG	3584
16	AG.NG.IBNG	HIVIBNG	L39106	AG	NG	3584
17	AGI.CY.94CY0323	94CY032-3	AF049337	AGI	CY	3584
18	AGI.ZR.Z321	HIVU76035, Z321B	U76035	AGI	ZR	3584
19	AGJ.AU.BFP90	HIVBFP90	AF064699	AGJ	AU	3584
20	B.CN.RL42	HCHRL42CG	U71182	B	CN	3584
21	B.DE.D31	HIV1D31	U43096	B	DE	3584
22	B.DE.HAN	HIVHAN2	U43141	B	DE	3584
23	B.FR.HXB2R	HIVHXB2	AF033819, K03455, M38432	B	FR	3584
24	B.GA.OYI	HIVYOI	M26727	B	GA	3584
25	B.GB.CAM1	HIVCAM1	D00917, D10112	B	GB	3584
26	B.GB.MANC	HIV1MANC	U23487	B	GB	3584
27	B.NL.ACH32OA	HIV1ACH32OA	U34604	B	NL	3584
28	B.US.ADA	HIV1AD8	AF004394	B	US	3584
29	B.US.DH123	HIV1DH123	AF069140	B	US	3584
30	B.US.JRCSF	HIVJRCSF	M38429	B	US	3584
31	B.US.JRFL	HIVJRFL	U63632	B	US	3584
32	B.US.MN	HIVMN	M17449	B	US	3584
33	B.US.P896	HIV1896	M96155, U39362	B	US	3584
34	B.US.RF	HIVRF	M12508	B	US	3584
35	B.US.SF2	HIVSF2CG	K02007	B	US	3584
36	B.US.WEAU160	HIVWEAU160	U21135	B	US	3584
37	B.US.WR27	HIV1WR27	U26546	B	US	3584
38	B.US.YU2	HIVYU2	M93258	B	US	3584
39	BF.BR.93BR029.4	93BR029	AF005495	BF	BR	3584
40	C.BR.92BR025	H92BR025	U52953	C	BR	3584
41	C.BW.BW96BW0502	96BW0502	AF110967	C	BW	3584
42	C.ET.ETH2220	HIVETH2220	U46016	C	ET	3584
43	C.IN.11246	1N11246	AF067159	C	IN	3584
44	C.IN.21068	C1N21068	AF067155	C	IN	3584
45	C.IN.301904	301904	AF067157	C	IN	3584
46	C.IN.301905	CIN301905	AF067158	C	IN	3584
47	C.IN.301999	CIN301999	AF067154	C	IN	3584
48	D.UG.94UG1141	94UG114	U88824	D	UG	3584
49	D.ZR.84ZR085	84ZR085	U88822	D	ZR	3584
50	D.ZR.ELI	HIVELICG	K03454, X04414	D	ZR	3584
51	D.ZR.NDK	HIVNDK	M27323	D	ZR	3584
52	F.BR.93BR0201	93BR020	AF005494	F	BR	3584
53	F.FN.FIN9363	FIN9363	AF075703	F	FN	3584
54	G.BE.DRCBL	DRCBL	AF084936	G	BE	3584
55	G.FI.HH87931	HH8793	AF061640, AF061641	G	FI	3584
56	G.SE.SE6165	SE6165	AF061642	G	SE	3584
57	H.BE.VI991	VI991	VI991	H	BE	3584
58	H.BE.VI997	VI997	VI997	H	BE	3584

	ID Number	Name	Accession Numbers	Subtype	Country	Length
59	H.CF.90CF056	90CF056	AF005496	H	CF	3584
60	J.SE.SE91733	SE91733	AF082395	J	SE	3584
61	J.SE.SE92809	SE92809	AF082394	J	SE	3584
62	N.CM.YBF3O	NCMYBF3O	AJ006022	N	CM	3584
63	O.CM.ANT7OC	HIVANT7OC	L20587	O	CM	3584
64	O.CM.MVP518O	HIVMVP518O	L20571	O	CM	3584

TABLE XXVII
in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A2-supertype binding capacity (IC50 nM)					alleles bound	
					total	B	A*0201	A*0202	A*0203	A*0206	A*6802		
1261.14	10	NEF	221	LTFGWCFKL	55	74	294.1	48.9	185.2	57.8	6.2	5	
1261.04	9	NEF	221	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4	
1261.06	9	POL	316	YTAFTIPS	58	68	26.3	6.1	9.1	7	16.7	5	
1261.15	10	POL	774	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5	
1069.32	9	GAG	386	VLAEMASQV	52	74	66.6	82.7	15.2	115.6	363.6	5	
1261.16	10	POL	182	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5	
1261.02	9	ENV	651	LLQLTVWGI	53	63	9.8	21.5	43.5	24.7	645.2	4	
1261.13	9	POL	448	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4	
1211.04	9	ENV	134	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4	
1261.08	9	POL	220	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4	
1261.11	9	VPR	59	AIIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4	
1261.09	9	POL	163	LVGPTPVNI	84	100	454.5	153.6	19.2	2846.2	67.8	4	
1261.12	9	VPR	62	RILQQLFI	56	74	19.2	1535.7	125	37	1818.2	3	
1261.05	9	POL	183	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3	
1261.03	9	GAG	271	MTNNPPIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3	
1261.17	10	POL	132	KMIGGIGGI	97	95	172.4	54.4	4.8	770.8	3333.3	3	
941.03	9	POL	498	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3	
1260.10	9	POL	772	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3	
1261.07	9	POL	879	KAACWWAGI	49	79	277.7	1075	83.3	160.9	2666.7	3	
1211.09	10	ENV	814	SLLNATDIIV	22	68	9.8	1303	238.1	28.5	5479.4	3	
1211.05	9	ENV	608	FLGAIGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2	
25.0053	9	VPR	66	QLLI IHFRI	69	89	94.3	21500	25000	1608.7	476.2	2	
25.0139	10	GAG	270	WMTNNPPIPV	31	89	98	3071.4	16.9	18500	2222.2	2	
1069.33	10	POL	993	LLWKGECAVV	95	100	111.1	632.4	25	770.8	3636.4	2	
25.0142	10	NEF	219	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2	
1069.34	9	POL	993	LLWKGECAV	97	100	172.4	10750	21.7	1608.7	2666.7	2	
25.0161	10	POL	452	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2	
1211.082	9	GAG	79	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2	
25.0037	9	GAG	486	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2	
25.0046	9	POL	91	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1	

TABLE XXVIII
in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A3-supertype binding capacity (IC50 nM)					alleles bound
					total	B	A*0301	A*1101	A*3101	A*3301	A*6801	
1273.01	9	GAG	163	MVHQAIQSPR	42	58	61.1	89.6	18.0	13.8	9.5	5
1193.0200	9	POL	572	IVWQKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5
1193.03	9	POL	931	AVFIHNFKR	97	100	64.7	3.3	5.1	107.4	4.2	5
1193.01	9	POL	724	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5
1211.32	10	POL	971	KIQNFRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5
1069.49	10	POL	929	QMAVFIHNFK	94	100	9.2	8.5	266.7	432.8	400.0	4
1273.03	10	GAG	162	QMVHQAIQSPR	42	58	42.3	6000.0	243.2	290.0	186.0	4
1193.09	9	POL	353	MTKILEPFR	67	84	13750.0	375.0	81.8	69.0	25.8	4
966.01	9	POL	347	AIPQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3
940.03	10	NEF	100	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	131.3	3
1069.43	10	ENV	48	TVYYGVPVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3
1069.48	10	POL	931	AVFIHNFKRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3
1273.05	9	POL	99	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3
1273.06	9	ENV	64	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3
1273.07	10	ENV	61	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3
1273.04	9	ENV	878	RIVELLGRR	34	89	200.0	600.0	138.5	13809.5	444.4	3
1273.09	10	POL	98	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3
1273.02	9	POL	246	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3
1150.14	9	POL	930	MAVFIHNFK	94	100	647.1	20.0	375.0	517.9	2.5	3
1273.08	9	VIF	7	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3
1069.47	11	ENV	47	VTYYGVPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3
1069.42	11	POL	722	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3
1069.44	9	POL	855	KLGRWPFVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3

TABLE XXIX

in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		B7-supertype binding capacity (IC50 nM)					alleles bound
					total	B	B*0702	B*3501	B*5101	B*5301	B*5401	
1146.01	9	NEF	94	FFVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5
1296.01	9	ENV	259	IPIHYCAPA	56	42	423	343	153	-	3.7	4
15.0268	10	GAG	545	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4
1261.01	9	POL	186	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3
1296.02	9	ENV	250	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3
1296.03	11	POL	893	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3
29.0028	8	REV	75	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3
1292.13	9	GAG	237	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3

Table XXX: A1-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
1.0431	EVNTVTDSQY	HIV pol 1187	83	93	472
1.0014	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	IYQYMDDL	HIV pol 359	78	87	391
1069.27	VIYQYMDDL	HIV pol 358	78	87	446
1069.26	VTVLVDGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
25.0113	IWGCSGKLI	HIV env 69	69	91	444
25.0127	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	TYQIYQEPFF	HIV pol 1033	78	93	67
25.0115	VWKEATTTL	HIV env 47	47	85	400
25.0218	VWKEATTTLF	HIV env 47	47	85	44
25.0219	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	Sequence	Protein	Conservancy			Immunogenicity		
			Total	Clade B	XRN	patients	transgenic	
1261.14	LTFGWCFKLV	HIV nef 221	55	74	5	0/1	0/6	
1261.04	LTFGWCFKL	HIV nef 221	61	74	4	4/12	3/3	
1261.06	YTAFTIPSI	HIV pol 316	58	68	5	0/1	0/6	
1261.15	MASDFNLPPV	HIV pol 774	39	68	5	1/15	2/6	
1069.32	VLAEMSQV	HIV gag 386	52	74	5	6/19	3/3	
1261.16	CTLNFPISPI	HIV pol 182	94	100	5	0/1	1/6	
1261.02	LLQLTVWGI	HIV env 651	53	63	4	2/8	1/6	
1261.13	KLVGKLNWA	HIV pol 448	95	95	4	3/15	3/3	
1211.04	KLTPLCVTL	HIV env 134	85	95	4	2/12	2/6	
1261.08	ALVEICTEM	HIV pol 220	23	79	4	0/2	1/6	
1261.11	AIIRILQQL	HIV vpr 59	61	74	4	5/9	0/6	
1261.09	LVGPTPVNI	HIV pol 163	84	100	4	1/9	1/6	
1261.12	RILQQLFI	HIV vpr 62	56	74	3	6/20	2/6	
1261.05	TLNFPISPI	HIV pol 183	97	100	3	1/7	0/6	
1261.03	MTNPPPIPV	HIV gag 271	31	89	3	2/17	4/6	
1261.17	KMIGGIGGFI	HIV pol 132	97	95	3	2/7	0/6	
941.03	ILKEPVHGV	HIV pol 498	64	79	3	8/19	3/6	
1261.10	RAMASDFNL	HIV pol 772	64	79	3	2/9	0/6	
1261.07	KAACWWAGI	HIV pol 879	49	79	3	1/8	0/6	
1211.09	SLLNATDIIV	HIV env 814	22	68	3			

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity	
			Total	Clade B	transgenic	patients
1211.32	KIQNFRVYYR	HIV pol 971	81	95	5	4/6
1193.02	IVIWGKTPK	HIV pol 572	75	79	5	0/6
1193.03	AVFIHFKR	HIV pol 931	97	100	5	3/6
1069.49	QMAVFIHFK	HIV pol 929	94	100	4	3/6
1150.14	MAVFIHFK	HIV pol 930	94	100	3	6/6
1069.48	AVFIHFKRK	HIV pol 931	91	100	3	0/6
1273.01	MVHQAI SPR	HIV gag 163	42	58	5	0/6
1273.03	QMVHQAI SPR	HIV gag 162	42	58	4	0/6
1193.01	YLA WVP AHK	HIV pol 724	34	95	5	0/6
1069.42	KVYLA WVP AHK	HIV pol 722	32	89	3	6/6
1193.09	MTKILEPFR	HIV pol 353	67	84	4	0/8
966.01	AIFQSSMTK	HIV pol 347	56	79	3	5/6
940.03	QVPLRPMTYK	HIV nef 100	72	79	3	0/6
1069.44	KLGRWPVK	HIV pol 855	78	68	3	
1273.02	NTPVFAIKK	HIV pol 246	58	95	3	0/6
1273.08	VMIVWQVDR	HIV vif 7	69	95	3	0/6
1273.04	RIVELLGRR	HIV env 878	34	89	3	
1273.07	TTLFCASDAK	HIV env 61	78	84	3	3/6
1273.06	TLFCASDAK	HIV env 62	81	84	3	0/6
1273.09	VTIKIGGQLK	HIV pol 98	27	63	3	6/6
1273.05	TIKIGGQLK	HIV pol 99	27	63	3	0/6
1069.43	TVYYGVPVWK	HIV env 48	64	95	3	28/33
1069.47	VTVYYGVPVWK	HIV env 47	64	94	3	6/6

Table XXXIV. HLA-DR screening panels

Screening Panel	Representative Assay				Phenotypic Frequencies					
	Antigen	Alleles	Allele	Alias	Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
Primary	DR1	DRB1*0101-03	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1	10.4
	DR4	DRB1*0401-12	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4
	DR7	DRB1*0701-02	DRB1*0701	(DR7)	26.2	11.1	1.0	15.0	16.6	14.0
	Panel total				59.6	24.5	49.3	38.7	51.1	44.6
Secondary	DR2	DRB1*1501-03	DRB1*1501	(DR2w2.01)	19.9	14.8	30.9	22.0	15.0	20.5
	DR2	DRB5*0101	DRB5*0101	(DR2w2.02)	-	-	-	-	-	-
	DR9	DRB1*09011.09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7	11.9
	DR13	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1
	Panel total				42.0	33.9	61.0	48.9	30.5	43.2
Tertiary	DR4	DRB1*0405	DRB1*0405	(DR4w15)	-	-	-	-	-	-
	DR8	DRB1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1
	DR11	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5
	Panel total				22.0	27.8	29.2	29.0	39.0	29.4
Quaternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4	11.9
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9
	Panel total				20.2	24.4	13.5	24.2	19.7	20.4

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	Sequence	Protein	Binding capacity (IC50 nM)										DR Allele bound		
			DR1	DR2w201	DR2w202	DR3	DR4w4	DR4w5	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53
27.0313	KRWILGLNKIVRAMY	HIV gag 298	4.2	5.1	24	188	633	404	54	124	0.36	379	49	58	12
27.0354	WEFVNTPLVVKLWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39	10
27.0377	QKQITKIQNFRVYYR	HIV pol 956	2.9	3.4	.80	-	357	49	53	124	25	75	577	75	11
1280.03	KVYLAWVPAHKGGIG	HIV pol 712	8.3	25	24	-	156	165	71	12598	2500	179	196	250	9
27.0311	GEIYKRWILGLNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536	9
27.0361	EKVYLAWVPAHKGG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144	9
27.0297	QHLLQLTVWGKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375	8
27.0304	QQQMVHQAIKPRILN	HIV gag 171	72	65	13	17647	60	400	-	-	412	455	7313	117	8
27.0344	SPAIQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33	8
F091.15	IKQFINMWQEVGRAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104
27.0341	FRKYTAFTIISINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39	7
27.0364	HISNWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872	7
27.0373	KTAVQMAVFIHFKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2386	7

A dash indicates IC50>20µM

Table XXXVI: DR3 binding peptides

Peptide	Sequence	Protein	DR3
35.0135	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	AETFYVDGAANRETK	HIV pol 619	769
35.0133	GAVVIQDNSDIKVVP	HIV pol 989	1000

TABLE XXXVII
Immunogenicity of HIV-derived DR-supernatant peptides

Peptide	Sequence	Protein	conservation (%)		DR Alleles bound	Patient Immunogenicity
			Total	clade B		
27.0313	KRWILGLNKIVRMY	HIV gag 298	85 [89] ¹	94 [95]	12	3/13
27.0311	GEYKRWILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	WEFVNTPTPLVKLWYQ	HIV pol 596	79 [89]	84 [95]	10	2/13
27.0377	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	QCQMVHQALSPRTLN	HIV gag 171	41 [42]	52 [58]	8	4/13
27.0344	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

¹: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Sequence
HLA-A2	1069.32	HIV gag 386	VLAEAMSQV
"	1261.03	HIV gag 271	MTNNPPIPV
"	1261.15	HIV pol 774	MASDFNLPPV
"	1261.13	HIV pol 448	KLVGKLNWA
"	1261.09	HIV pol 163	LVGPTPVNI
"	941.03	HIV pol 498	ILKEPVHGV
"	1261.07	HIV pol 879	KAACWWAGI
"	1261.17	HIV pol 132	KMIGGIGGFI
"	1261.10	HIV pol 772	RAMASDFNL
"	1261.05	HIV pol 183	TLNFPISPI
"	1211.04	HIV env 134	KLTPLCVTL
"	1261.02	HIV env 651	LLQLTVWGI
"	1211.09	HIV env 163	SLLNATDIAV
"	1261.04	HIV nef 221	LTFGWCCKL
"	1261.11	HIV vpr 59	AJIRILQQL
"	1261.12	HIV vpr 62	RILQQLFI
HLA-A3	1069.49	HIV pol 929	QMAVFIHNFK
"	1069.42	HIV pol 722	KVYLAWVPAHK
"	1211.32	HIV pol 971	KIQNFRVYYR
"	1193.09	HIV pol 353	MTKILEPFR
"	966.01	HIV pol 347	AIFQSSMTK
"	1273.09	HIV pol 98	VTIKIGGQLK
"	1273.07	HIV env 61	TTLFCASDAK
"	1069.47	HIV env 47	VTVYYGVPVWK
"	940.03	HIV nef 100	QVPLRPMTYK
"	1273.08	HIV vif 7	VMIVWQVDR
"	1273.03	HIV gag 162	QMVHQAISPR
HLA-B7	15.0268	HIV gag 545	YPLASLRSLF
"	1292.13	HIV gag 237	HPVHAGPIA
"	1261.01	HIV pol 186	FPISPIETV
"	1296.03	HIV pol 893	IPYNPQSQGVV
"	1296.01	HIV env 259	IPIHYCAPA
"	1296.02	HIV env 250	CPKVSFEPI
"	1146.01	HIV nef 94	FPVRPQVPL
"	29.0028	HIV rev 75	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	EVNIVTDSQY
"	1.0014	HIV gag 317	FRDYVDRFY
"	1069.27	HIV pol 368	VYQYMDDL Y
"	1069.26	HIV pol 295	VTVLDVGDAY
HLA-A24	1069.60	HIV pol 533	IYQEPFKNL
"	25.0123	HIV pol 244	PYNTPVFAI
"	1069.59	HIV pol 530	TYQIYQEPF
"	25.0219	HIV pol 597	YWQATWIPEW
"	25.0113	HIV env 681	IWGC SGKLI
"	1069.57	HIV env 671	RYLKDQQLL
"	25.0115	HIV env 55	VWKEATTLF
"	25.0127	HIV vpr 46	IYETYGDTW
"	25.0128	HIV vpr 14	PYNEWTLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Sequence	Protein
DR	27.0313	KRWIILGLNKIVRMY	HIV gag 298
	27.0354	WEFVNTPLVVKLWYQ	HIV pol 596
	27.0377	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	QHLLQLTVWGIKQLQ	HIV env 729
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171
	27.0344	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915
DR3	35.0135	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	EVNIVTDSQYALGII	HIV pol 674
	35.0125	AETFYVDGAANRETK	HIV pol 619
	35.0133	GAVVIQDNSDIKVVP	HIV pol 989

TABLE XL
Estimated population coverage by a panel of HIV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes ²	Population coverage (phenotypic frequency)					
				Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
DR1	DRB1*0101-03	DR1	13	18.5	8.4	10.7	4.5	10.1	10.4
DR2	DRB1*1501-03	DR2w2 β1	12	19.9	14.8	30.9	22.0	15.0	20.5
DR2	DRB5*0101	DR2w2 β2	12	-	-	-	-	-	-
DR3	DRB1*0301-2	DR3	5	17.7	19.5	0.40	7.3	14.4	11.9
DR4	DRB1*0401-12	DR4w4	10	23.6	6.1	40.4	21.9	29.8	24.4
DR4	DRB1*0401-12	DR4w15	13	-	-	-	-	-	-
DR7	DRB1*0701-02	DR7	11	26.2	11.1	1.0	15.0	16.6	14.0
DR8	DRB1*0801-5	DR8w2	9	5.5	10.9	25.0	10.7	23.3	15.1
DR9	DRB1*09011,09012	DR9	11	3.6	4.7	24.5	19.9	6.7	11.9
DR11	DRB1*1101-05	DR5w11	9	17.0	18.0	4.9	19.4	18.1	15.5
DR13	DRB1*1301-06	DR6w19	8	21.7	16.5	14.6	12.2	10.5	15.1
Total ¹				98.5	95.1	97.1	91.3	94.3	95.1

1. Total opulation coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.

2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 13. Additional alleles possibly bound by nested epitopes have not been accounted.

WHAT IS CLAIMED IS

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope consisting of an amino acid sequence selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAI SPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVVP	WEFVNTPLVLKLYQ,
KVYLAWVPAHKGIGG,	GEIYKRWILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAI SPRTL N,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,
YRKILRQRKIDRLID,	EVNIVTDSQYALGII, and	AETFYVDGAANRETK.

2. The composition of claim 1, wherein the epitope is selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAI SPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	WEFVNTPLVLKLYQ,	KVYLAWVPAHKGIGG,
GEIYKRWILGLNKI,	EKVYLAWVPAHKGIG,	QHLLQLTVWGIKQLQ,

QGGMVHQAI SPRTL N, SPAIFQSSMTKILEP, FRKYTAFTIPSINNE,
HSNWRAMASDFNLPP, KTAVQMAVFIHNFKR, YRKILRQRKIDRLID,
EVNIVTDSQYALGII, and AETFYVDGAANRETK.

3. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

4. The composition of claim 3, comprising three epitopes selected from the group in claim 1.

5. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLE, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

6. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.

7. The composition of claim 6, wherein the HTL epitope is a pan DR binding molecule.

8. The composition of claim 1, wherein the epitope is on or within a liposome.

9. The composition of claim 1, wherein the peptide is joined to a lipid.

10. The composition of claim 1, wherein the epitope is bound to an HLA heavy chain, β 2-microglobulin, and strepavidin complex, whereby a tetramer is formed.

11. The composition of claim 1, wherein the epitope is bound to an HLA molecule on an antigen presenting cell.
12. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.
13. The composition of claim 1, the composition further comprising a pharmaceutical excipient.
14. The composition of claim 1, wherein the epitope is in a unit dose form.
15. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.
16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
EVNIVTDSQY,	FRDYVDRFY,	VIYQYMDDLY,
VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVP	WEFVNTPLVLKLYQ,
KVYLAWVPAHKGIGG,	GEIYKRWIILGLNKI,	EKVYLAWVPAHKGIG,
QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK, wherein the peptide comprises less than 50 contiguous amino acids that have 100% identity with a native peptide sequence.

17. The composition of claim 16, wherein at least two epitopes are linked via a spacer.
18. The composition of claim 16, further comprising a third epitope.
19. The composition of claim 18, wherein the third epitope is selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMY, MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.
20. The composition of claim 16, further comprising a third epitope that is a helper T lymphocyte (HTL) epitope.
21. The composition of claim 20, wherein the HTL epitope is a panDR binding molecule.
22. The composition of claim 16, wherein the peptide is on or within a liposome.
23. The composition of claim 16, wherein the peptide is joined to a lipid.
24. The composition of claim 16, wherein the peptide further comprises at least three of the epitopes in the group of claim 16.
25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.

26. The composition of claim 16, wherein the peptide further comprises at least five of the epitopes in the group of claim 16.

27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.

28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.

29. The composition of claim 16, further wherein the peptide is in a unit dose form.

30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.

AMENDED CLAIMS

[received by the International Bureau on 12 March 2001 (12.03.01);
original claims 1-30 replaced by new claims 1-36 (6 pages)]

1. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences:
- | | | | |
|----|------------------|--------------------|----------------------|
| 5 | VLA EAMSQV, | MTNNPPIPV, | KL VGKLNWA, |
| | LVGPTPVNI, | KMIGGIGGFI, | TLNFPISPI, |
| | KLTPLCVTL, | LLQLTVWGI, | SLLNATDIAV, |
| | LTFGWCFKL, | AIIRILQQL, | RILQQLLFI, |
| 10 | KVYLAWVPAHK, | MTKILEPFR, | AIFQSSMTK, |
| | VTIKIGGQLK, | TTLFCASDAK, | VTVYYGVPVWK, |
| | QMVHQAI SPR, | PYNTPVFAL, | YWQATWIPEW |
| | IWGCSGKLI, | VWKEATTTLF, | IYETYGDTW, |
| | PYNEWTLEL, | KIQNFRVYYR, | IPYNPQSQGVV, |
| 15 | EVNIVTDSQY, | FRDYVDRFY, | VYQYMDDL Y, |
| | VTVLDVGDAY, | IYQEPFKNL, | TYQIYQEPF, |
| | QMAVFIHNFK | QKQITKI QNFRVYYR, | IKQFINMWQEVGKAMY, |
| | WAGIKQEFGIPYNPQ, | GAVVIQDNSDIKVVP | WEFVNTPLVLWYQ, |
| | KVYLAWVPAHKGIGG, | GEIYKRWILGLNKI, | EKVYLAWVPAHKGIG, |
| 20 | QHLLQLTVWGIKQLQ, | QGQMVHQAI SPRTL N, | SPAIFQSSMTKILEP, |
| | FRKYTAFTIPSINNE, | HSNWRAMASDENLPP, | KTAVQMAVFIHNFKR, |
| | YRKILRQRKIDRLID, | EVNIVTDSQYALGII, | and AETFYVDGAANRETK. |

2. The composition of claim 1, comprising two epitopes selected from the group in claim 1.

3. The composition of claim 1, comprising three epitopes selected from the group in claim 1.

4. The composition of claim 1, wherein the composition further comprises a cytotoxic T lymphocyte (CTL) epitope selected from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR, FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWIILGLNKIVRMV, MASDFNLPPV,
5 KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA, IPIHYCAPA, and VPLQLPPL.

5. The composition of claim 1, wherein the composition further comprises a helper T lymphocyte (HTL) epitope.

10

6. The composition of claim 5, wherein the HTL epitope is a pan DR binding molecule.

7. The composition of claim 1, wherein the epitope is on or within a
15 liposome.

8. The composition of claim 1, wherein the peptide is joined to a lipid.

9. The composition of claim 1, wherein the epitope is bound to an
20 HLA heavy chain, β 2-microglobulin, and strepavidin complex, whereby a tetramer is formed.

10. The composition of claim 1, wherein the epitope is bound to an
25 HLA molecule on an antigen presenting cell.

11. The composition of claim 1, wherein the antigen presenting cells is a dendritic cell.

12. The composition of claim 1, the composition further comprising a
30 pharmaceutical excipient.

13. The composition of claim 1, wherein the epitope is in a unit dose form.

5 14. The composition of claim 1, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

15. An expression vector comprising a recombinant nucleic acid molecule encoding a prepared epitope set out in claim 1.

10

16. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of:

	VLAEAMSQV,	MTNNPPIPV,	KLVGKLNWA,
15	LVGPTPVNI,	KMIGGIGGFI,	TLNFPISPI,
	KLTPLCVTL,	LLQLTVWGI,	SLLNATDIAV,
	LTFGWCFKL,	AIIRILQQL,	RILQQLLFI,
	KVYLAWVPAHK,	MTKILEPFR,	AIFQSSMTK,
	VTIKIGGQLK,	TTLFCASDAK,	VTVYYGVPVWK,
20	QMVHQAISPR,	PYNTPVFAI,	YWQATWIPEW
	IWGCSGKLI,	VWKEATTTLF,	IYETYGDTW,
	PYNEWTLEL,	KIQNFRVYYR,	IPYNPQSQGVV,
	EVNIVTDSQY,	FRDYVDRFY,	VTYQYMDDL Y,
	VTVLDVGDAY,	IYQEPFKNL,	TYQIYQEPF,
25	QMAVFIHNFK	QKQITKIQNFRVYYR,	IKQFINMWQEVGKAMY,
	WAGIKQEFGIPYNPQ,	GAVVIQDNSDIKVP	WEFVNTPLVKLWYQ,
	KVYLAWVPAHKIGG,	GEIYKRWILGLNKI,	EKVYLAWVPAHKIG,
	QHLLQLTVWGIKQLQ,	QGQMVHQAISPRTLN,	SPAIFQSSMTKILEP,
	FRKYTAFTIPSINNE,	HSNWRAMASDFNLPP,	KTAVQMAVFIHNFKR,

YRKILRQRKIDRLID, EVNIVTDSQYALGII, and AETFYVDGAANRETK,
wherein the peptide comprises less than 50 contiguous amino acids that have 100%
identity with a native peptide sequence.

- 5 17. The composition of claim 16, wherein at least two epitopes are
linked via a spacer.
18. The composition of claim 16, further comprising a third epitope.
- 10 19. The composition of claim 18, wherein the third epitope is selected
from the group consisting of ILKEPVHGV, QVPLRPMTYK, VMIVWQVDR,
FPISPIETV, CPKVSFEPI, FPVRPQVPL, RYLKDQQLL, KRWILLGLNKIVRMY,
MASDFNLPPV, KAACWWAGI, RAMASDFNL, YPLASLRSLF, HPVHAGPIA,
IPIHYCAPA, and VPLQLPPL.
- 15 20. The composition of claim 16, further comprising a third epitope
that is a helper T lymphocyte (HTL) epitope.
21. The composition of claim 20, wherein the HTL epitope is a panDR
20 binding molecule.
22. The composition of claim 16, wherein the peptide is on or within a
liposome.
- 25 23. The composition of claim 16, wherein the peptide is joined to a
lipid.
24. The composition of claim 16, wherein the peptide further
comprises at least three of the epitopes in the group of claim 16.
- 30

25. The composition of claim 16, wherein the peptide further comprises at least four of the epitopes in the group of claim 16.
26. The composition of claim 16, wherein the peptide further
5 comprises at least five of the epitopes in the group of claim 16.
27. The composition of claim 16, wherein the peptide further comprises at least six of the epitopes in the group of claim 16.
- 10 28. The composition of claim 16, the composition further comprising a pharmaceutical excipient.
29. The composition of claim 16, further wherein the peptide is in a unit dose form.
15
30. The composition of claim 16, wherein the peptide is expressed from a recombinant nucleic acid that encodes the peptide.
31. An expression vector comprising a recombinant nucleic acid
20 encoding a prepared peptide as set out in claim 16.
32. A composition comprising a prepared human immunodeficiency virus-1 (HIV-1) epitope, said epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.
25
33. A composition of claim 32, wherein the composition comprises a further epitope consisting of an amino acid sequence selected from the group consisting of the sequences set forth in Tables VII-XX.
- 30 34. The composition of claim 32, wherein the epitope is expressed from a recombinant nucleic acid molecule that encodes the epitope.

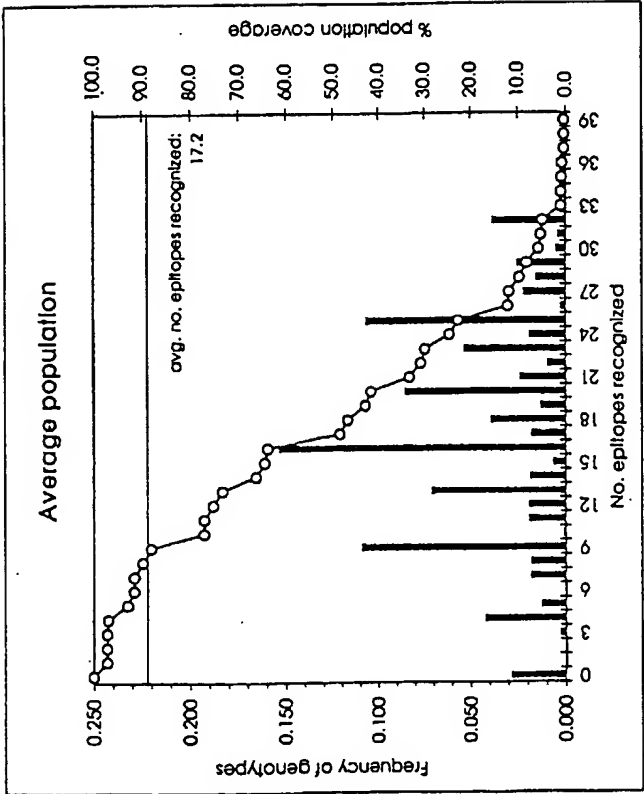
35. A composition comprising a prepared peptide of less than 500 amino acid residues comprising at least two human immunodeficiency virus-1 (HIV-1) peptide epitopes selected from the group consisting of the sequences set out in Tables
- 5 VII-XX.

36. The composition of claim 35, wherein the prepared peptide is expressed from a recombinant nucleic acid molecule that encodes the peptide.

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Figure 1



Plot of total frequency of genotypes as a function of the number of candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

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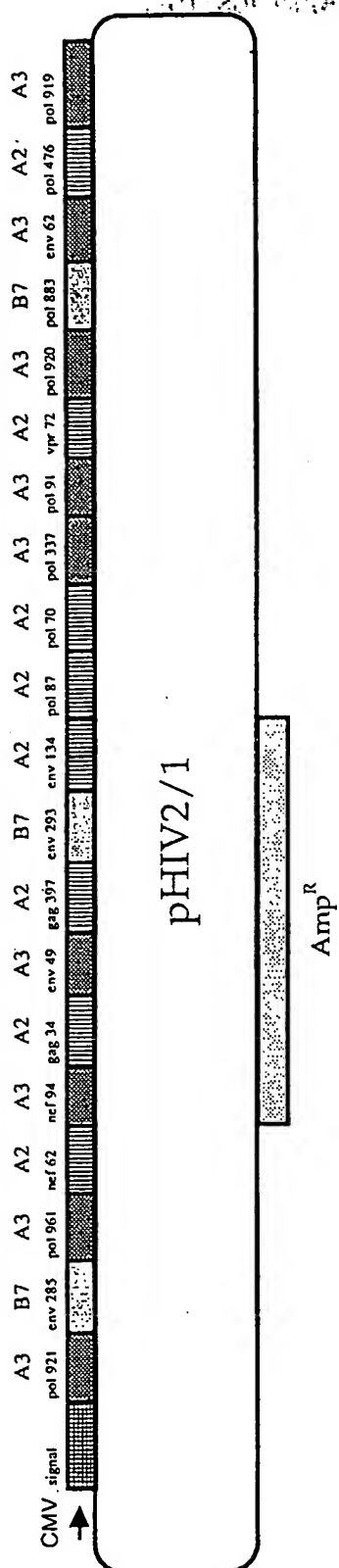
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FIGURE 2

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